

Result	No.	Score	Query	Match	length	DB	ID	Description
	1	2121	100.0		2121	6	AR371346	AR371346 Sequence
	2	2036.2	96.0		2722	9	AF120491	AF120491 Homo sapi
	3	2025	95.5		2041	9	AF187963	AF187963 Homo sapi
	4	1997	94.2		2064	6	AR371347	AR371347 Sequence
	5	1963.2	92.6		1968	9	AF048873	AF048873 Homo sapi
	6	1962	92.5		2072	6	AR85166	AR85166 Sequence
	7	1962	92.5		2072	6	AR204885	AR204885 Sequence
	8	1960	92.4		1968	6	AX956786	AX956786 Sequence
	9	1959.6	92.4		1968	9	AF205857	AF205857 Homo sapi
	10	1901	89.6		1984	9	AF187964	AF187964 Homo sapi
	11	1839.2	86.7		1911	9	AF048872	AF048872 Homo sapi
	12	1838	86.7		2104	6	AR85164	AR85164 Sequence
	13	1838	86.7		2104	6	AR204884	AR204884 Sequence
	14	1836	86.6		1911	9	AF205856	AF205856 Homo sapi
	15	1830	86.3		2104	6	AR85168	AR85168 Sequence
	16	1830	86.3		2104	6	AR204886	AR204886 Sequence
	17	1816.4	85.6		2057	4	AF454388	AF454388 Mus mus
	18	1780.4	84.0		1968	4	AF198445	AF198445 Oryzotola
	19	1718.4	81.0		1968	10	AB003587	AB003587 Rattus no

20	1769.8	80.9	1968	10	AF3344791	Rattus norvegicus
21	1692.2	80.1	1968	10	AF107781	Mus musculus
22	1631	76.9	7258	10	RN052975	Rattus norvegicus
23	1621	76.4	1996	10	RN075448	Rattus norvegicus
24	1576.8	74.3	1911	10	AF107782	Mus musculus
25	1543.8	70.5	4262	10	RAT3543R	L48619 Rattus norvegicus
26	1494.8	67.6	1665	4	AF493549	Oryzotylagus
27	1394.6	55.8	1977	5	AF209722	Gallus gallus
28	1178.2	55.5	1754	9	AF166009	Homo sapiens
29	1178.2	55.5	149322	2	AC016039	Homo sapiens
30	1178.2	55.5	169599	2	AL512665	Human DNA
31	1178.2	55.5	16656	2	AL592143	Homo sapiens
32	1138.6	53.7	2840	5	XLU898265	Xenopus laevis
33	1107.8	52.2	1114	6	CQ7898922	Sequence
34	1000	47.1	223192	2	AC127011	Rattus norvegicus
35	1000	47.1	228013	2	AC105582	Rattus norvegicus
36	992.4	46.8	1907	4	AF508735	Oryzotylagus
37	962.2	46.3	3056	5	BC045304	Danio rerio
38	982	46.3	189689	10	AC123847	Mus musculus
39	964.2	45.5	2918	4	AY147192	Mus musculus
40	959.4	45.2	1801	4	AF493547	Oryzotylagus
41	939.2	44.3	2314	5	AF075160	Gallus gallus
42	935.4	44.1	2351	9	HSAT10969	Homo sapiens
43	935.4	44.1	5333	9	AB028967	Homo sapiens
44	924.2	43.6	1859	9	AF121104	Homo sapiens
45	920.2	43.6	4562	10	BC079667	Mus musculus

## ALIGNMENTS

RESULT 1				
AR37j346				
LOCUS	AR37j346	2121 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 6395477.			PAT 12-SEP-2002
ACCESSION	AR37j346			
VERSION	AR37j346.1	GI:34608278		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 2121)			
AUTHORS	Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.			
TITLE	Human potassium channel polynucleotide and polypeptides and uses thereof			
JOURNAL	Patent: US 6395477-A, 1 28-MAY-2002;			
FEATURES	Location/Qualifiers			
source	1..2121			

## ORIGIN

	Query Match	Similarity	Score 2121;	DB 6;	Length 2121;
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	Matches 2121;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
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Db	1	GATTTCGTGAACCTA	ATCTCCAAAGCTGTGTGCTTAAGCGTCCGCGCGGCTCCCGGCCCAAGA	60	
QY	61	GCTGGAACTCAAC	ATATGGGCGGCGCGAGTTGCGGCGCTGGCGTGCCTTTTGTCCCGGAGCTGGGCG	120	
Db	61	GCTGGAACTCAAC	ATATGGGCGGCGCGAGTTGCGGCGCTGGCGTGCCTTTTGTCCCGGAGCTGGGCG	120	
QY	121	ATCGGGTGATATG	CCCGGTGGCCAACTGCCCCATATGCCCTTGAGCCCGCGCCGACAAAGAACAG	180	
Db	121	ATCGGGTGATATG	CCCGGTGGCCAACTGCCCCATATGCCCTTGAGCCCGCGCCGACAAAGAACAG	180	
QY	181	CGGAGAGATAGAG	CTGATTTCTCTCAACGTGATGGGCGGAGATTCACAGCTGAGGAGAC	240	
Db	181	CGGAGAGATAGAG	CTGATTTCTCTCAACGTGATGGGCGGAGATTCACAGCTGAGGAGAC	240	
QY	241	ACGCTGAGAGCTA	CCCGGACACCTCTGTGGGACACGAGAAAGAGATCTTTCTTCAAC	300	

Db	241	ACCGTGAAGCCCTACCCGGACAACCCCTGTGGGCAAGCAGAGAAAGAGTTCTTTCAAC	300
Qy	301	GAGGACACCAAGAGTACTTCTTCGACCGGGACCCCGAGGTTCCGTGCTCAAC	360
Db	301	GAGGACACCAAGAGTACTTCTTCGACCGGGACCCCGAGGTTCCGTGCTCAAC	360
Qy	361	TTCTACCGCACGGGGAACTGCACTACCCCGGCTACAGATGCATCTTGCTTACAGCAGC	420
Db	361	TTCTACCGCACGGGGAACTGCACTACCCCGGCTACAGATGCATCTTGCTTACAGCAGC	420
Qy	421	GAGCTGGCCTTCTACGGCATCCTCCCGGAGATCATCCGGGAGCTGTGTGCTACAGAGTAC	480
Db	421	GAGCTGGCCTTCTACGGCATCCTCCCGGAGATCATCCGGGAGCTGTGTGCTACAGAGTAC	480
Qy	481	AAGGACCGCAAGAGGAGAACGCCGAGCGGCTCATGACGACAACTCCGAGAACAC	540
Db	481	AAGGACCGCAAGAGGAGAACGCCGAGCGGCTCATGAGCAGCAACAACTCCGAGAACAC	540
Qy	541	CAGGATGTCATGCTCCTCGCTCAAGCTTCCGCAAGCATGTGGCGGGCTTTCAGAACCCC	600
Db	541	CAGGATGTCATGCTCCTCGCTCAAGCTTCCGCAAGCATGTGGCGGGCTTTCAGAACCCC	600
Qy	601	CACACCAAGCAGCTGGCCCTGTGTTCTACATGACACTGGCTTCTTATGTGCTGTCCG	660
Db	601	CACACCAAGCAGCTGGCCCTGTGTTCTTCTACATGAGTGGCTTCTTATGTGCTGTCCG	660
Qy	661	GTCAATCAACCAAGTGTGTGAGACGGGTGCCGTGCGGACAGGTCCCGGGCAGCAAGAGCTG	720
Db	661	GTCAATCAACCAAGTGTGTGAGACGGGTGCCGTGCGGACAGGTCCCGGGCAGCAAGAGCTG	720
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Db	721	CCGTGCGGGGAGCCGTACTCGGTGGCCCTTCTTGTGCTTGACACAGCGGTGCTCATATC	780
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Db	781	TTTCAACCGTGAATACCTCTCGCGGCTTTCGCGGGTCCCAACCGGTACCGCTTATCCGC	840
Qy	841	AGCGTCATGACATCATGACGATGTGGTGCATCATAGCCCTTACATCGATGATGATG	900
Db	841	AGCGTCATGACATCATGACGATGTGGTGCATCATAGCCCTTACATCGATGATGATG	900
Qy	901	ACCAACCAAGAGAGCTGTCCGGCGCTTTCGTACAGCTCCGGGATCTTCCGGCTTTCAGG	960
Db	901	ACCAACCAAGAGAGCTGTGTCCGGCGCTTTCGTACAGCTCCGGGATCTTCCGGCTTTCAGG	960
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Db	1021	TGTGCTCCGAACTGGGGCTTTCCTCTCTTCCCTCAACATGGGCAATCATGATTTGGCC	1080
Qy	1081	ACTGTGATGTTTTATGCGGAGAGGGCTCTCGGCAAGCAATTCACAAAGCATCCCTGCC	1140
Db	1081	ACTGTGATGTTTTATGCGGAGAGGGCTCTCGGCAAGCAATTCACAAAGCATCCCTGCC	1140
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Qy	1201	ACGATGAGGAGAAAGATCTTGGGCTCCCATGCTGCTTGAATGGCGCTCTGTGATTTGCC	1260
Db	1201	ACGATGAGGAGAAAGATCTTGGGCTCCCATGCTGCTTGAATGGCGCTCTGTGATTTGCC	1260
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Db	1261	CTGCCAGTCCCTGTGATTTGTTCCAACTTATAGCCGATTTTACACAGAAATCAAGAGCT	1320
Qy	1321	GATTAACGCAAGGCAAAAGAGGCCCGCTTTCAGAGATCCGTGTGGCCAAAACAGGC	1380

D	1321	GTATAAGCAGGGGACAAAGAAAGAGGCCGCCGCTTGGCCAGATCCGTGTGGCCAAACAGAGC	1380
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D	1381	AGTTGGAATGATPACTCTGCACAGCAGCGCATCGGCTCTCTCTCAACGAGCGCTGGAGCTG	1440
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D	1441	ACGGGGACCCCGAAGAGGGAGCATATGGGCAAGACACCTCACTCATATCGAGAGCGAGCAT	1500
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D	1561	CTGTTATCTGTAGCAACCTTCCACATTAAGAACACGAGTTTATGTATGACGATGTTT	1620
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D	1621	GAGCAGAACTGCATATGAGAGGTTCATATGCAGAACTAACCATCCACAAGAAATCCCTCACTG	1680
Q	1681	TCCAGCCACCCAGGCTCACTACCACTCTGCTCTCCGCTGTATGAGAAAGACACACAC	1740
D	1681	TCCAGCCACCCAGGCTCACTACCACTCTGCTCTCCGCTGTATGAGAAAGACACACAC	1740
Q	1741	CTGCGCCAATTTCTAACCTTGCAGACTACTCTGCTGGCAGCATGTCAAGAGCTCAGACGATC	1800
D	1741	CTGCGCCAATTTCTAACCTTGCAGACTACTCTGCTGGCAGCATGTCAAGAGCTCAGACGATC	1800
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D	1801	CACATCCAGGGGAGTGAAGCAGCCCTCCCTCACAACAGCTGCTCCAGCCTTTAATTGGAA	1860
Q	1861	GCAGACGACGGACTGAGAACCAAACTGTCAAAACATCCAGATCACACAGCATCATCAGC	1920
D	1861	GCAGACGACGGACTGAGAACCAAACTGTCAAAACATCCAGATCACACAGCATCATCAGC	1920
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D	1921	ATCCCCACTCCCCCAGGCGTTAACCCCGAGGGGGAAATGTGGCCACCCCCCTGCAGGCCCA	1980
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D	1981	GGCCCCAACAAGAACATTTCTTCATATACAGCAATTTGTTCAAAGGTCTGTCTTGTAA	2040
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D	2041	AAATCCCGCGGCATGGCGGCGCGGAGCATGCACTCGGGCCCAATTGCGCCCTATATGTG	2100
Q	2101	AGTGTATTTAAAGCCGAATTC	2121
D	2101	AGTGTATTTAAAGCCGAATTC	2121

RESULT 2	
LOCUS	AF120491
DEFINITION	Homo sapiens Shal-related potassium Channel Kv4.3 (KCND3) mRNA,
	long splice variant, complete cds.
ACCESSION	AF120491
VERSION	AF120491.1
KEYWORDS	GI:5059059
SOURCE	.
ORGANISM	Homo sapiens (human)
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 2722)
AUTHORS	Ishiyama,D., Leichter,T., Walschutz,R., Zhu,X., Luhmann,U.,
TITLE	Michel,U., Sauter,K. and Pongs,O.
JOURNAL	Gene structures and expression profiles of three human KCND (Kv4)
	potassium channels mediating A-type currents I(TO) and I(SA)
	Genomics 64 (2), 144-154 (2000)

MEDLINE 20195625  
PUBMED 107299221  
2 (bases 1 to 2722)  
AUTHORS Zhu, X. R., Waldischuetz, R., Isbrandt, D., Sauter, K. and Pongs, O.  
TITLE Direct Submision  
JOURNAL Submitted (15-JAN-1999) ZMNH, Institut fuer Neurale  
Signalverarbeitung, Martinistrasse 52, Hamburg 20246, Germany  
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gene  
CDS

ORIGIN

Query Match 96.0%; Score 2036.2; DB 9; Length 2722;  
Beet Local Similarity 97.5%; Pred. No. 1.2e-306;  
Matches 2068; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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QY 61 GCTGAGTCAACATGCGCGCGGAGTGGCGCTGCGCTTTGCCCGGCGTCCGCGC 120  
Db 477 GCTGAGTCAACATGCGCGCGGAGTGGCGCTGCGCTTTGCCCGGCGTCCGCGC 536  
QY 121 ATCGGATGATGCGCGCGGAGTGGCGCTGCGCTTTGCCCGGCGTCCGCGC 180  
Db 537 ATCGGATGATGCGCGCGGAGTGGCGCTGCGCTTTGCCCGGCGTCCGCGC 596  
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QY 241 ACGTGAAGCGCTACCGGAGACCTGTGCGGAGACACGAGAGAGAGTTCCTTCAAC 300  
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DB 2457 AATCCCGCGGAGTGAAGAGCCCTCCCTCACAACCAAGTGGCTCCAGCTTAATTGAAA 2516
QY 2101 AGTCGATTAAGCCGAATTC 2121
DB 2517 GGTGTCATGAGACCACTCC 2537

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RESULT 3
LOCUS AF187963
DEFINITION Homo sapiens voltage gated potassium channel Kv4.3 long splice
ACCESSION AF187963
VERSION AF187963.1 GI:6007794
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2041)
TITLE Dllks,D., Lang,H.P., Cockett,M., Sokol,P. and Numann,R.
JOURNAL Cloning and expression of the human kv4.3 potassium channel
MEDLINE 99218223
PUBMED 10200233
REFERENCE 2 (bases 1 to 2041)
AUTHORS Dllks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN
8000, Room 1119A, Princeton, NJ 08543-8000, USA
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ORIGIN
Query Match 95.5%; Score 2025; DB 9; Length 2041;
Best local Similarity 99.5%; Pred. No. 7e-305;
Matches 2031; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 61 GCTGAGATCACTGCGGCGGAGTGTGCGGCTGCTTTTCCGCGGCTGCGGCC 120
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DB 121 ATCGGATGATGCGGATGCGCACTGCGGATGCGGATGCGGATGCGGATGCGG 180
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DB 181 CGGACAGATGAGTGAATGCTCTCAACGTAAGTGGCGGAGTTCCAGACTGAGAAC 240
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DB 361 TTCTACCGACGCGGAGAACTGCACTACCGGCTGACGATGCTCTGCTTCAACGAC 420
QY 421 GACCTGCTCTTCAAGGACATCTCCCGGAGATCATGTGGGACCTGCTGAGAGTAC 480
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Db 1801 CACATTCAGAT 1860  
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Qy 1981 GCGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2040  
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Qy 2041 A 2041  
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RESULT 4  
AR371347  
LOCUS AR371347 2064 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 3 from patent US 6395477.  
ACCESSION AR371347  
VERSION AR371347.1 GI:34608279  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE  
1 (bases 1 to 2064)  
AUTHORS Cockett,M.I., Dilke,D.W., Ling,H.-P.C. and Sokol,P.T.  
TITLE Human potassium channel polynucleotide and polypeptides and uses thereof  
JOURNAL Patent: US 6395477-A 3 28-MAY-2002;  
FEATURES  
location/Qualifiers  
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ORIGIN  
Query Match 94.2%; Score 1997; DB 6; Length 2064;  
Best Local Similarity 97.3%; Pred. No. 1.6e-300;  
Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;  
Qy 1 GATTTGCTGAATCTAATCTCAAGCTGTGTGCTGAGCTGCGGCTGCGGCTCAAGA 60  
Db 1 GATTTGCTGAATCTAATCTCAAGCTGTGTGCTGAGCTGCGGCTGCGGCTCAAGA 60  
Qy 61 GCTGAGTCAACATGAGGCGGCGGAGTTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
Db 61 GCTGAGTCAACATGAGGCGGCGGAGTTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
Qy 121 ATCGGAGTGAAGTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 180  
Db 121 ATCGGAGTGAAGTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 180  
Qy 181 CCGAGAGATGAGTGTGTCTTCAAGTGAAGTGGGAGAGAGAGAGAGAGAGAT 240  
Db 181 CCGAGAGATGAGTGTGTCTTCAAGTGAAGTGGGAGAGAGAGAGAGAGAT 240  
Qy 241 ACGCTGAGAGGCTTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300  
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Db 361 TTCTAACGAT 420  
Qy 421 GAGCTGAGCTTTCTAGGAGATCTCTCGGAGAGATATGAGGAGAGATGCTGCTAGAGAGAT 480  
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ORIGIN

Query Match 92.6%; Score 1963.2; DB 9; Length 1968;  
Best Local Similarity 99.8%; Pred. No. 2.8e-295;  
Matches 1965; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	73	ATGGGCGCGGAGTTGCGGCTGCTGCTTTGCGCGGCTGCGGCATCGGATGAGT	132
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Qy	133	CCGGTGGCAACCTGCGCCATGCTGCGCCCGCGCGACAGAACAGCGGATGAG	192
Db	61	CCGGTGGCAACCTGCGCCATGCTGCGCCCGCGCGACAGAACAGCGGATGAG	120
Qy	193	CTGATGCTCAACGTAGTGGGCGAGGTTCCAGACTGGAGGACACGCTGAGGCG	252
Db	121	CTGATGCTCAACGTAGTGGGCGAGGTTCCAGACTGGAGGACACGCTGAGGCG	180
Qy	253	TACCGGACACCTGCTGCTGCGAGCAGCAGAGAGAGTTCTTCTTCAAGAGACAC	312
Db	181	TACCGGACACCTGCTGCTGCGAGCAGCAGAGAGAGTTCTTCTTCAAGAGACAC	240
Qy	313	GAGTACTTCTTGACCGGAGACCCGAGGTGTTCCGCTGCTGCTCACTTACCGCA	372
Db	241	GAGTACTTCTTGACCGGAGACCCGAGGTGTTCCGCTGCTGCTCACTTACCGCA	300
Qy	373	GGGAGGCTGCACTCCGCGGCTAGAGTGCATCTGCTGCTAGAGAGAGTGGCTTC	432
Db	301	GGGAGGCTGCACTCCGCGGCTAGAGTGCATCTGCTGCTAGAGAGAGTGGCTTC	360
Qy	433	TACGCGATCTCCGCGAGATCATCGGAGACTGCTGCTAGAGAGTACAGAGCCGCA	492
Db	361	TACGCGATCTCCGCGAGATCATCGGAGACTGCTGCTAGAGAGTACAGAGCCGCA	420
Qy	493	AGGAGAAACCCGAGCGGCTCATGAGCAACAGACTGGAGAACACAGAGTCCATG	552
Db	421	AGGAGAAACCCGAGCGGCTCATGAGCAACAGACTGGAGAACACAGAGTCCATG	480
Qy	553	CCCTGCGTCACTCCGCGAGACCATGAGGCGGCTTCCAGAACCCCAACCGACAG	612
Db	481	CCCTGCGTCACTCCGCGAGACCATGAGGCGGCTTCCAGAACCCCAACCGACAG	540
Qy	613	CTGGCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	672
Db	541	CTGGCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	600
Qy	673	GTGGTGGAGAGCGTCCGCGGACGCGTCCCGGCGAGAACAGAGCTGCGCGGAG	732
Db	601	GTGGTGGAGAGCGTCCGCGGACGCGTCCCGGCGAGAACAGAGCTGCGCGGAG	660
Qy	733	CGTACTCGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	792
Db	661	CGTACTCGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	720
Qy	793	TACCTCTGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	852
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Qy	853	ATCATCGAGCGTGGGCGCATGATGCTTCAATCGGCTGTCATGACCAACAGAG	912
Db	781	ATCATCGAGCGTGGGCGCATGATGCTTCAATCGGCTGTCATGACCAACAGAG	840
Qy	913	GACGTGTCGGCGGCTTCTGTCACGCTCCGCGTCTTCCGCTTCCAGATCTTCA	972
Db	841	GACGTGTCGGCGGCTTCTGTCACGCTCCGCGTCTTCCGCTTCCAGATCTTCA	900
Qy	973	TCCGCGCATCTCCAGGCGCTCGGATCTCGGCTTCAACACTGAGAGAGCTGTC	1032
Db	901	TCCGCGCATCTCCAGGCGCTCGGATCTCGGCTTCAACACTGAGAGAGCTGTC	960
Qy	1033	CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1092
Db	961	CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1020
Qy	1093	TATGCCGAGAGGCGCTCCGCGAGCAGAGTTCACAGACATCCCTGCTTGTATC	1152
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Qy	1213	AAGATCTTCCGCTCATCTGCTCTTGAAGTGGCGCTCCGCTGATGCTGCTGCT	1272
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Qy	1273	GTGATGTTTCAACTTTAGCCGATTTTACACAGATCAGAGAGCTGATTAACGCA	1332
Db	1201	GTGATGTTTCAACTTTAGCCGATTTTACACAGATCAGAGAGCTGATTAACGCA	1260
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Db	1261	GCACAAAAGAGGCGCGCTTTCAGAGATCCGTGTGCAAAACAGAGGATTCAG	1320
Qy	1393	TACCTGCAACAGAGCGGAGAGGCTCTTCAACAGAGGCTGAGAGTGAAGGCA	1452
Db	1321	TACCTGCAACAGAGCGGAGAGGCTCTTCAACAGAGGCTGAGAGTGAAGGCA	1380
Qy	1453	GAGAGGAGCAGATGGGCAAGACCACTCATTCAGAGAGCCAGATCATCCTGCTG	1512
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Qy	1573	CGAATCTCCACATCAAGAAACAGAGTTTATGATGAGAGATGTTGAGAGAACTG	1632
Db	1501	CGAATCTCCACATCAAGAAACAGAGTTTATGATGAGAGATGTTGAGAGAACTG	1560
Qy	1633	ATGAGAGTTCAATGAGAACTAACCATCCATCCAGAAAGTCCCTCATCTGCCAC	1692
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Qy	1693	GCGCTCACTACACCTGCTGCTCCGCTGTAAGTAAAGAACACACCTGCCAATCT	1752
Db	1621	GCGCTCACTACACCTGCTGCTCCGCTGTAAGTAAAGAACACACCTGCCAATCT	1680
Qy	1753	AACCTGCGAGTATCTGCTGCGGAGCATGGAAGAGTCCACAGATTCACAGGGC	1812
Db	1681	AACCTGCGAGTATCTGCTGCGGAGCATGGAAGAGTCCACAGATTCACAGGGC	1740
Qy	1813	AGTAGAGAGCCCTCCCTCAACAGAGTGCCTCAAGCTTAATTTGAAGAGAGCGA	1872
Db	1741	AGTAGAGAGCCCTCCCTCAACAGAGTGCCTCAAGCTTAATTTGAAGAGAGCGA	1800
Qy	1873	CTGAGACCAAACTGCAAAACATCCAGATTCACAGAGCATCATGAGATCCCATCC	1932
Db	1801	CTGAGACCAAACTGCAAAACATCCAGATTCACAGAGCATCATGAGATCCCATCC	1860
Qy	1933	CGAGGCTAACCCCAAGAGGAGAAAGTGGCCACCCCTGCGAGGCCCAACAG	1992

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QY 1993 AACATTCCTTCCATAACACAGCAATGTGTCAAGTCTCTGTCTTGTAA 2040  
Db 1921 AACATTCCTTCCATAACACAGCAATGTGTCAAGTCTCTGTCTTGTAA 1968

RESULT 6  
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LOCUS A85166 2072 bp DNA linear PAT 21-JAN-2000  
DEFINITION Sequence 3 from Patent WO9842833.  
ACCESSION A85166  
VERSION A85166.1 GI:6733868  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2072)  
AUTHORS Bril,A.M. and Calmel's,T.P.  
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL Patent: WO 9842833-A 3 01-OCT-1998;  
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ORIGIN  
Query Match 92.5%; Score 1962; DB 6; Length 2072;  
Best Local Similarity 99.7%; Pred. No. 4.2e-295;  
Matches 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 133 CCGGTGCGCAACTGCGCCCATGCGCTTGCGCGCGCGCAAGAAAGAGAGATGAG 192  
Db 61 CCGGTGCGCAACTGCGCCCATGCGCTTGCGCGCGCGCAAGAAAGAGAGATGAG 120  
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Db 121 CTGATTGTCTCAACGTGAGTGGCGGAGTTCCAGACTGAGAGACACGCTGAGCGC 180  
QY 253 TACCGCGACACCTGCTGGGAGAGAGAGAGAGTTCTTTCACAGAGAGACACCAAG 312  
Db 181 TACCGCGACACCTGCTGGGAGAGAGAGAGAGTTCTTTCACAGAGAGACACCAAG 240  
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Db 241 GAGTACTTCTTCAACCGGAGACCGCGAGTGTTCGCTGCTGCTCAACTTCAACGACG 300  
QY 373 GGGAGCTGCACTACCGCGCTACAGATGCTTTCCTTCAACGAGAGCTGAGCTTTC 432  
Db 301 GGGAGCTGCACTACCGCGCTACAGATGCTTTCCTTCAACGAGAGCTGAGCTTTC 360  
QY 433 TAGGGACTGCTCCCGGAGATCATGGGAGAGTCTGCTGCTACAGAGAGTCAAGACCGGAG 492  
Db 361 TAGGGACTGCTCCCGGAGATCATGGGAGAGTCTGCTGCTACAGAGAGTCAAGACCGGAG 420  
QY 493 AGGAGAGACCGAGCGGCTCATGAGACGACACTCGAGAGAACAGAGAGTCCATG 552  
Db 421 AGGAGAGACCGAGCGGCTCATGAGACGACACTCGAGAGAACAGAGAGTCCATG 480  
QY 553 CCTCGCTCAAGCTTCCGCGAGACCATGTGGGGCTTTCAGAAACCCCAACAGACAG 612  
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QY 613 CTGGCGCTGCTTCTTCACTGAGCTGGCTTCTTCAACGCTGCTGCTGCTACCAAC 672  
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QY 673 GTGTGAGAGCGGTGCGGTGCGGACGATCCGAGGAGAGAGAGTCCGTCGGGAG 732  
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Db 1561 ATGAGAGTTCAATGAGAGATACCATTCACAAAGATCTCTCACTGTCAAGCCCA 1620  
QY 1693 GGCCTCATACCACTGCTGCTCCGATGTAAGAGAGCAACACCTGACCAATTC 1752  
Db 1621 GGCCTCATACCACTGCTGCTCCGATGTAAGAGAGCAACACCTGACCAATTC 1680

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1881 AACCTGACGAGTCTGCGCTGCGAGCATGCAAGAGCTCAGACGATCCACATCCAGGAGC 1740  
1813 AGTGAAGACGCTCCCTCCCTCACAACAGTGTCTCCAGCTTAAATTTGAAAGACAGACGGA 1872  
1741 AGTGAAGACGCTCCCTCCCTCACAACAGTGTCTCCAGCTTAAATTTGAAAGACAGACGGA 1800  
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1933 CCAAGCGTAAACCCAGAGGGGGAAGTGGGCAACCCCTGCAAGCCAGGCCCCCAACAG 1992  
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RESULT 7  
AR204885 2072 bp DNA linear PAT 20-JUN-2002  
LOCUS Sequence 3 from patent US 6368823.  
ACCESSION AR204885  
VERSION AR204885.1 GI:21502325  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
1 (bases 1 to 2072)  
AUTHORS Brill,A.Michel,Alain., Calmels,T.Paul, Gerard.,  
Favre,J.-F., Simon,Pierre., Javre,J.-L. and Rouanet,S.  
TITLE Kv potassium channel polypeptides and polynucleotides  
JOURNAL Patent : US 6368823-A 3 09-APR-2002;  
FEATURES  
location/Qualifiers  
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ORIGIN

Query Match 92.5%; Score 1962; DB 6; Length 2072;  
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Matches 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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193 CTGATTTGCTTCAACGTGAGTGGGGGAGGTTTCCAGACTTGGAGGACCACTGGAGGCC 252  
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253 TACCGGAGCAACCTGCTGGGAGGAGCAAGGAGGTTCTTCTTCAAGAGAGCAACCAAG 312  
181 TACCGGAGCAACCTGCTGGGAGGAGCAAGGAGGTTCTTCTTCAAGAGAGCAACCAAG 240

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421 AGGAGAAACGCGGAGCGGCTCATGAGACGACAGACTTCGGAGAACACAGAGATCCATG 480

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733 CGTACTGCGTGGCGCTTCTTCTGCTGGAACAGCGGCGTGCATGATCTTCAACGCTGAG 792  
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793 TACCTCTGCGGCTTCTTCTGCGGCTCCAGCGGCTTCAATCCGAGCGTCATGAGC 852  
721 TACCTCTGCGGCTTCTTCTGCGGCTCCAGCGGCTTCAATCCGAGCGTCATGAGC 780

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973 TCCCGCACTTCCAGAGCGGCTGCGGATCCTGGGCTTACACATGAAAGAGTGGCTCCGA 1032  
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1453 GAAAGAGAGCAAGAGGCGGAGCAACCTCACTATGAGAGCGAGCATCATCTGCTG 1512  
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QY	1573	CGAACCTTCAACATCAAGAAACCAAGAGTTTATGATGAGAGATGTTTGAACAGAACTGC	16132
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QY	1633	ATGAGAGTTCAATGACAGAACTACCCATCCACAAGAAAGTCCCTCACTGTCCAGCCACCCA	16929
Db	1561	ATGAGAGATTCAATGACAGAACTACCCATCCACAAGAAAGTCCCTCACTGTCCAGCCACCCA	16208
QY	1693	GGCCTCACTACCACTGTGCTGCCCGTGTGATGAAGAGACACACACCTGCCAAATCT	17532
Db	1621	GGCCTCACTACCACTGTGCTGCCCGTGTGATGAAGAGACACACACCTGCCAAATCT	1680
QY	1753	AACCTGCAGCTACTCGCTCGCTCGAGACATGAGAAAGCTCAGACACATCCATCCAGGCG	1812
Db	1681	AACCTGCAGCTACTCGCTCGCTCGAGACATGAGAAAGCTCAGAGATCCATCCAGGCG	1740
QY	1813	AGTGAAGCAGCCTCTCCCTCAACAACAGTGTCTCCACCTTAATTGGAAGCAGACGCGGA	18727
Db	1741	AGTGAAGCAGCCTCTCCCTCAACAACAGTGTCTCCACCTTAATTGGAAGCAGACGCGGA	1800
QY	1873	CTGAGACCAAACTGCAAAACATCCCAATCACACAGCCATCATGAGATCCCACTCC	1932
Db	1801	CTGAGACCAAACTGCAAAACATCCCAATCACACAGCCATCATGAGATCCCACTCC	1866
QY	1933	CCAGCGCTAACCCCAAGAGGGGAAAAGTGGCCACCCCTGCGACGCCAGGCCCAACG	19929
Db	1861	CCAGCGCTAACCCCAAGAGGGGAAAAGTGGCCACCCCTGCGACGCCAGGCCCAACG	1920
QY	1993	AAACATTCCTTCATTAACAGCAATGTTGTCAAGGCTCTGTCTTGTAATA	2042
Db	1921	AAACATTCCTTCATTAACAGCAATGTTGTCAAGGCTCTGTCTTGTAATA	1970

RESULT	8			
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LOCUS				
DEFINITION	AX956786	1968 bp	DNA	linear
ACCESSION	Sequence	4 from Patent WO03097682.		PAT 08-JAN-2004
VERSION	AX956786			
KEYWORDS	AX956786.1	GI:40785267		
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 Kaelin, T.J., Dewulf, N.E. and Placetinck, G.K.			
	Methods for identifying and developing compounds that interact with			
	voltage-gated potassium channels of the kv4 family			
	Patent: WO 03097682-A 4 27-NOV-2003;			
	Devgen NV (BE)			
FEATURES	Location/Qualifiers			
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Query Match	92.4%	Score 1960:	DB 6: Length 1668:
Best Local Similarity	99.7%	Pred. No. 8.7e295;	
Matches 1963: Conservative	0;	Mismatches 5;	Indels 0;
			Gaps 0;

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QY	133	CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCGCAAGAACACGGCAGGATGAG	192
Db	61	CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCGCAAGAACACGGCAGGATGAG	120
QY	193	CTGATTGTCCCAACGTGAGTGGGGCGAGGTTCCAGACATCGGAGGACCAACGCTGGAGGCG	252
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QY	253	TACCCGGACACCCGCTGGGAGACGCGAAGAGGATCTTCTTCAACGAGACACCAAG	312
Db	181	TACCCGGACACCCGCTGGGAGACGCGAAGAGGATCTTCTTCAACGAGACACCAAG	240
QY	313	GAGTACTTCTTCGACCGGAGACCCCGAGGATGTTCCGCTGCGGTCTCAACTTCTTACCGGACG	372
Db	241	GAGTACTTCTTTCGACCGGAGACCCCGAAGTGTTCGCTGCGGTCTCAACTTCTTACCGGACG	300
QY	373	GGGAAGCTGCATACCGCGCTTACGAGTGCACTCTCTGCTTACGACGACGAGCTGACCTTC	432
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QY	433	TACGGCAATCCCTCCGGAGATCATATGCGGGACCTGCTCTACGAGGAGTCAAGAGACCGCAAG	492
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QY	493	AGGAGAAACGCCGAGCGGCTCATGGAACGACACACTCGAGAAACAACAGAGTCCATG	552
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QY	553	CCCTTGCTCAGCTTCCGCGACACATGTGCGGGGCTTTCGAGAACCCCCACACGACGACG	612
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QY	853	ATCATTCGACGTGTGGACCATATGCAATCCGATCGGTCTGATGATGACCAACAGAG	912
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QY	913	GACGTGTCCGGCGGCTTGTGACGCTCCGGGCTCTTCCGCGCTTACAGAGTCTTCAAGTTT	972
Db	841	GACGTGTCCGGCGGCTTGTGACGCTCCGGGCTCTTCCGCGCTTACAGAGTCTTCAAGTTT	900
QY	973	TCCGCGCACTCCCAAGGGCTGCGGATCTTGCGGCTTACACTGAAAGCTGTGCTCGAA	1032
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QY	1033	CTGGGCTTCTTCTCTCTCTCCCTACCATATGGCCCATCATCTTGTGACCTGATGTTT	1092
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Db	1081	ACCAATTGTACCATGACCAACTGCGGATACGGAACATGTGTCTTAAGACGATTCGAGGG	1140
QY	1213	AAGATCTTCCGCTCAATCTGTCTCTTGAATGCGGCTCTGATGCTTCCCTGCGACGTCCCT	1272
Db	1141	AAGATCTTCCGCTCAATCTGTCTCTTGAATGCGGCTCTGATGCTTCCCTGCGACGTCCCT	1200
QY	1273	GTGATTTGTTTCAACTTTAGCCGATTTTACACAGAAATCAGAGAGCTGATTAACGCGAGG	1332
Db	1201	GTGATTTGTTTCAACTTTAGCCGATTTTACACAGAAATCAGAGAGCTGATTAACGCGAGG	1260
QY	1333	GCACAAAAGAGGCGCGCTTTCGACGAGTCCGTGTGCGCAAAACAGGACGATTCGATGCA	1392



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Qy	1453	GAAGGAGAGCACTATGGGCGAAGACCACTTCATCTCATGAGAGCGACAGATCATCACTGCTG	1512
Db	1381	GAAGGAGAGCACTATGGGCGAAGACCACTTCATCTCATGAGAGCGACATCATCACTGCTG	1440
Qy	1513	CACCTCCCTGGAAGAAACCACTGGGTGTGCTATCTTGTGAGATGATCCCTGTATCTGTA	1572
Db	1441	CACCTCCCTGGAAGAAACCACTGGGTGTGCTATCTTGTGAGATGATCCCTGTATCTGTA	1500
Qy	1573	CGAACCTTCACCATCATGAAGAACCAAGATTATTTGATGAGAGATTTTGAAGAAACTGC	1632
Db	1501	CGAACCTTCACCATCATGAAGAACCAAGATTATTTGATGAGAGATTTTGAAGAAACTGC	1560
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Db	1561	ATGAGAGTTCAATGACAGAACTAATCCATTCACAGAGAAGTCCCTCACTGTCCAGCCCA	1620
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Db	1621	GGCTTCATTAACCACTGCTGTCTCCGTGTGTAGTAAGAAAGACCAACACTTGGCCAAATCT	1680
Qy	1753	AACCTGCAGGCTACTCGCTGCGAGAGACATGCAAGAGCTCAGCAGCATCAATCCAGGGC	1812
Db	1661	AACCTGCAGGCTACTCGCTGCGAGAGATGCAAGAGCTCAGCAGCATCAATCCAGGGC	1740
Qy	1813	AGTGAAGCAGCCCTCTCCATCAACAACAGTCCGCTTCAGCTTAATTGAAAGACAGACGGA	1872
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Qy	1873	CTGAGAGCCAACTGTGAAAACATCCCAATCACCAAGCATCATGAGATCCCACTGCC	1932
Db	1801	CTGAGAGCCAACTGTGAAAACATCCCAAGATCAACAGCATCATGAGATCCCACTGCC	1860
Qy	1933	CCAGGCGCTAACCCCAAGAGGGGAAAGTGGGCAACCCCTGCGACGCGCCCAACG	1992
Db	1861	CCAGGCGCTAACCCCAAGAGGGGAAAGTGGGCAACCCCTGCGACGCGCCCAACG	1920
Qy	1993	AACATTCCTTCATTAACGAGCAATTTGTCAAGGTCTGTCTTTGTA 2040	
Db	1921	AACATTCCTTCATTAACGAGCAATTTGTCAAGGTCTGTCTTTGTA 1968	
RESULT 9			
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LOCUS			linear
DEFINITION	Homo sapiens potassium ion channel Kv4.3 long isoform mRNA,		PRI 29-DEC-1999
ACCESSION	AF205857		
VERSION	AF205857.1		GI:6644151
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1968)		
	Calmele,T.P.G., Faivre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.		
	and Bril,A.		
	Long and Short Human isoforms of the Kv4.3 Channel: Cloning,		
	Expression, Electrophysiology, Pharmacology and Phosphorylation by		
	Protein Kinase C		
	Unpublished		
	2 (bases 1 to 1968)		
	Calmele,T.P.G., Faivre,J.-F., Javre,J.-L. and Bril,A.		
	Direct Submission		
	Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline		
	Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France		
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Query Match	92.4%; Score 1959.6; DB 9; Length 1968;	
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Dd	61	CCGGTGGCACTGCCCCCATGCCCCCGCGCCGACAAGAAGCGGAGATGAG 120
OY	193	CTGATTGCTCCAAGGTAGTGGGGGAGGTTCCAGACCCTGAGGACACGCTGAGCGC 252
Dd	121	CTGATTGCTCCAACGTAGTGGGGGAGGTTCCAGACCCTGAGGACACGCTGAGCGC 180
OY	253	TACCCGACACCTGCTGGGAGCAGCAGGAAGAGTTCCTTCAACAGAGCACCAAG 312
Dd	181	TACCCGACACCTGCTGGGAGCAGCAGGAAGAGTTCCTTCAACAGAGCACCAAG 240
OY	313	GAGTACTTCTTGACCGGAGACCCCGAGGTTCGCTGCTCTCACTTCAACGCAAG 372
Dd	241	GAGTACTTCTTGACCGGAGACCCCGAGGTTCGCTGCTCTCACTTCAACGCAAG 300
OY	373	GGGAAGCTGCACTACCGCGGCTACGAGTGACATCTGTGCTACGAGCAGAGCTGCTTC 432
Dd	301	GGGAAGCTGCACTACCGCGGCTACGAGTGACATCTGTGCTACGAGCAGAGCTGCTTC 360
OY	433	TACGGCATCTCCCGGAGATCATCGGGAGCTGCTCTACGAGAGTACAGAGCCGCAAG 492
Dd	361	TACGGCATCTCCCGGAGATCATCGGGAGCTGCTCTACGAGAGTACAGAGCCGCAAG 420
OY	493	AGGAGAAACGCCGAGCGGCTATGAGCAGACCAACTCGAGAACCAACGAGATTCATG 552
Dd	421	AGGAGAAACGCCGAGCGGCTATGAGCAGACCAACTCGAGAACCAACGAGATTCATG 480
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Dd	481	CCCTGCTCAGCTTCCGCGACACCATGTGGCGGGGCTTCGAGAACCCCAACACAGCAAG 540
OY	613	CTGGCCCTGCTCTTCTACTAGTGAAGTGGCTTCTTCAATGCTGTCTCGGTATCAACAAC 672
Dd	541	CTGGCCCTGCTCTTCTACTAGTGAAGTGGCTTCTTCAATGCTGTCTCGGTATCAACAAC 600
OY	673	GTGGTGAAGACGATGCGGTGCGGACCGGTCCCGGACAGAAAGAGCTGCTGTCGGGAG 732
Dd	601	GTGGTGAAGACGATGCGGTGCGGACCGGTCCCGGACAGAAAGAGCTGCTGTCGGGAG 660



QY 733 CGCTACTCGGTGGCTTTCTTCTGCTGAGACAGCGCGTGCATGATCTTACCGTGGAG 792  
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 QY 793 TACCTCTGGGGCTTTCTGCGGCTCCAGCGCTTACCTGCTTATCCGAGCGCTCATGAGC 852  
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 variant (Kv4.3) mRNA, complete cds.  
 AF187964  
 AF187964.1 GI:6007796  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 1 (bases 1 to 1984)  
 Dilks,D., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.  
 Cloning and expression of the human Kv4.3 potassium channel  
 J. Neurophysiol. 81 (4), 1974-1977 (1999)  
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 10200233

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN  
 8000, Room 1119A, Princeton, NJ 08543-8000, USA  
 Location/Qualifiers

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DEFINITION Homo sapiens Kv4.3 potassium channel short splice variant (Kv4.3)  
mRNA, complete cds.

ACCESSION AF048712 GI:2935433  
VERSION AF048712.1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1911)  
AUTHORS Kong, W. and Tomasetti, G.F.  
TITLE Direct Submission  
JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA  
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ORIGIN  
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Best Local Similarity 97.0%; Pred. No. 5.1e-276;  
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## RESULT 12

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DEFINITION Sequence 1 from Patent WO9842833.

ACCESSION A85164  
VERSION A85164.1 GI:6733867

KEYWORDS  
SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 2104)  
Brill,A.M. and Calmels,T.P.

AUTHORS KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE Patent: WO 9842833-A 1 01-OCT-1998;

JOURNAL BRIL ANTOINE MICHEL, ALAIN (FR); CALMELS THIERRY PAUL, GERARD (FR)

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## ORIGIN

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Matches 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;

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DEFINITION Sequence 1 from patent US 6368823.  
ACCESSION AR204884  
VERSION AR204884.1 GI:21502324  
KEYWORDS  
SOURCE .  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2104)  
AUTHORS Bill,A.Michel,Alain., Calmels,T.Paul.Gerard.,  
Favre,J.-F.Simon,Pierre., Javre,J.-L. and Rouanet,S.  
TITLE Kv potassium channel polypeptides and polynucleotides  
JOURNAL Patent: US 6368823-A 1 09-Apr-2002;  
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Location/Qualifiers  
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ORIGIN  
Query Match 86.7%; Score 1838; DB 6; Length 2104;  
Best Local Similarity 96.4%; Pred. No. 7,7e-276;

Matches 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;  
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 DB 1924 GAGGAGC 1929

RESULT 14  
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 ACCESSION AF205856  
 VERSION AF205856.1 GI:6644149

KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Calmeis,T.P.G., Faltre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.  
 and Brill,A.  
 TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,  
 Expression, Electrophysiology, Pharmacology and Phosphorylation by  
 Protein Kinase C  
 JOURNAL 2 (bases 1 to 1911)  
 AUTHORS Calmeis,T.P.G., Faltre,J.-F., Javre,J.-L. and Brill,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, Smithkline  
 Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France

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## ORIGIN

Query Match 86.6%; Score 1836; DB 9; Length 1911;  
 Best Local Similarity 96.8%; Pred. No. 1.66-275;  
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Db 1804 CCAGCGCTAACCCAGAGGAGGAAAGTCCGCCACCCCTGCGCAGGCCAGCCCAACAG 1863
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DEFINITION Sequence 5 from Patent WO9842833.
ACCESSION A85168
VERSION A85168.1 GI:6733869
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2104)
AUTHORS Bril,A.M. and Calmels,T.P.
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JOURNAL Patent: WO 9842833-A 5 01-OCT-1998;
BRIL ANTOINE MICHEL,ALAIN (FR); CALMELS THIERRY PAUL GERRARD (FR)
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ORIGIN
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Best Local Similarity 96.1%; Pred. No. 1.3e-274;
Matches 1909; Conservative 0; Mismatches 20; Indels 57; Gaps 1;

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Search completed: April 6, 2005, 00:35:29  
Job time : 11022.4 secs

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RESULT 2
US-09-178-109-3
; Sequence 3, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cocke, Mark T.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hwai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polymucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
; US-09-178-109-3

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Query Match 94.2%; Score 1997; DB 3; Length 2064;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

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## RESULT 4

US-09-142-791A-1  
; Sequence 1, Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Bril  
; APPLICANT: Thierry Paul Gerard Calmels  
; APPLICANT: Jean-Francois Simon Pierre Falvire  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142,791A  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2104  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-142-791A-1

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Best local similarity 96.4%; Pred. No. 0;  
Matches 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;

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QY	1993	AACATTCTCTTCATTAACAGCAATGTTGTCAAAGTCTGTGTTGTAAAAAATCCCGCGGC	2052
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/ RESULT 5
/ Sequence 5, Application US/09142791A-5
/ Patent No. 6368823
/ GENERAL INFORMATION:
/ APPLICANT: Antoine Michel Alain Brill
/ APPLICANT: Thierry Paul Gerard Calmels
/ APPLICANT: Jean-Francois Simon Pierre Faivre
/ APPLICANT: Jean-Luc Dautre
/ APPLICANT: Sabine Rouanet
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GH-30012
/ CURRENT APPLICATION NUMBER: US/09/142,791A
/ CURRENT FILING DATE: 1999-02-02
/ PRIOR APPLICATION NUMBER: PCT/EP98/01901
/ PRIOR FILING DATE: 1998-03-23
/ PRIOR APPLICATION NUMBER: UK 9706377.0
/ PRIOR FILING DATE: 1997-03-27
/ PRIOR APPLICATION NUMBER: EP 97402971.2
/ PRIOR FILING DATE: 1997-12-09
/ PRIOR APPLICATION NUMBER: EP 97403007.4
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: FaesSEQ for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 2104
/ TYPE: DNA
/

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ORGANISM: HOMO SAPIENS  
US-09-142-791A-5

Query Match	86.3%	Score 1830;	DB 3;	Length 2104;
Best Local Similarity	96.1%	Score, No. 0;		
Matches 1909;	Conservative	0;	Mismatches 20;	Indels 57;
				Gaps 11

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Db	1	ATGGCGCGAGGAGTTGCAGCTGGCTGCTTTTGGCCCGGCGCTGGCGCATCGGCTGGGATG	60
QY	133	CCGGTGGCCAACTGCGCCCATATGCCCTTGGCCCCCGGCGCAAGAAACAAGCGGCGAGATGAG	192
Db	61	CCGGTGGCCAACTGCGCCCATATGCCCTTGGCCCCCGGCGCAAGAAACAAGCGGCGAGATGAG	120
QY	193	CTGATTGCTCTCAACGTGATGGGGCGGAGGTTCCAGACTGTGAGAGCAACGCTGAGCGC	252
Db	121	CTGATTGCTCTCAACGTGATGGGGCGGAGGTTCCAGACTGTGAGAGCAACGCTGAGAGCGC	180
QY	253	TACCCGGACACCCCTGCTGGGCGAGCACGAGAGAGATTCTTTCAACGAGAGCACCAAG	312
Db	181	TACCCGGACACCCCTGCTGGGCGAGCACGAGAGAGATTCTTTCAACGAGAGCACCAAG	240
QY	313	GAGATCTTCTTCCAGCGGGGACCCCGAGGTTGCCGCGCGTGCTCAACTTACCGGACG	372
Db	241	GAGATCTTCTTCCAGCGGGGACCCCGAGGTTGCCGCGCGTGCTCAACTTACCGGACG	300
QY	373	GGGAGCTGCACTACCCCGCGCTACGATGCACTTCTGCTTACGACGACGAGCTGGCTTC	432
Db	301	GGGAGCTGCACTACCCCGCGCTACGATGCACTTCTGCTTACGACGACGAGCTGGCTTC	360
QY	433	TACGGCATCTCTCCCGAGATCATTGGGGACCTGCTGCTTACGAGGAGTACAAGATCCGACG	492
Db	361	TACGGCATCTCTCCCGAGATCATTGGGGACCTGCTGCTTACGAGGAGTACAAGATCCGACG	420
QY	493	AGGAGAAACGCCGAGCGCTCATATGACAGACACACTCGGAGAACACAGAGATCCATG	552
Db	421	AGGAGAAACGCCGAGCGGCTCATATGAGACACACACTCGGAGAACACAGAGATCCATG	480
QY	553	CCCTGCTCAGCTTCGGCCAGACCATATGTGGCGGCTTTGAGAAACCCCTCACACGACG	612
Db	481	CCCTGCTCAGCTTCGGCCAGACCATATGTGGCGGCTTTGAGAAACCCCTCACACGACG	540
QY	613	CTGGCCCTGGCTCTTACTACGTGACGTGGCTTCTTACGCTGCTGTGATCATCAAC	672
Db	541	CTGGCCCTGGCTCTTACTACGTGACGTGGCTTCTTACGCTGCTGTGATCATCAAC	600
QY	673	GTGGTGAAGACGATGCGCGACCGTCCCGGGCAGCAAGAGACTGCGTGCGGGAG	732
Db	601	GTGGTGAAGACGATGCGGTGCGGACCGTCCCGGGCAGCAAGAGACTGCGTGCGGGAG	660
QY	733	CGCTACTGGTGCCTTCTTCTGCTTGGACAGCGCGTGCTCATGATCTTCAACCTGTGAG	792
Db	661	CGCTACTGGTGCCTTCTTCTGCTTGGACAGCGCGTGCTCATGATCTTCAACCTGTGTAG	720
QY	793	TACCTCCGCGGCTTCTTGGGCGTCCAGCGGCTTACATCCGAGCGTATGAGC	852
Db	721	TACCTCCGCGGCTTCTTGGGCGTCCAGCGGCTTACATCCGAGCGTATGAGC	780
QY	853	ATCATCGACGTGATGGCATCATGCCCTTACTATGAGTCTGATCATGACCAACAGAG	912
Db	781	ATCATCGACGTGATGGCATCATGCCCTTACTATGAGTCTGATCATGACCAACAGAG	840
QY	913	GACGTGTCGGGCGCTTGTGACGCTCCGGGATCTTCGCGCTTCAGAGATTCACAAGTT	972
Db	841	GACGTGTCGGGCGCTTGTGACGCTCCGGGATCTTCGCGCTTCAGAGATTCACAAGTT	900
QY	973	TCCGCGCACTCCACAGGCGCTCGGATCTGGGGCTACACTGAAAGCTGTGCTCCGAA	1032
Db	901	TCCGCGCACTCCACAGGCGCTGGGATCTGGGGCTACACTGAAAGCTGTGCTCCGAA	960
QY	1033	CTGGGCTTCTTCTCTTCTCCCTACATGAGGCATCATCTTTGCCACTGTGATGTTT	1092



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Db 1619 ACTGCCCTGTGAGAGCGGTATGCTGTGCGCTTCTTCTGTGAGACAGCGCTCGCTCAT 1678
Qy 777 GATCTTCAACGGTGAAGTACCTCTCGCGGCTCTTTCGCGGCTCCAGCGGCTACCGCTTCAT 836
Db 1679 GATCTTCAACGGTGAAGTATTTGCTTCCGCTCGGCTGAGCGGCTAGTGTGTTTGT 1738
Qy 837 CCGGAGCGTATGAGCATTCATCGAGTGTGGCCATGATGCGCTTATCATCATCGTCTGGT 896
Db 1739 GCGTAGTGTATGATGATTCATCGAGTGTGGCCATGCTGCTTATTAATGAGGCTGTGT 1798
Qy 897 CATGACAAACAGAGAGACGCTGCTCCGCGCTCTGCTGACGCTCCGCGCTCTCCGCGCTCT 956
Db 1799 GATGACAGACATATGAGACGTCAGCGGAGCTTGTGTACACTCCGATCTTCTCCGCGCTCT 1858
Qy 957 CAGGATCTTCAAGTTTCTCCGCGCACTCCAGAGGCTCGGATCTCTGGGCTATACACTGAA 1016
Db 1859 CAGGATCTTCAAGTTTCTCCGCGCACTCTCAAGGCTCGGATCTCTGGGCTATACACTGAA 1918
Qy 1017 GAGCTGTGCTCCGAGTGGGCTTCTCTTCTCTCCCTGACATGGCCATCATCATCTT 1076
Db 1919 GAGTGTGCTCCGAGTGGGCTTCTCTTCTCTCCCTGACATGGCTATCATCATCTT 1578
Qy 1077 TGCCACATGTATGTTTATATCCGAGAGGCTCTCTCGGCGAGGAGTTTCAAGCATCCC 1136
Db 1979 CGCTACAGTTATGTTTATCGAGAGAGGAGGCTCTTGGCTAGCAAGTTTCAACAGCATCCC 2038
Qy 1137 TGCTCTGTTTGTATACCATATTTGACATGACATGACACACTGAGGATACAGGATATGTC 1196
Db 2039 TGCAAGCTTCTGTATATCATCTGTCACATGACATGACATGAGGATATGTCATGTC 2098
Qy 1197 TAAGACATTTGAGAGAGAGATCTTGGCTTCATCTGCTCTTGAAGTGGCTCTGTCAT 1256
Db 2099 AAAAACCATATGAGAGAGAGATTTTGGTCTATCTGTCGAGTGGGCTCTGTCAT 2158
Qy 1257 TGCCCTGCGCGCTCCCTGATGTTGTTTCAACTTAAAGCGGATTTACACAGAGATTCAG 1316
Db 2159 TGCTCTACCTGTTCCGATGATGATTCATCACTTACATGATGATTCACACAGATTCAG 2218
Qy 1317 AGCTGATTAACGACAGGCAACAAAGAGCGGCTTGGCGAGATCCGTTGCGCAAAAC 1376
Db 2219 AGCAGACAAACGAGAGGCAACAAAGAGCTAGCTAGCTGCGGAGGATCCGAGCAAAAG 2278
Qy 1377 AGGCAATTCGATGATCTGTCACAGACAGCGAGCGGCTCTCAACAGAGCGCTGGA 1436
Db 2279 CGGAAAGCGCAATCTTATCATGACAGCAAAAGGATGTTTACTAGTATCATGTCGA 2338
Qy 1437 GCTGACGGGCAACCCGAGAGAGGACATGAGGAGAAACCATCTCATCTCAGAGCCA 1496
Db 2339 GTCTCTAGAGGA--TGAAGAGGCTTTTGTGAAGAAATCGGCTCCAGCTTTGAAACCA 2395
Qy 1497 GCATCATCACTGCTGACCTGCTGCAAAACCATCTGAGTGTGCTATCTTGTGATGA 1556
Db 2396 GCACACACACCTGCTTCACTGCTGCAAAACCATCTGAGTGTGATGA 2431
Qy 1557 TCCCTGTTATCTGATGAACTTCCACCATCAAGAACAGAGTTTATGATGAGCAT 1616
Db 2432 -----GAAATCAAGATTTGTGAGCAAGAT 2458
Qy 1617 GTTTGAGACAACTGATGAGATTCATGACAGAACTAACCATCCACAGAAATCCCTC 1676
Db 2459 CTTTGAAGAAAGTGTGATGAGAACTGAACTGTTAATGCTTCAAGTCACACTCTTC 2518
Qy 1677 ACTGTCAAGCAACCGAGGCTCTCATACACCTGCTGCTCCGTTAGTAAAGAGACAC 1736
Db 2519 ACTGTCTTCAACAAAGAGTCAACAGCACTGCTGTTTCAAGAGACACAAAGAACTTT 2578
Qy 1737 ACACCTGCCCAATTTCTAATCTGACGACTCTGCTGCGAGCATGAGAGCTCAGAC 1796
Db 2579 TCGCATCCAAATGCTCATGATATCAGAGAGCATCAAGATGATATCAAGAACTCAGAC 2638
Qy 1797 GATTCACATCGAGGAGTGTGAGAGCTCTCTCTCAACAACAGTGTCTCAGCTTAATTT 1856
Db 2639 GATTCAGATGATGTGTGAGAGAACCTCTCTCTAACAGCGGATCCAGTTTAAATGC 2698

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Qy 1857 GAAAGCAGACGACGAGTGAAGACCAAACTGCAAAACATCCAGATCAACAGCCATCAT 1916
Db 2699 CAAATATGAAAGATGTATTAACCTAACTGTGAAACAACCTTATGTGATACAGCAATAT 2758
Qy 1917 CAGATCCCACTCTCCCGAGCGCTAACCCCAAGAGGAGGAAAGTCCGCCA 1965
Db 2759 AAGCATCCCAACACCTTCAGTAAACCAACACAGAGAGAGATAGGCCA 2807

RESULT 7
US-09-336-643A-9
; Sequence 9, Application US/0936643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Muller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Ruter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-09-336-643A-9

Query Match 37.6%; Score 798.2; DB 3; Length 3424;
Best Local Similarity 72.8%; Pred. No. 1,2e-162;
Matches 1079; Conservative 1; Mismatches 379; Indels 24; Gaps 3;

Qy 65 GATTCACATGAGGAGCGGAGTTCGCGCTGCTGCTTTTGGCGGAGTGGGCGCATG 124
Db 249 GTGACAGATGAGGAGCGGAGTTCGCGCTGCGCTGCTTTTGGCGGAGTGGGCGCATG 308
Qy 125 GGTGATGCGCGTGGCAACTGCGCCCATGCGCTGCGCGCGCGCAAGAACAGCGC 184
Db 309 GCTGCGTCCCGCGCGCGCGCGCAACCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
Qy 185 AGATGAGTGTATGCTCTCAACGTGAGTGGGCGAGGTTCCAGACTGAGAGCAAGC 244
Db 369 GATATGAGTGTGCTGCTGAGTGAAGTGAAGCGAGCGGCTTTGAGACTTGGAAATACGC 428
Qy 245 TGAAGGCTTACCGGAGACCTCTGCGGAGCGAGCAAGAGAGGTTCTTTGAAGAG 304
Db 429 TGAAGGCTTACCGGAGACCTCTGCGGAGCGAGCGAGCGAGGAGGAGGAGGAGGAG 488
Qy 305 ACACCAAGAGTACTTCTTGAACGGGAGACCCGAGGAGTTCGCTGCGCTCAACTTCT 364
Db 489 ACTCAGGCGATCTTCTTGAATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 548
Qy 365 ACCGACAGGAGAGTGTGACTTACCGCGGCTAGAGTGTCTGTGCTTACAGAGAGC 424
Db 549 ACCGACAGGAGAGTGTGACTTACCGCGGCTAGAGTGTCTGTGCTTACAGAGAGC 608
Qy 425 TGCGCTTCTACGCGATCTCCCGAGATCATCGGAGATGCTCTTACAGAGATTAAG 484
Db 609 TGCGCTTCTACGCGATCTCCCGAGATCATCGGAGATGCTCTTACAGAGATTAAG 668

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QY 485 ACCGGAAGAGGAGGAGAACCGGCGCTCATGAGACGACGACTCGAGAAACACGAG 544
DB 669 ACCGGAAGAGGAGGAGAACCGGCGCTCATGAGACGACGACTCGAGAAACACGAG 728
QY 545 AGTCATGACCCCTCGC-----TCAGCTTCGCGCAGACCAATGTGGCGGGCTTCGAGA 595
DB 729 ACGCGCCAGCCCTCGCAGCAGGACGACTCCCTCGGCGAGGGGCTCTGGCGGGCTTCGAGA 788
QY 596 ACCCCACACGACGACGCTGCGCTGTCTTCTACTACGTGACGTGCTTCTTCATCGCTG 655
DB 789 ATCCACACGACGACGCGGACGCTCGTTTCTACTATGTGACCGGCTTCTTCATCGCGG 848
QY 656 TCTCGTATCATCCACGCTGTGTGAGAGGCTGCGGGGACGCGTCCCGGGAG----- 710
DB 849 TGTGCTATCGCCCAATGTGTGTGAGACATCCATGCGCGGCTCTGACGCGAGTCTCT 908
QY 711 -CAAGGAGCTGCGCGGCGGAGCGCTACTCGGTGAGCTTCTTCTGCTGACGAGCGT 769
DB 909 CAGGAGACGACGCTGTGTGCGGACGCTTCCACAGGCTTCTTCTGATGACACAGCTCT 968
QY 770 GCGTCATGATCTTCAACGCTGAGTACCTCTGCGGCTCTTCCGCGCTCCGACGCGTAC 829
DB 969 GTGTACTATATTCACAGGTGATATCTCTGCGGCTGTGTGCGCGCCGACGCGTGGC 1028
QY 830 GCTTCATCCGACGCTCATGAGCATCATGACGTGTGCGCATCATGCCCTTACTCATG 889
DB 1029 GCTTCCTCGGAGTGTCAATGACCTCATGACGTGTGCGCATCTGCTCATCATG 1088
QY 890 GTCTGTGATGACCAACAGGAGCGTGTGCGGGGCTGTGCTACGCGTCCGGGCTTCC 949
DB 1089 GCGTTTGTGTGCGGAGGAGCGATGTCTGTGGGCTGTGTGCTACCGCTGTGTGTTC 1148
QY 950 GCGTCTTCAAGATCTTCAAGTTCCTCCGCACTCCGAGGCGCTGCGGATCTCGGCTACA 1009
DB 1149 GGGTGTTCGATCTTCAAGTTCCTCCGCACTCAAGGCGCTGAGGATTCGGGCTACA 1208
QY 1010 CACTGAAGAGCTGTGCTCCGACGCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 1069
DB 1209 CACTCAAGAGCTGTGCTTCTGAGCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 1268
QY 1070 TCATCTTGTGCACTGTGATGTTTATGCGAGAAAGGCGCTCGCGGCGAGGATTCACA 1129
DB 1289 TCATCTTGTGCACTGTGATGTTTATGCTGAGAAAGGCGCAAAACAAACCACTTTACA 1328
QY 1130 GCATCCCTGCTGCTTGTGTGTAACACATGTGTACCATGACCACTGGGATTCGAGACA 1189
DB 1329 GCATCCCTGCGGCTTCTGTATATCATTTGTCAACATGACCAAGCTTGGCTAGAGACA 1388
QY 1190 TGTGTCTTAAGACGATTCGAGGAAAGATCTTCTGCTCACTGTCTTGTAGTGGCTTC 1249
DB 1389 TGTGTCTTCCAGACCACTTGTCTGCAAGATTTTCTGCTCACTGTCTTGTAGTGGCTTC 1448
QY 1250 TGTGTATGCTGCTGCACTGCTGTGATGTTTCACTTGAACGAGATTTACCAACGAGA 1309
DB 1449 TGTGTATGCTGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508
QY 1310 ATCAGAGAGCTGATTAACGAGGAGCAAAAGAGGCGCGCTTCCAGGATCCGCTGG 1369
DB 1509 ACGAGCGGCTGTGACAGGCGCGAGACGAGAGAGTGTGCTTGGCAGAGATCCGATTTG 1568
QY 1370 CCAAAAACGAGGATTCGATGATCTGACACAGAGGCAACGCGCTCTCTCAACGAGG 1429
DB 1569 CAAAGAGGTGTACCAACCAATGCTTCTGCAAGTACAGAGAGATGGGGGCTTTGA----- 1623
QY 1430 CGCTGAGCTGTGCGGAGCAACCGAGAGAGGACATGGGCAAGACCACTGATCATG 1489
DB 1624 -----GGAAGCGGCGAGTGGCAAGGCTCTTGTGTACGAAACGCTTCTGCTTTG 1679
QY 1490 AGAGCAGCATCATCATCTGTGCACTGCTGCACTGCTGCAAAACCAAC 1532
DB 1680 AACAGCAACATCAACATTTGCTGCACTGTCTGTAGAGAGCAAC 1722
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RESULT 8
US-09-949-016-2456
; Sequence 2456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2456
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2456

Query Match      12.3%; Score 261; DB 4; Length 3260;
Best Local Similarity 61.5%; Pred. No. 8.3e-47;
Matches 488; Conservative 0; Mismatches 245; Indels 60; Gaps 2;

QY 1173 ACTGGATACGGAACATGCTGCTAAGACGATTCGAGGAGAAAGTCTGGCTCATCTG 1232
DB 2 ACTGAGATGTGTGACATGAGTGTGCAAAACCATGACAGGAGAAATTTGTGTATCTG 61
QY 1233 CTCCTGAGTGGCGCTGCTGATTCCTCCGACGCTGCTGTGATGTTTCAACTTAG 1292
DB 62 TTCCTGATGAGGCTTGTGATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 121
QY 1293 CCGATTTTACCAACGAGATTCAGAGCTGATTAACGAGGCGCAAAAGAGGCGCT 1352
DB 122 TCGCATTCACACGAGATTCAGAGCAGACAAAGAGGCGCAAAAGAGCTAGACT 181
QY 1353 TGCAGATTCCTGTGCGCAAAACAGGAGCTGATTAACGAGGCGCAAAAGAGGCGCA 1412
DB 182 GCGCAGATTCGCGGCGAGCAAAAGGAGGCAAAAGCTTTCATGACGAGCAAAAGGCA 241
QY 1413 CGGCTCTCTCAAGAGGCGTGTGAGCTGACGCGGACCCAGAGAGGAGCAGATGGGCA 1472
DB 242 TGTGTACTAGTATACGCTGCACTGCTCAG---AGATGAGAGAGCTTTTGTAGCA 298
QY 1473 GACCACTCACTCATGAGAGCAGACATCATCTGCTGCTGAGTGTGAAAAACAC 1532
DB 299 ATCCGGCTCCGAGCTTTGAAACCAAGCACACCACTGCTTCACTGCTGAAAAACAC 358
QY 1533 TGGTGTCTTATCTTGTGATGATCCCTGTATCTGTACGAACCTCACATCAAGAA 1592
DB 359 -----GAA 361
QY 1593 CCAGAGTTTATGATGAGAGATGTTTGTGAGCAGACTGAGAGATTCATGACAGAA 1652
DB 362 TCAGAGTTTGTGAGAGCAAGTCTTTGAGAAAGCTGTGATGAGAGTGTGACAGTGTAA 421
QY 1653 CTACCATTCACAAAGATTCCTGACTGTTCAGGACCCAGAGCTCTACTACCTGCTG 1712
DB 422 TGTGCTTTCAAGTACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 481
QY 1713 CTCCTGTGTGTGAGAGAGACACACACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1772
DB 482 TTCAGAGACACAAAAATCTTTCGATTCCAAATGCAATGTATGAGAGCATCA 541
QY 1773 GCGCAGATGCAAGAGCTCAGACGATTCATTCAGGAGGAGTGTGAGAGAGCCCTCTAC 1832
DB 542 AGTATGTATACAGAACTCAGCAGATTCAGATTCAGATGTGTGAGAGAAACCTCTGTCTC 601
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QY 1833 AACAGTGGCTCCAGCTTAAATTGAAAGCAGACGAGCTGAGCAACCAACTGCAAAAC 1892  
| | | | |  
Db 602 TACAGCCGATCCAGTTTAAATGCAAAATGAAAGATGTGTTAACTAAACTGTGAACA 661  
| | | | |  
QY 1893 ATCCGATATACACCAAGCCATCATCAGATCCCACTCCCGGCGGTAAACCCCAAGAGG 1952  
| | | | |  
Db 662 ACCTTATGTACTACAGCAATTAATAGCATCCCAACCTTGATTAACACACCAAGAGG 721  
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QY 1953 GGAAGTCGGCCA 1965  
| | | | |  
Db 722 AGACGATAGGCCA 734  
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RESULT 9  
US-09-949-016-2293  
; Sequence 2293, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CI001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2293  
; LENGTH: 3004  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-2293  
Query Match 11.3%; Score 240; DB 4; Length 3004;  
Best Local Similarity 53.4%; Pred. No. 2,7e-42;  
Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;  
QY 19 CAAGCTGTGTGCTTACGCTGCTGCGCGCTGCGCGCCCAAGAGCTGAGTGCACCATGCG 78  
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Db 72 CGAGCTCGCGCCGACATGACCGGTGTGCGCGGACACACGTGTGAG--CGAGAGTG 129  
| | | | |  
QY 79 GCGGAGTGTGCGCTGCTGCTGCTTTTGGCCGCGCTGCGCGCATGCGGTGATGCGCGTG 138  
| | | | |  
Db 130 GCGGATGTGAGAGGCGCGCGCTCAAGCGCGCTGTGCGCGCGCGCTGCGACCGCTAC 189  
| | | | |  
QY 139 GCGCAATGCGCCATGCGCTGCGCGCGCGCGCGCAAGAAAGAGCGGAGATGAGCTATT 198  
| | | | |  
Db 190 GAGCGGCTGCGCGCTCACTGCTGCGCGCGCGCGAGAGAGAGTCTGCGGAGAGCGCTG 249  
| | | | |  
QY 199 GTCTCAAGCTGAGTGTGCGGAGGTTTCAAGCTGAGAGACCAAGCTGAGCGCTACCG 258  
| | | | |  
Db 250 GTATCAACATCTCGCGGCTGCGCTTGAAGCGAGCTGAAGACCTTTTGCAAGTTCCC 309  
| | | | |  
QY 259 GACACCTGCTGCGGAGAGAGAGAGAGAGTTC--TTCTTCAAGAGAGACCAAGAGAG 315  
| | | | |  
Db 310 GAGACGCTGCTGCGGAGAGAGAGAGAGAGAGTTC--TTCTTCAAGAGAGAGAGAGAG 369  
| | | | |  
QY 316 TACTTCTTGAAGCGGAGAGAGAGAGAGAGTTCGCGGAGAGAGAGAGAGAGAGAGAG 375  
| | | | |  
Db 370 TACTTCTTGAAGCGGAG 429  
| | | | |  
QY 376 AAGC---TGACATACCGCGCTACAGATGATCTCTGCTTACAGAGAGAGAGAGAGAG 432  
| | | | |  
Db 430 GCGCGAGATCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489  
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QY 433 TAGGCAATCTCTCCGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492  
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Db 490 TACAGCTGGCGAG 549  
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QY 493 AGGAG 552  
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Db 550 GAG 606  
| | | | |  
QY 553 CCGTGTGAG 612  
| | | | |  
Db 607 TACCCGAG 666  
| | | | |  
QY 613 CTGGCCCTGATCTTCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666  
| | | | |  
Db 667 ATCTCATTTGTATCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
| | | | |  
QY 667 ACCAG 726  
| | | | |  
Db 727 CCGCGCTGAG 786  
| | | | |  
QY 727 GGGAG-----CGTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
| | | | |  
Db 787 GAG 846  
| | | | |  
QY 781 TTACAG 840  
| | | | |  
Db 847 TTCTCTTGAAG 906  
| | | | |  
QY 841 AGGTCATGAG 900  
| | | | |  
Db 907 AACATCATGAG 966  
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QY 901 ACCAA-----CAAG 945  
| | | | |  
Db 967 GAGCTGCGGAG 1026  
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QY 946 TTCCGC-----GTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996  
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Db 1027 ATCCGCTGTGAG 1086  
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QY 997 ATCTGAG 1056  
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Db 1087 ATCTGAG 1146  
| | | | |  
QY 1057 ACCATGAG 1116  
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Db 1147 TTATATGAG 1206  
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QY 1117 AGCAATGAG 1176  
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Db 1207 TCAAGTTTGAAG 1266  
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QY 1177 GATATGAG 1236  
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Db 1267 GTTATGAG 1326  
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QY 1237 TTGAGTGTGCTGCTGATGATGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1296  
| | | | |  
Db 1327 ATGCGCGGTGTGAG 1386  
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QY 1297 ATTACACAGAG 1310  
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Db 1387 TTCTACACAGAGAG 1400  
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RESULT 10  
US-09-949-016-12066  
; Sequence 12066, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CI001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 12066  
 LENGTH: 7055  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-12066

Query Match 11.3%; Score 240; DB 4; Length 7055;  
 Best Local Similarity 53.4%; Pred. No. 3.4e-42;  
 Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

19 CAAGCTGTGTGCTAGCTGCTGCGCGCTGCGCGCCCAAGAGCTGAGTACCATGCGG 78  
 2072 CGAGCTGCGCGCCGACATGACCTGTGTGCTGCGCGGACCACTGTGAG--CCGAGGATG 2129  
 79 GCCGAGTGTGCGGCTGAGCTGCTTTTCCCGGCTGCGGCTGAGGATGCGCGG 138  
 2130 GCCATGTGTGAGGGGCGCCCGCTTCAGGCGGCTGTGCGGCGCGGCTGCGACTAC 2189  
 139 GCCAATGCGCCGATGCGCTTGTGCGCGCGGACCAAGAAACAAGCGGAGATGAGCTGATT 198  
 2190 GAGCGGCTGCGCGCTTCACTGCGCGCGCGGCGGAGAGACTGTGCGGGAGCGCGTG 2249  
 199 GTCTCTCAACGTAGTGTGCGGAGGTTCCAGACTGTGAGAGACCACTGTGAGCGTACCCG 258  
 2250 GTCAATCAACATCTCGGCGCTGCGCTTCAGAGAGAGCTGAAGACCTTTGCGAGTTCC 2309  
 259 GACACCTGTGCTGCGGAGAGAGAGAGGTTCTTCTCAACAGAGAGACCAAGAG 315  
 2310 GAGAGCGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2369  
 316 TACTTCTTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375  
 2370 TACTTCTTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2429  
 376 AAGC---TGCACTACCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432  
 2430 GCGCGAG 2489  
 433 TAGGAGATCTTCCGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492  
 2490 TACCACTGTGCGGAG 2549  
 493 AGGAG 552  
 2550 GAG 2606  
 553 CCTGTGCTGAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612  
 2607 TACCCGAG 2666  
 613 CTGAGCGCTGCTTCTTACTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666  
 2667 ATCTTCATTTGATCTTCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2726  
 667 ACCAAGCTGTGAG 726  
 2727 CCCGCTGAG 2786  
 727 GGGAG 780  
 2787 GAG 2846  
 781 TTCAACGAG 840

DB 2847 TTCTCTTGAAG 2906  
 QY 841 AGCTCATGAGATCATGAG 900  
 DB 2907 AACATCATGAG 2966  
 QY 901 ACCAA-----CAAG 945  
 DB 2967 GAGCTGCGGAG 3026  
 QY 946 TTCCGC-----GTCTTGAAGATCTTCAAGTTTTCGCCCACTCCAGAGAGAGAGAGAG 996  
 DB 3027 ATCCGCTGTAAG 3086  
 QY 997 ATCTGAGCTTCAACATGAG 1056  
 DB 3087 ATCTGAGCTTCAACATGAG 3146  
 QY 1057 ACCATGAGCTATCATCTTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1116  
 DB 3147 TTATTTGAGGATCTTCTTCTCAAGCGGCTTCACTTTGCGAGAGAGAGAGAGAGAGAG 3206  
 QY 1117 AGCAAGTTCACAG 1176  
 DB 3207 TCAGGTTTCAAG 3266  
 QY 1177 GATATGAG 1236  
 DB 3267 GATATGAG 3326  
 QY 1237 TTGAGTGTGCTGAG 1296  
 DB 3327 ATCCGCGGTCTTGAAG 3386  
 QY 1297 ATTACCAACAGAA 1310  
 DB 3387 TTCTACACCGGGA 3400

RESULT 11  
 US-09-949-016-14035  
 Sequence 14035, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C0001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 PRIOR FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 14035  
 LENGTH: 7056  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-14035

Query Match 11.3%; Score 240; DB 4; Length 7056;  
 Best Local Similarity 53.4%; Pred. No. 3.4e-42;  
 Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

19 CAAGCTGTGTGCTAGCTGCTGCGCGCTGCGCGCCCAAGAGCTGAGTACCATGCGG 78  
 2072 CGAGCTGCGCGCCGACATGACCTGTGTGCTGCGCGGACCACTGTGAG--CCGAGGATG 2129  
 79 GCCGAGTGTGCGGCTGAGCTGCTTTTCCCGGCTGCGGCTGAGGATGCGCGG 138





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Db      486 TACACGCTGGGAGAGAGCCATGAGAAAGTCCCGGAGAGAGAGGCTTCTCGGGAG 545
Qy      493 AGGGAGAACCCGAGCGGCTATGAGCAACAGACTCGAGAACACAGAGATCCATG 552
Db      546 GAGGAGCGCCCTTCCCGCGCGCATTCAGCCAGGTTG---TGCGTCTTCGAG 602
Qy      553 CCTTCGCTCAGTTCCGACAGCATGTGGCGGCTTCGAGAACCCCAACAGCAG 612
Db      603 TACCCGAGAGCTCGGCGCGCGCGCATGCGATGTCGTGCTGATCTTC 662
Qy      613 CTGGCCCTGCTTCTTACTAGTGAAGTCTT-----CTTATGCTGTCTCGATC 666
Db      663 ATCTCATTTGTCATTTTCTGCTGAGAGAGCTCCGAGTTCCGAGAGAGAGATAC 722
Qy      667 ACCAAGCTGTGAGAGCGGTGCGGCAAGCTCCGAGAGAGAGAGAGTCCGTC 726
Db      723 CCGGCTCGAGCTGCAAGACTATTCAGAGCAGCGGCAAGAGCAGTCCGAGTCCG 782
Qy      727 GGGAG-----CGTACTCGGTGCTTCTTCTGCTGAGACAGCGCTGCTATGATC 780
Db      783 GAGAGAGCTTCAGCTTCTCCGATCCCTTCTGAGAGAGCCTGTGATCATCTG 842
Qy      781 TTCAACGAGATACCTCTGAGGCTTTCGCGCTCCAGCGGCTAACCGCTTCAATCC 840
Db      843 TTTCTCTTGAATCTGAGTGGTTCCTGCTTCTGCTTCTGAGAGAGCCTTCTGCGA 902
Qy      841 AGCGTCATGAGATCATGAGCTGTGAGCATCATGCTTCTTCTGAGTCTGATG 900
Db      903 AACATCATGAGCTGATGAGATGTGGCATCTTCTTATTTATCATCTTGGATACC 962
Qy      901 ACCAA-----CAAGAGAGCTGTCCGCGCTTGTGTCAGCTCCGAGT 945
Db      963 GAGCTGCGGAGAGCAAGGAGATGAGAGAGAGCATGTCTGCGCATCTTGAAGGTC 1022
Qy      946 TTCCG-----GTCTGAGATCTTCAAGTTTCCCGCATCCAGGCGCTGCG 996
Db      1023 ATCCGCTGAGAGGCTTTCGCGATCTTCAAGCTGTGCGGCACTCCAGGAGCTGAG 1082
Qy      997 ATCTGAGGCTACACAGTGAAGCTGTGCGCTCGAATGAGGCTTCTTCTTCTCC 1056
Db      1083 ATCCCTCGGAGAAAGCTGAGAGGCTGCAATGCGGAGCTGGATGTCTATCTTCTCC 1142
Qy      1057 ACCATGCGCATCATCTTTGCGCATGTGATGTTTATGCGAGAGGCTCTCGGCT 1116
Db      1143 TTTATTTGGGTCATCTTTTCTCCAGCGGCTTCTTCTTTCGAGAGAGACCCCACT 1202
Qy      1117 AGCAAGTTCAGAGATCCCTGCGCTGTTTGTACACATGTGACATGACAGACATG 1176
Db      1203 TCAGGTTTCAGAGATCCCGGATCTTCTGTGGGAGTGAACATGACAAAGTG 1262
Qy      1177 GGAATACGAGAGATGCTGCTTAAGACATGTCAGAGAGATCTTGGGCTCATCTGCTCC 1236
Db      1263 GGTATCGCGAGATTCACACAGTGAACATGAGGAGAGATGTGGATCTCTGTGCTC 1322
Qy      1237 TTGAGTGGCTGCTGTGATGCTGCTGCGATGCTCTGTGATGTTTCAACTTTA 1296
Db      1323 ATCGCGGCTGCTTGAACATGATGCGATGCGAGTTCCGATGATGTTTCAATTA 1382
Qy      1297 ATTAAACAGAGAA 1310
Db      1383 TTCTAACACCGGA 1396

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RESULT 13
US-09-949-016-1604
; Sequence 1604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1604
; LENGTH: 1802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1604

Query Match      10.2%; Score 216; DB 4; Length 1802;
Best Local Similarity 53.7%; Pred. 3.6e-37;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy      294 CTTCAAGAGAGACACCAAGAGTACTTTCGACCGGAGCCCGAGTGTTCGCTGCT 353
Db      207 CTACGAGCCCGGCAAGCGCGAGTTCTTACTTTGACAGGAGCCGAGCCTTCAATGTT 266
Qy      354 GCTCAACTTTCACCGGAGGAGTCACTACCCGGGCTTACAGATGATCTGCTT 413
Db      267 CATCAGAGTATCTATTTTCGGGAGTCCACATGAAAGGAGCATCTGCCATCTGCT 326
Qy      414 CGACGAGAGCTGCGCTTCTACGCGATCTCCGAGATCAATCGGAGACTGCTGCTA 470
Db      327 CAAGAACAGATGAGCTTCTGGAAGTGAACCTCAAGTTCTGAGACGATGTGGAAG 386
Qy      471 -----CGAGAGTACAAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 521
Db      387 CCACCTGAGAGAGAGCGCGAGAGTGAAGAGATTCGCGCGCGCTGAGCTCATCT 446
Qy      522 CAAGAGCTGAGAGAACACAGAGAGTCCATGCTCGCTCGCTTCCGCGAGACATG 581
Db      447 GAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
Qy      582 GCGGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
Db      507 GAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
Qy      642 CTTCTTATGCTGTCTGCTGATCAACAGGTGTGAGAGAGAGAGAGAGAGAGAG 701
Db      567 CTTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
Qy      702 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
Db      627 GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
Qy      762 CAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
Db      678 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737
Qy      822 CCGTACAGCTTTCATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
Db      738 CAAGCTGAGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
Qy      882 CTACATGCTGTGCTGATGACCAACAGAG-----AGTGTG 920
Db      798 CTACGTGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857
Qy      921 CGGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Db      858 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 917
Qy      981 CTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Db      918 CTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 977
Qy      1041 TCTTCTCTTTCCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100

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Db 978 GCTGCTCATCTACTGCGACGTGGATATCTTCCTTCGCCCCGTGGGCTACACCATGGA 1037  
Qy 1101 GAAGGGCTCTCGGGCCGACGAAGTTTACAGAGATCCCTCGCTTGTGTAGACCATTTG 1160  
Db 1038 GCGAGGCTATCCAGAGACCTGTTTAAAGATCCCACTCTTCTGTGGGCTCATCAT 1097  
Qy 1161 CACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGCAAGGAATCTT 1220  
Db 1098 CACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGCAAGGAATCTT 1157  
Qy 1221 CGGCTCATCTGCTCTTGTAGTGGCGCTGCTGCTATTCCTTGCATCTTGTATTT 1280  
Db 1158 CGGGGCTCATGCTCTTGTGTGTGTGTCATGCGCATGCGCTGCTGCTGCTGCTGCT 1217  
Qy 1281 TTCCACTTAAAGCGGATTTACCAACGAGATC 1312  
Db 1218 CAACACTTGTGTAGGTACTACAAACAGCAGC 1249

## RESULT 14

US-08-464-340A-3  
; Sequence 3, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILIAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,340A  
; FILING DATE: June 5,1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449  
; FILING DATE: 28 JUL 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA  
; US-08-464-340A-3

Query Match 10.2%; Score 216; DB 1; Length 2483;  
Best Local Similarity 53.7%; Pred. No. 3.9e-37;  
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy 294 CTTCAAGAGAGACCAAGAGTACTTCTTGCACCGGAGCGGAGGTTTCCGCTGCGT 353  
Db 891 CTAGAGACCCCGGAGAGCGAGTCTTCTTGAAGAGGAGACCCGAGCCCTTCAAGTGTGT 950  
Qy 354 GCTCAACTTGTACGCAAGGAGAGTGTGACTACCCGCGTACGAGTGTCTTGTGCTTA 413

Db 951 CATCGAGTGTATATTTTGGGGAGGTCCACATGAAGAAAGGATCTGCCCATCTGCTT 1010  
Qy 414 CGACGACGAGCTGGCTTCTTACAGGATCTCTCCGAGATCATATGAGGAGCTGCTGCTA--- 470  
Db 1011 CAAAGACGAGATGATCTTCTGAAAGTGAACCTCAAGTTCTTGAAGACCTGTTGCAAGAG 1070  
Qy 471 -----CGAGAGTAAAGAGACCGCAAGAGGAGAAACCGGACGGCTCATGAGCA 521  
Db 1071 CCACTGAGGAGAAACGAGAGAGTGAAGAGATGCGCGCGCGGTGAGCTCATCTT 1130  
Qy 522 CAACGATGAGAGAAACACAGAGATTCATGCTTCTGCTCAGTTTCCGCAACATGTG 561  
Db 1131 GAGCGACTGGGGCTGAGAGCGCGGCGAGGAGCGCTGCGCGCTGCGCAGAAAGTGCCTTG 1190  
Qy 582 GCGGGGCTTGAAGACCCCAACACAGACACGCTGGGCGCTGCTTCTTAACTAGTGA 641  
Db 1191 GAAGTTCTGGAAGAACCGAGATGTCGTGCTCCGAGCGGGTGTGAGCGAGCTTCTT 1250  
Qy 642 CTTCTTCACTGCTGTCTGCTGCTATCAACAGTGTGAGAGACGCTGCGGACAGGT 701  
Db 1251 CTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310  
Qy 702 CCGGCGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761  
Db 1311 GCTGAGACGCGAGAG-GCAACCGGCTGAGAGACCGAGCTGAG-----AACGTGA 1361  
Qy 762 CACGGGCTGCTGATGATCTTCAACGAGTACCTCTGCGGCTCTTGCAGCTCCAG 821  
Db 1362 GACGGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421  
Qy 822 CCGCTACCGCTTATCGAGAGCTGCTGATGAGCATCATGAGTGTGAGCATATGCTCTA 881  
Db 1422 CAAGTGAACCTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481  
Qy 882 CTACATCGCTGTGTGTATGACCAACAGAG-----ACGTGTC 920  
Db 1482 CTACGAGAGCTTACCGCTACCGACCTGAGTGGCCGATGAGAGCTGACCAACGTGA 1541  
Qy 921 CGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980  
Db 1542 GAGGCGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601  
Qy 981 CTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040  
Db 1602 CTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1661  
Qy 1041 TCTTCTCTTCTCTCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100  
Db 1662 GCTGCTCATGTATCTGAGTGTGTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721  
Qy 1101 GAAGGGCTCTGCGGAGCAAGTTTCAAGCATCCCTGCTGCTTGTGAGACCATTTG 1160  
Db 1722 GAGAGCATCAAGAGACCTGTTTAAAGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1781  
Qy 1161 CACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGCAAGGAATCTT 1220  
Db 1782 CACCATGACCACTGGGATACGAGACATGTGCTTAAAGCATTTGCAAGGAATCTT 1841  
Qy 1221 CGGCTCATCTGCTCTTGTAGTGGCGCTGCTGCTATTCCTTGCATCTTGTATTT 1280  
Db 1842 CGGCGCATGACTTCTTGTGTGTGTGTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901  
Qy 1281 TTCCACTTAAAGCGGATTTACCAACGAGATC 1312  
Db 1902 CAACACTTGTGTAGGTACTACAAACAGCAGC 1933

## RESULT 15

PCT-US94-08449A-3  
; Sequence 3, Application PC/TUS9408449A  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.

TITLE OF INVENTION: Potassium Channel Protein 1 and 2  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESS: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08449A  
FILING DATE: SUBMITTED HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
PCT-US94-08449A-3

Query Match 10.2%; Score 216; DB 5; Length 2483;  
Best Local Similarity 53.7%; Pred. No. 3.9e-37;  
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

QY 294 CTTCAACGAGACACCAAGAGTACTTTTTCACCGGACCCCGAGGTTCCTCGTGGT 353  
DB 891 CTACGACCCCGCAGACCGGAGTTCTTCTTGACGAGACCGGACGCTTCAAGTGT 950  
QY 354 GCTCAACTTCTACCGCAGCGGAGAGTCACTACCGCGCTACGAGTCACTTGTGCTTA 413  
DB 951 CATGAGGTGATCTATTTTCGGGAGGTCCACATGAAAGGCACTGCCCCATCTGCTT 1010  
QY 414 CGACGACGAGTGTGCTTCTTACGAGCATCTCCCGAGATCATCGGGAATGCTGCTA 470  
DB 1011 CAAGAACGAGATGACTTCTGGAAGTGAAGCTCAAGTTCTTGACGAGTGTGCAAG 1070  
QY 471 -----CGAGAGTACAAAGAACCGCAAGAGAGAAACCGGAGCGCTCATGACGA 521  
DB 1071 CCACCTGACGAGAGACCGCAGAGAGTGAAGATCGCGCGCCGCTGCACTCATCT 1130  
QY 522 CAACGACTCGAGAACCAACGAGAGTCCATGCGCTCGCTCAGCTTCCGCGAGACATG 581  
DB 1131 GAGACACTTGGCGGTGAGCGGCGCGAGAGGCTGCGGCGCGCTGCGAGATGCGTCTG 1190  
QY 582 GCGGCGCTTGAAGAACCCCAACAGCAGCAGCTGAGCCCTGATCTTCTACTAGTAC 641  
DB 1191 GAAGTTCTGAGAGAGCCGAGTCTGCGGCGCGGAGTGTGCGCGAGACTCTCTT 1250  
QY 642 CTTCTTCACTCGCTGCTGCTGATCAACAGTGTGAGACGTCGCGGAGCGTGGAGCGT 701  
DB 1251 CTTGCTCATCTCTGCTGCTGCTGATGATGACACCATCCCGAATGCAAGT 1310  
QY 702 CCGGCGAGAGAGTGTGCGGAGAGCGTACTGAGTGTCTTCTTCTGCTGGA 761  
DB 1311 GCTGAGCGCGAGG--GCAACCGCGTGAAGCAACCGACGCTGAG-----AAGTGA 1361

QY 762 CAAGCGGTGCTCATGATCTTACCGTGAAGTACTCTCTGAGGCTTTCGGGCTCCAG 821  
DB 1362 GAGCGGTGACATGAGCTGTGACCCCGAGATGACTGTGAGGCTTCTGTACACCA 1421  
QY 822 CCGTCAACGCTTCAATCCGACAGCTCATGAGCATATCAGCTGTGAGCATATGACCTTA 881  
DB 1422 CAAGTGCATCTTCCGCTGTCTTATGAAATATGTGACGCTGTGAGCATCTCTCC 1481  
QY 882 CTACATCGGTGTGCTATGACCAACAGAG-----ACGTGC 920  
DB 1482 CTACGTGAGCTTCAAGCTCAGCAGCAGCTGGGCGCGCATGATGAGTGAACCAAGTCA 1541  
QY 921 CCGGCGCTTGTCAACGCTCGCGGTCTTCCGCTTTCAGATCTTCCGCGCA 980  
DB 1542 GCAGCGCTGTGAGGCGGTGCGGATCATGCGATGCGCGCATCTTCAAGCTGCGCGCA 1601  
QY 981 CTCCAGGCGCTGCGGATCTGAGCTACACACTGAAGAGTGTGCTCCGAATGAGCTT 1040  
DB 1602 CTCTCGGCGCTGACAGACCTTCACTATGCTTCAAGGCGAGCTTCAAGAACTGGGCT 1661  
QY 1041 TCTTCTTCTTCCCTACACATGCGCATCATCTTTGCACTGTATGTTTATGCGGA 1100  
DB 1662 GCTGCTCATGATCTGAGGAGTGTATCTTCTCTGCGCTGCGGCTACACATGGA 1721  
QY 1101 GAAGGCTCTCTGCGGAGAGTTCACAGATCTCTGCTCTGTTTGTATACCATGT 1160  
DB 1722 GCAGGCGCATCCAGAGACCTGTTTAAGAAATATCCCGAGTCTTGTGTGGCCATCAT 1781  
QY 1161 CACCATGACCACTGAGGATGAGAGACATGATGCTTAAGAGATGAGGAGAGATCTT 1220  
DB 1782 CACATGACCACTGAGGATGAGAGACATGATGCTTAAGAGATGAGGAGAGATCTT 1841  
QY 1221 CCGCTCATCTGCTCTTGAAGTGTGCTGCTGATGATGCTGCGAGTCCCTGATGT 1280  
DB 1842 CGCGGCGATGAGCTTCTTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1901  
QY 1281 TTCCACTTGAACCGGATTTACACAGATC 1312  
DB 1902 CAACAACTTGTGAGTACTTCAACAAAGAC 1933

Search completed: April 6, 2005, 04:45:33  
Job time : 365.767 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 07:58:39 ; Search time 2500.09 Seconds  
(without alignments)  
5022.120 Million cell updates/sec

Title: US-10-062-879-1

Perfect score: 2121  
Sequence: 1 gatttgcgtgaactaactcca.....gtcgtatcaagccgaattc 2121

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2004as:\*  
12: Geneseqn2004bs:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1962	92.5	2072	2	AAV61572 Human Kv
4	1960	92.4	1968	12	ADFP1397 Wild-type
5	1838	86.7	2104	2	AAV61571 Human Kv
6	1830	86.3	2104	2	AAV61573 Human Kv
7	935.4	44.1	2351	4	AAH21247 Human Kv4
8	935.4	44.1	2351	11	ADM10922 Human O64
9	935.4	44.1	2351	12	ADJ11252 Human Ova
10	935.4	44.1	2351	12	ADM43513 Human Ova
11	935.4	44.1	5333	11	ADM10923 Human O64
12	935.4	44.1	5333	11	ADM10921 Human O64
13	935.4	44.1	5333	12	ADJ11253 Human Ova
14	935.4	44.1	5333	12	ADJ11251 Human Ova
15	935.4	44.1	5333	12	ADM43512 Human Ova
16	935.4	44.1	5333	12	ADM43514 Human Ova
17	935.4	44.1	5333	12	ADP21361 Gene KCND
18	800.2	37.1	2711	4	AAH21246 Human Kv4
19	798.2	37.6	3424	2	AAZ11901 Human pot
20	795.4	37.5	2578	4	AAH99538 Human pot

21	739.8	34.9	1716	4	ABL29811	Abi29811 Drosophila
22	679	32.0	5404	11	ADM10924	Adm10924 Human O64
23	679	32.0	5404	12	ADJ11254	Adj11254 Human Ova
24	679	32.0	5404	12	ADM43515	Adm43515 Human Ova
25	637.8	30.1	2033	4	AAH21248	AAH21248 Human KCN
26	634.2	29.9	1121	12	ACH91582	ACH91582 Human gen
27	540	20.5	8075	4	ABL29810	Abi29810 Drosophila
28	435	20.5	1737	12	ADFP1396	ADFP1396 Worm Kv4
29	357	16.8	1083	4	AAH21264	AAH21264 Human Kv4
30	354.4	16.7	1597	11	ADM10925	Adm10925 Human O64
31	354.4	16.7	1597	12	ADJ11255	Adj11255 Human Ova
32	354.4	16.7	1597	12	ADM43516	Adm43516 Human Ova
33	338	15.9	612	4	AAI28128	AAI28128 Probe #18
34	338	15.9	612	4	ABA76453	ABA76453 Human foe
35	338	15.9	612	4	AAI57133	AAI57133 Probe #25
36	338	15.9	612	4	ABA40984	ABA40984 Probe #19
37	338	15.9	612	4	AAK51097	AAK51097 Human bon
38	338	15.9	612	4	AAK25090	AAK25090 Human bra
39	338	15.9	612	4	ABS50654	ABS50654 Human liv
40	338	15.9	612	6	ABS24615	ABS24615 Human gen
41	266	12.5	2882	13	ADSI6307	ADSI6307 Rabbit vo
42	259.2	12.2	3254	11	ADM10920	Adm10920 Human O64
43	259.2	12.2	3254	12	ADJ11250	Adj11250 Human Ova
44	259.2	12.2	3254	12	ADM43511	Adm43511 Human Ova
45	240	11.3	3004	13	ABD33130	ABD33130 Human can

## ALIGNMENTS

RESULT 1  
ID AEN84400 standard; cDNA; 2121 BP.  
AC AEN84400;  
DT 01-OCT-2002 (first entry)  
XX Human Kv4.3 potassium channel (long form) cDNA.  
DE Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;  
KW nootropic; neuroprotective; cardiac; gene therapy; gene; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 73..2040  
FT /tag= a  
FT /product= "Kv4.3"  
XX  
XX US6395477-B1.  
XX  
XX 28-MAY-2002.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX (AMHP) AMERICAN HOME PROD CORP.  
XX  
XX Cockett MI, Dilks DW, Ling HC, Sokol PT;  
XX  
XX WPI; 2002-556093/59.  
XX P-PSDB; ABB79584.  
XX  
XX New isolated polynucleotide encoding human Kv4.3 potassium channel  
XX polypeptide, useful as probe in a diagnostic method for detecting nucleic  
XX acid encoding human Kv4.3, and for treating Alzheimer's and heart  
XX diseases.  
XX  
XX Claim 5; Col 15-18; 19pp; English.  
XX  
XX The present sequence is that of cDNA encoding the long isoform of novel  
XX  
XX CC

CC human p15ssingham channel Kv4.3. To obtain the cDNA, oligonucleotides based  
CC on the published rat sequence were used to screen a whole heart cDNA  
CC library. A 511 bp fragment was obtained and used as a probe to rescreen  
CC the library. The resulting clones lacked the extreme 5' and 3' coding  
CC regions, and 5' and 3' RACE was therefore used to amplify these sequences  
CC from a human brainstem cDNA library. 2 isoforms of human Kv4.3 were  
CC identified. One form is full-length (hKv4.3 long) while the second form  
CC has a deletion of 19 amino acids in the carboxy domain after the  
CC predicted sixth transmembrane domain (hKv4.3 short). Human heart  
CC primarily expresses hKv4.3 long, whereas human brain contains both forms.  
CC The invention provides Kv4.3 polypeptides, polynucleotides, and methods  
CC for producing these polynucleotides. The Kv4.3 polypeptides and  
CC polynucleotides are useful in the diagnosis, treatment and screening of  
CC human diseases relating to an excess or deficiency of hKv4.3 activity,  
CC including Alzheimer's disease and heart disease

Sequence 2121 BP; 457 A; 694 C; 557 G; 413 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2121;	DB 6;	Length 2121;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2121; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	GATTTGCAGAACTAACTCAAGCTGGTGGCCCTACGGTCCGGCGGGCTGGCCGGCCCAAGA	60
Db	1	GATTTGTGAACTAACTCAAGCTGGTGGCCCTACGGTCCGGCGGGCTGGCCGGCCCAAGA	60
QY	61	GCTGGAGTCACCATGGCCGGCCGGGAATTGGGCTGGCTGGCTGGCTGGCTGGCTGGCC	120
Db	61	GCTGGAGTCACCATGGCCGGCCGGGAATTGGGCTGGCTGGCTGGCTGGCTGGCTGGGTC	120
QY	121	ATCGGGTGGATTGCGCGGTGGCCAACTGGCCCCATGGCCCCCTGGCCCCGGACGAACAAG	180
Db	121	ATCGGGTGGATTGCGCGGTGGCCAACTGGCCCCATGGCCCCCTGGCCCCGGACGAACAAG	180
QY	181	CGGACGAGTGAAGCTGATTGTGCTCAACGTGAAGTGGGCGGAGGTTCCAAACCTGGAGAGCC	240
Db	181	CGGACGAGTGAAGCTGATTGTGCTCAACGTGAAGTGGGCGGAGGTTCCAAACCTGGAGAGCC	240
QY	241	ACGCTGAGCGCTAACCCGGACAACCCCTGGCTGGGACACACGGAAGAAAGATTCTTCTTCAAC	300
Db	241	ACGCTGAGCGCTAACCCGGACAACCCCTGGCTGGGACACACGGAAGAAAGATTCTTCTTCAAC	300
QY	301	GAGGACACCAAGAGATCTTCTTGGACCGGGACCCCGAGGTTCGCTGGCTGCTCAAC	360
Db	301	GAGGACACCAAGAGATCTTCTTGGACCGGGACCCCGAGGTTCGCTGGCTGCTCAAC	360
QY	361	TTCTAACCGCAAGGGGAGCTGACACTAACCCGCGCTACGATGCTGCTGCTTCCCTTACGACGAC	420
Db	361	TTCTAACCGCAAGGGGAGCTGACACTAACCCGCGCTACGATGCTGCTGCTTCCCTTACGACGAC	420
QY	421	GAGCTGGCTTCTTACGGCATCTCTCCCGGAGATCATCGGGGAACTGGCTGTTACGAGAGTAC	480
Db	421	GAGCTGGCTTCTTACGGCATCTCTCCCGGAGATCATCGGGGAACTGGCTGTTACGAGAGTAC	480
QY	481	AAGGACCGCAAGAGGAGAAACGCGGAGCGGCTCATGAGACGACCAACGACTTCGGAGAACAC	540
Db	481	AAGGACCGCAAGAGGAGAAACGCGGAGCGGCTCATGAGACGACCAACGACTTCGGAGAACAC	540
QY	541	CAGGAGTCATAGCCCTCGCTCAAGCTTCCGCGCAACCATGTGGCGGGCTTTCGAGAAACCC	600
Db	541	CAGGAGTCATAGCCCTCGCTCAAGCTTCCGCGCAACCATGTGGCGGGCTTTCGAGAAACCC	600
QY	601	CACACCAACGACTGGACCTGGTCTTCTTACTACGATGACTGGCTTCTTCACTCGCTGCTTCG	660
Db	601	CACACCAACGACTGGACCTGGTCTTCTTACTACGATGACTGGCTTCTTCACTCGCTGCTTCG	660
QY	661	GTCAATCAACAACTGGTGGAGACGCGTGCCTGTCGCGACGAGTCCCGGAGCAAGAGGCTG	720
Db	661	GTCAATCAACAACTGGTGGAGACGCGTGCCTGTCGCGACGAGTCCCGGAGCAAGAGGCTG	720
QY	721	CCGTCGCGGAGAGCTGACTCGGTGGCTTCTTCTGCTGAGACACGAGCTGGCTCATGATC	780
Db	721	CCGTCGCGGAGAGCTGACTCGGTGGCTTCTTCTGCTGAGACACGAGCTGGCTCATGATC	780

QY	781	TTCAACCGTGAAGTATCTCTCCGCGGCTCTTGCGGCTCCACAGCGCTACCGCTTAATCCG	840
Db	781	TTCAACCGTGAAGTATCTCTCCGCGGCTCTTGCGGCTCCACAGCGCTACCGCTTAATCCG	840
QY	841	AGCGTCATGAGCATCATCGAGTGAGGCGCATCTAGCCCTACTACATCGATCTGGTCATG	900
Db	841	AGCGTCATGAGCATCATCGAGTGAGGCGCATCTAGCCCTACTACATCGATCTGGTCATG	900
QY	901	ACCAACAACGAGGACGTGTCCGGGGCTTTCGTCAACGCTCCGGGCTTCGGGCTTTCAAG	960
Db	901	ACCAACAACGAGGACGTGTCCGGGGCTTTCGTCAACGCTCCGGGCTTCGGGCTTTCAAG	960
QY	961	ATCTTCAAGTTTCCCGCACCTCCAGGCGCTGCGGATCTCGGGCTACACACTGAAGC	1020
Db	961	ATCTTCAAGTTTCCCGCACCTCCAGGCGCTGCGGATCTCGGGCTACACACTGAAGC	1020
QY	1021	TGTGCTTCGAACTGGGCTTCTTCTCTCTCTCCCTCAACATGCGCATCATCTTTGCC	1080
Db	1021	TGTGCTTCGAACTGGGCTTCTTCTCTCTCTCCCTCAACATGCGCATCATCTTTGCC	1080
QY	1081	ACTGGAATGTTTATGCGGAGAGGGCTCCCGGCGAGCAAGTTCAAGCATCCCTGCC	1140
Db	1081	ACTGGAATGTTTATGCGGAGAGGGCTCCCGGCGAGCAAGTTCAAGCATCCCTGCC	1140
QY	1141	TCGTTTTGATCAACACATTTGTCAACCATGACCACTGSGGATACGAGACATGGTCCTAAG	1200
Db	1141	TCGTTTTGATCAACACATTTGTCAACCATGACCACTGSGGATACGAGACATGGTCCTAAG	1200
QY	1201	ACGATTTGAGGGAAGATCTTGGGCTCCATCTGCTCTCTTGAATGGCGTCTGGTATTGCC	1260
Db	1201	ACGATTTGAGGGAAGATCTTGGGCTCCATCTGCTCTCTTGAATGGCGTCTGGTATTGCC	1260
QY	1261	CTGCACGCTCCGTGATTTGTTCCACTTTTAGCGCGAATTTACCAACAATCAAGAGCT	1320
Db	1261	CTGCACGCTCCGTGATTTGTTCCACTTTTAGCGCGAATTTACCAACAATCAAGAGCT	1320
QY	1321	GATTAACGCGAGGCGACAAAGAAGGCGCCGCTTGCCAGGATCCGTGGCCAAACAGGC	1380
Db	1321	GATTAACGCGAGGCGACAAAGAAGGCGCCGCTTGCCAGGATCCGTGGCCAAACAGGC	1380
QY	1381	AGTTGGAATGATTAACCTGCGACAGGAGGCGGCGCTCCCAAGGCGCTGAGAGTG	1440
Db	1381	AGTTGGAATGATTAACCTGCGACAGGAGGCGGCGCTCCCAAGGCGCTGAGAGTG	1440
QY	1441	ACGGGCAACCCAGAGAGGAGCACATGSGGCAAGACCATCTCATCTGAGAGCCAGCAT	1500
Db	1441	ACGGGCAACCCAGAGAGGAGCACATGSGGCAAGACCATCTCATCTGAGAGCCAGCAT	1500
QY	1501	CATCACCTGCTGCACTGCTTGGAACCACTGGGTGTCCTATCTTTGAGAGATCCC	1560
Db	1501	CATCACCTGCTGCACTGCTTGGAACCACTGGGTGTCCTATCTTTGAGAGATCCC	1560
QY	1561	CTGTTATCTGACCAACCTCCACCATCAAGAACAAGGTTTATTTGATGAGCAATGTTT	1620
Db	1561	CTGTTATCTGACCAACCTCCACCATCAAGAACAAGGTTTATTTGATGAGCAATGTTT	1620
QY	1621	GAGCGAATCTGCATGAGAGATTCAATGCAAGTAATCCATCCACAGAAGTCCCTCACTG	1680
Db	1621	GAGCGAATCTGCATGAGAGATTCAATGCAAGTAATCCATCCACAGAAGTCCCTCACTG	1680
QY	1681	TCGAGGCAACGAGGCTCATTAACAACCTGCTGCTCCGTCGTAAGTAAGAACAACAAC	1740
Db	1681	TCGAGGCAACGAGGCTCATTAACAACCTGCTGCTCCGTCGTAAGTAAGAACAACAAC	1740
QY	1741	CTGCCAATTTCTAACCCTGCGACTAAGCTGCGGCAAGCATGAAGCTCAGACGATC	1800
Db	1741	CTGCCAATTTCTAACCCTGCGACTAAGCTGCGGCAAGCATGAAGCTCAGACGATC	1800
QY	1801	CACATCCAGGGGAGTGAAGACCTCTCTCAACAACAATCGCTCCAGCTTAATTTGAAA	1860
Db	1801	CACATCCAGGGGAGTGAAGACCTCTCTCAACAACAATCGCTCCAGCTTAATTTGAAA	1860

QY 1861 GCAGACGACGACCTGAGACCAACTGCAAAACATCCAGATGACCAAGCCATCATCAGC 1920  
 DB 1861 GAGACGACGACCTGAGACCAACTGCAAAACATCCAGATGACCAAGCCATCATCAGC 1920  
 QY 1921 ATCCCACTCCCGCCGCTAAACCCAGAGGGGAAAGTCGSCCAACCCCTCCAGCCCA 1980  
 DB 1921 ATCCCACTCCCGCCGCTAAACCCAGAGGGGAAAGTCGSCCAACCCCTCCAGCCCA 1980  
 QY 1981 GGGCCCAACAGCAATTCCTTCCTAAACAGCAATGTTGTCAGGTCCTCTGTTGTA 2040  
 DB 1981 GGGCCCAACAGCAATTCCTTCCTAAACAGCAATGTTGTCAGGTCCTCTGTTGTA 2040  
 QY 2041 AAATCCGCGGCGATGCGGCGGAGCATGCGAGTGGGCGCAATTCGCTTAAGG 2100  
 DB 2041 AAATCCGCGGCGATGCGGCGGAGCATGCGAGTGGGCGCAATTCGCTTAAGG 2100  
 QY 2101 AGTCGATTAAAGCCGAATTC 2121  
 DB 2101 AGTCGATTAAAGCCGAATTC 2121

## RESULT 2

ABN84401 standard; cDNA; 2064 BP.

ABN84401;

01-OCT-2002 (first entry)

Human Kv4.3 potassium channel (short form) cDNA.

Kv4.3; potassium channel; human; Alzheimer's disease; heart disease; nootropic; neuroprotective; cardiant; gene therapy; gene; ss.

Homo sapiens.

Location/Qualifiers

73..1983

/tag= a

/product= "Kv4.3"

US6395477-B1.

28-MAY-2002.

23-OCT-1998; 98US-00178109.

23-OCT-1998; 98US-00178109.

(AMHP) AMERICAN HOME PROD CORP.

Cockett MI, Dicks DW, Ling HC, Sokol PT;

WPI: 2002-556093/59.

P-PSDB: ABB79585.

New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting nucleic acid encoding human Kv4.3, and for treating Alzheimer's and heart diseases.

Claim 7; Col 21-22; 199p; English.

The present sequence is that of cDNA encoding the short isoform of novel human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been identified. One form is full-length (hkV4.3 long) while the second form has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hkV4.3 short). Human heart primarily expresses hkV4.3 long, whereas human brain contains both forms. To obtain the present hkV4.3 short cDNA, PCR amplification was performed using primers that flanked the 57 bp insert in hkV4.3 long. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are

CC useful in the diagnosis, treatment and screening of human diseases  
 CC relating to an excess or deficiency of hkV4.3 activity, including  
 CC Alzheimer's disease and heart disease  
 CC

Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;

Query Match 94.2%; Score 1997; DB 6; Length 2064;

Best Local Similarity 97.3%; Pred. No. 0; Mismatches 0; Indels 57; Gaps 1;

Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

QY 1 GATTTCGTAACCTCAACTGAGTGTGTGCTGACGCTCCGCGGCTGCGGCCCAAGA 60  
 DB 1 GATTTCGTAACCTCAACTGAGTGTGTGCTGACGCTCCGCGGCTGCGGCCCAAGA 60  
 QY 61 GCTGAGTCAACATGCGCGCGGAGTTGCGGCTGCTGCTTTTGGCGGCTGCGGCC 120  
 DB 61 GCTGAGTCAACATGCGCGCGGAGTTGCGGCTGCTGCTTTTGGCGGCTGCGGCC 120  
 QY 121 ATCCGCTGATGCGCGTGGCCCACTGCGCCCAATGCGCCCTGCGCGCGGAGCAAG 180  
 DB 121 ATCCGCTGATGCGCGTGGCCCACTGCGCCCAATGCGCCCTGCGCGCGGAGCAAG 180  
 QY 181 CGGACGATGAGTGTATGCTCTCAACGATGAGTGGCGGAGTTCCAGACCTGAGAGCC 240  
 DB 181 CGGACGATGAGTGTATGCTCTCAACGATGAGTGGCGGAGTTCCAGACCTGAGAGCC 240  
 QY 241 ACGCTGAGCGCTACCCGAGACCTGCTGCGGAGCAAGAGAGTCTTCTTCAAC 300  
 DB 241 ACGCTGAGCGCTACCCGAGACCTGCTGCGGAGCAAGAGAGTCTTCTTCAAC 300  
 QY 301 GAGGACACCAAGAGTACTTTTTCGACCGGAGACCCCGAGTGTTCGCTGCTCAAC 360  
 DB 301 GAGGACACCAAGAGTACTTTTTCGACCGGAGACCCCGAGTGTTCGCTGCTCAAC 360  
 QY 361 TTCTACCGCAGCGGAGAGCTGACATCCCGGCTTACGAGTGCATCTGCTTCAAGCAG 420  
 DB 361 TTCTACCGCAGCGGAGAGCTGACATCCCGGCTTACGAGTGCATCTGCTTCAAGCAG 420  
 QY 421 GAGCTGGCTTCTTACCGGATCTCCGAGATCATCGGAGCTGCTGCTTACGAGAGTAC 480  
 DB 421 GAGCTGGCTTCTTACCGGATCTCCGAGATCATCGGAGCTGCTGCTTACGAGAGTAC 480  
 QY 481 AAGGACCGCAAGAGAGAGAAAGCCGAGAGGCTCATGACCAACCAAGTCCGAGAAC 540  
 DB 481 AAGGACCGCAAGAGAGAGAAAGCCGAGAGGCTCATGACCAACCAAGTCCGAGAAC 540  
 QY 541 CAGAGTCCATGCGCTGCTGAGCTCCGCGAGACATGTGGCGGAGCTTCCGAGAACCC 600  
 DB 541 CAGAGTCCATGCGCTGCTGAGCTCCGCGAGACATGTGGCGGAGCTTCCGAGAACCC 600  
 QY 601 CACACAGACGCTGCGCTGCTGCTTCTTACATGATGAGCTTCTTATGCTGCTCG 660  
 DB 601 CACACAGACGCTGCGCTGCTGCTTCTTACATGATGAGCTTCTTATGCTGCTCG 660  
 QY 661 GTCTATACCAACGCTGCTGAGAGCGGTGCGGAGCAAGTCCGCGGAGCAAGAGCTG 720  
 DB 661 GTCTATACCAACGCTGCTGAGAGCGGTGCGGAGCAAGTCCGCGGAGCAAGAGCTG 720  
 QY 721 CCGTGGCGGAGCGCTACTGCTGCTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 780  
 DB 721 CCGTGGCGGAGCGCTACTGCTGCTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 780  
 QY 781 TTCAACGCTGAGTACTTCTGCTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 840  
 DB 781 TTCAACGCTGAGTACTTCTGCTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 840  
 QY 841 AGCTCATGAGCATCATGAGAGTGTGTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 900  
 DB 841 AGCTCATGAGCATCATGAGAGTGTGTGCTTCTTCTGCTGAGCAGCGGCTGCTGATGC 900  
 QY 901 ACCAACAAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 901 ACCAACAAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960



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QY 961 ATCTTCAAGTTTTCCGGCCACTCCCAAGGCGCTGCGATCTCGGAGCTTACACACTGAAGAGC 1020
Db 961 ATCTTCAAGTTTTCCGGCCACTCCCAAGGCGCTGCGATCTCGGAGCTTACACACTGAAGAGC 1020
QY 1021 TGTGCTCCGAACTGGGCTTTCTTCTCTTCTCCCTCAACATGGCCATCATCTTTGGCC 1080
Db 1021 TGTGCTCCGAACTGGGCTTTCTTCTCTTCTCCCTCAACATGGCCATCATCTTTGGCC 1080
QY 1081 ACTGTGATGTTTATGTCGGAAGGGGCTCTCGGCGCAGAAAGTTTCAACATCCCTGGCC 1140
Db 1081 ACTGTGATGTTTATGTCGGAAGGGGCTCTCGGCGCAGAAAGTTTCAACATCCCTGGCC 1140
QY 1141 TCGTTTGGTACACATTTGTCAACATGACCACTGGGATACGAGACATGTGCTTAAG 1200
Db 1141 TCGTTTGGTACACATTTGTCAACATGACCACTGGGATACGAGACATGTGCTTAAG 1200
QY 1201 ACGATTGCGAGGAAGATCTTGGCTCATCTGCTCTTGTGAGGCGCTCTGTCTATTGGC 1260
Db 1201 ACGATTGCGAGGAAGATCTTGGCTCATCTGCTCTTGTGAGGCGCTCTGTCTATTGGC 1260
QY 1261 CTGCGAGTCCCTGTGATTTTTCACATTTAGCGGAGTTTACCAACGATTCAGAGACT 1320
Db 1261 CTGCGAGTCCCTGTGATTTTTCACATTTAGCGGAGTTTACCAACGATTCAGAGACT 1320
QY 1321 GATTAACGAGGACAAAAGAGCCGCTTTCAGAGATCCGTGTGACCAAAACAGGC 1380
Db 1321 GATTAACGAGGACAAAAGAGCCGCTTTCAGAGATCCGTGTGACCAAAACAGGC 1380
QY 1381 AGTTTCAATGATCTTGTGACACAGGAGGAGGAGGCTCTTCAACGAGGCGCTGAGCTG 1440
Db 1381 AGTTTCAATGATCTTGTGACACAGGAGGAGGAGGCTCTTCAACGAGGCGCTGAGCTG 1440
QY 1441 ACGGAGCAGCCAGAAAGAGAGCAATGGGCAAGCACTCATCTGAGAGGAGCAT 1500
Db 1441 ACGGAGCAGCCAGAAAGAGAGCAATGGGCAAGCACTCATCTGAGAGGAGCAT 1500
QY 1501 CATCACTGCTGCACTGCTGGAAGAAACCACTGGGTTGTCTTCTTGTGATGATCCC 1560
Db 1501 CATCACTGCTGCACTGCTGGAAGAAACCACTGGGTTGTCTTCTTGTGATGATCCC 1560
QY 1561 CTGTATCTGTAGGAAGCTCCACATCAAGAACAGAGTTTATGATGAGAGATGTTT 1620
Db 1561 CTGTATCTGTAGGAAGCTCCACATCAAGAACAGAGTTTATGATGAGAGATGTTT 1620
QY 1621 GAGCAGAACTGATGAGAGTTCAATGAGAACTCAACCTCAACCAAGAGCTCCCTCACTG 1680
Db 1621 GAGCAGAACTGATGAGAGTTCAATGAGAACTCAACCTCAACCAAGAGCTCCCTCACTG 1680
QY 1681 TCCAGCAGCCAGGCTCACTACCACTGCTGCTCCGCTGTAGTAAAGAACCAACAC 1740
Db 1681 TCCAGCAGCCAGGCTCACTACCACTGCTGCTCCGCTGTAGTAAAGAACCAACAC 1740
QY 1741 CTGCGCAATTTCTAATCTGCAAGTCTGCTGCGAGCATTCGCAAGGCTCAGACATC 1800
Db 1741 CTGCGCAATTTCTAATCTGCAAGTCTGCTGCGAGCATTCGCAAGGCTCAGACATC 1800
QY 1801 CATATCAGGAGAGTGAAGAGCTCCCTCAACCAAGTGTGCTGAGCTTAAATTTGAAA 1860
Db 1801 CATATCAGGAGAGTGAAGAGCTCCCTCAACCAAGTGTGCTGAGCTTAAATTTGAAA 1860
QY 1861 GCAAGCAGAGGAGTGAAGAGCTGCAAAACATCCAGATTCACACAGCATCATCAGC 1920
Db 1861 GCAAGCAGAGGAGTGAAGAGCTGCAAAACATCCAGATTCACACAGCATCATCAGC 1920
QY 1921 ATGCGCACTCCCGCAGGCTTAAACCCAGAGGAGGAAAGTGGGCAACCCCTGCGACGCCA 1980
Db 1921 ATGCGCACTCCCGCAGGCTTAAACCCAGAGGAGGAAAGTGGGCAACCCCTGCGACGCCA 1980
QY 1981 GGGCCCAAGAGAACTTCTTCAATACAGCAATGTGTGCAAGAGTCTGTCTTGTAA 2040
Db 1981 GGGCCCAAGAGAACTTCTTCAATACAGCAATGTGTGCAAGAGTCTGTCTTGTAA 2040
QY 1993 GGGCCCAAGAGAACTTCTTCAATACAGCAATGTGTGCAAGAGTCTGTCTTGTAA 1993

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QY 2041 AAATCCCGGCGCATGAGCGCGGAGAGATCGGAGCTGCGGCGCAATTCGCTTATAGTG 2100
Db 1984 AAATCCCGGCGCATGAGCGCGGAGAGATCGGAGCTGCGGCGCAATTCGCTTATAGTG 2043
QY 2101 AGTCGATTTAAAGCCGAATTC 2121
Db 2044 AGTCGATTTAAAGCCGAATTC 2064

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## RESULT 3

AAV61572 standard; cDNA; 2072 BP.

AAV61572;

11-JAN-1999 (first entry)

Human Kv potassium channel hKv4.3 (longer isoform) cDNA.

Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia; therapy; diagnosis; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..1965

FT /tag= a

PN M09842833-A2.

PD 01-OCT-1998.

PF 23-MAR-1998; 98WC-EP01901.

PR 27-MAR-1997; 97GB-0006377.

PR 09-DEC-1997; 97EP-00402971.

PR 11-DEC-1997; 97EP-00403007.

XX (SMIK ) SMITHKLINE BEECHAM LAB PHARM.

XX Bill NMA, Calmels TPG, Falvire JSP, Javre J, Rouanet S;

XX WPI, 1998-542277/46.

XX DR P-PSDB; AAW79590.

XX PS Claim 2; Page 26; 47pb; English.

XX CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see

XX CC AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.

XX CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated

XX CC from human heart cDNA by PCR amplification (see AAV61574-77). Another

XX CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589)

XX CC of hKv4.3 having 19 fewer amino acid residues. The invention relates to

XX CC these hKv4.3 polynucleotides and polypeptides and to methods for

XX CC producing such polypeptides by recombinant techniques. Also claimed are

XX CC methods for utilizing the hKv4.3 polynucleotides for the treatment of

XX CC subjects in need of enhanced or reduced activity or expression of hKv4.3

XX CC polypeptide. These include the treatment of cardiac arrhythmias and

XX CC Alzheimer's disease. The invention can also be used to identify agonists

XX CC and antagonists of hKv4.3, and to detect disease associated with

XX CC inappropriate hKv4.3 expression or activity

SQ Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;

Query Match 92.5%; Score 1962; DB 2; Length 2072;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 ATGGCGCGGAGAGTTCGCGCTGCTGCTTTTCCCGGAGCTGCGGCATCGGGTGGATG 132

Db 1 ATGGGGGAGAGAGTTGACAGCTGCTGCTTTTGCCCGGCTGCGGCACTGGGTGATG 60  
Qy 133 CCGGTGGCAACTGCCCCCATGTCCTTGGCCCCGGCCGACAAAGAGGCGAGATGAG 192  
Db 61 CCGGTGGCAACTGCCCCCATGTCCTTGGCCCCGGCCGACAAAGAGGCGAGATGAG 120  
Qy 133 CTGATTTCTTCAAGTGTGAGGCGGAGAGTTCCAGACTTGAGAGCCAGCTGAGAGCC 252  
Db 121 CTGATTTCTTCAAGTGTGAGGCGGAGAGTTCCAGACTTGAGAGCCAGCTGAGAGCC 180  
Qy 253 TACCCGAGACCCCTGCTGGGAGACAGAGAGAGAGTTCTTCTTCAACAGGACACCAAG 312  
Db 181 TACCCGAGACCCCTGCTGGGAGACAGAGAGAGAGTTCTTCTTCAACAGGACACCAAG 240  
Qy 313 GAGTACTTCTTGAACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCAACTTCTTACCGCAG 372  
Db 241 GAGTACTTCTTGAACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCAACTTCTTACCGCAG 300  
Qy 373 GGGAGAGCTGCACTACCCGCGCTACAGAGTGCATCTGCTGCTACAGAGAGCTGCGCTTC 432  
Db 301 GGGAGAGCTGCACTACCCGCGCTACAGAGTGCATCTGCTGCTACAGAGAGCTGCGCTTC 360  
Qy 433 TACGCACTCTCTCCGAGATCATCGGAGAGCTGCTGCTACAGAGAGTACAGAGACCGCAG 492  
Db 361 TACGCACTCTCTCCGAGATCATCGGAGAGCTGCTGCTACAGAGAGTACAGAGACCGCAG 420  
Qy 493 AGGAGAGACCGCGAGCGGCTCATGAGACAGACGACTCGAGAGACAGACGAGAGTCCATG 552  
Db 421 AGGAGAGACCGCGAGCGGCTCATGAGACAGACGACTCGAGAGACAGACGAGAGTCCATG 480  
Qy 553 CCTGCTGCTGCTTCCGCGACACATGTGCGGCGCTTGAAGAACCCCGACACGAGCAG 612  
Db 481 CCTGCTGCTGCTTCCGCGACACATGTGCGGCGCTTGAAGAACCCCGACACGAGCAG 540  
Qy 613 CTGGCCCTGCTTCTTCACTAGCTGAGCTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCT 672  
Db 541 CTGGCCCTGCTTCTTCACTAGCTGAGCTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 673 GTGGTGAAGACGGTCCGTCGCGACAGTCCCGGCGAGAGAGCTGCGCGGAG 732  
Db 601 GTGGTGAAGACGGTCCGTCGCGACAGTCCCGGCGAGAGAGCTGCGCGGAG 660  
Qy 733 CGCTACTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792  
Db 661 CGCTACTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Qy 793 TACCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852  
Db 721 TACCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 853 ATCATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912  
Db 781 ATCATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 913 GACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972  
Db 841 GACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 973 TCCCGGCACTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032  
Db 901 TCCCGGCACTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1092  
Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020  
Qy 1093 TATGCGGAGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1152  
Db 1021 TATGCGGAGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080  
Qy 1153 ACCATTGTACCATGACCACTGGGATTCGAGACATGTGCTTAAAGCATGTCAGAG 1212

Db 1081 ACCATTGTACCATGACCACTGGGATTCGAGACATGTGCTTAAAGCATGTCAGAG 1140  
Qy 1213 AAGATCTTGGCTCCATCTGCTCTTGAAGTGGCGCTGCTGCTATGTTGCTTCCCTGCACTGCT 1272  
Db 1141 AAGATCTTGGCTCCATCTGCTCTTGAAGTGGCGCTGCTGCTATGTTGCTTCCCTGCACTGCT 1200  
Qy 1273 GTGATTTGTTCCAACTTTAAGCGGATTTACACACGAAATCAGAGAGTGAATAAGCAGG 1332  
Db 1201 GTGATTTGTTCCAACTTTAAGCGGATTTACACACGAAATCAGAGAGTGAATAAGCAGG 1260  
Qy 1333 GCACAAAAGAGGCGCGCTTGCAGAGTCCGCTGTCGCAAAACAGGAGTTGATGA 1392  
Db 1261 GCACAAAAGAGGCGCGCTTGCAGAGTCCGCTGTCGCAAAACAGGAGTTGATGA 1320  
Qy 1393 TACCTGCAACGAGCGCAAGGCTCTTCAACGAGCGCTGAGCTGACGGGACCCCA 1452  
Db 1321 TACCTGCAACGAGCGCAAGGCTCTTCAACGAGCGCTGAGCTGACGGGACCCCA 1380  
Qy 1453 GAAGAGAGCACTAGGAGAGACCACTCACTCACTCACTCACTCACTCACTCACTCACTGCTG 1512  
Db 1381 GAAGAGAGCACTAGGAGAGACCACTCACTCACTCACTCACTCACTCACTCACTCACTGCTG 1440  
Qy 1513 CACTGCTGAGAAAAACCACTGAGTGTCTATCTTGTGATGATCCCTGTTATCTGTA 1572  
Db 1441 CACTGCTGAGAAAAACCACTGAGTGTCTATCTTGTGATGATCCCTGTTATCTGTA 1500  
Qy 1573 CGAACCTTCACCATCAGAACCAAGTTTATGATGAGAGATGTTTGAAGCACTGC 1632  
Db 1501 CGAACCTTCACCATCAGAACCAAGTTTATGATGAGAGATGTTTGAAGCACTGC 1560  
Qy 1633 ATGAGAGTTCAAGTCAACTACCACTCACTCACTCACTCACTCACTCACTCACTCACTGCTG 1692  
Db 1561 ATGAGAGTTCAAGTCAACTACCACTCACTCACTCACTCACTCACTCACTCACTCACTGCTG 1620  
Qy 1693 GGCCTCACTACCACTGCTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752  
Db 1621 GGCCTCACTACCACTGCTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
Qy 1753 AACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1812  
Db 1681 AACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
Qy 1813 AGTGAAGCGCTTCCCTCAACACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1872  
Db 1741 AGTGAAGCGCTTCCCTCAACACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
Qy 1873 CTGAGACCAAACTGAGAAACATCCAGATCAACAGGCTCATGAGATCCCACTGCC 1932  
Db 1801 CTGAGACCAAACTGAGAAACATCCAGATCAACAGGCTCATGAGATCCCACTGCC 1860  
Qy 1933 CCAGGCTTAACCCGAGAGGAGAAAGTGGCCACCCCTGCGAGGCCAGGCCCAACAG 1992  
Db 1861 CCAGGCTTAACCCGAGAGGAGAAAGTGGCCACCCCTGCGAGGCCAGGCCCAACAG 1920  
Qy 1993 AACATTCTTCAATACCAAGATGTTGCTCAAGTCTGCTGTTGATAA 2042  
Db 1921 AACATTCTTCAATACCAAGATGTTGCTCAAGTCTGCTGTTGATAA 1970

RESULT 4  
ADP91397  
ID ADP91397 standard; cdna; 1968 BP.  
XX AC ADP91397;  
XX DT 26-FEB-2004 (first entry)  
XX DE wild-type hkv4.3 cdna #SEQ ID 4.  
XX XX  
XX Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
XX tranquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;  
XX nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
XX blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;

KW tachycardia; congestive heart failure; epilepsy; stroke;  
 KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
 KW Parkinson's disease; gene; ss.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 1.1968  
 FT /\*tag= a  
 FT /product= "hKv4.3"

XX MO2003097682-A1.

XX 27-NOV-2003.

XX 14-MAY-2003; 2003MO-IB02453.

XX 15-MAY-2002; 2002GB-00011123.

XX 15-MAY-2002; 2002US-0378076P.

XX 15-MAY-2002; 2002US-0378131P.

XX (DEVG-) DEVGEN NV.

XX Kaletta TJ, Dewulf NE, Plaetinck GM,

XX WPI; 2004-061981/06.

XX P-PSDB; ADP91398.

XX New nematode worm expressing a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, useful for determining compounds that interact with the voltage-gated potassium channel.

XX Example 1; SEQ ID NO 4; 82pp; English.

XX The invention relates to a nematode worm that expresses a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, or its analog, mutant, variant, homolog, ortholog, part or fragment. The nematode worm is useful in determining whether a compound interacts with the voltage-gated potassium channel of the Kv4 family or whether a compound is an agonist, antagonist, opener and/or blocker of the voltage-gated potassium channel expressed by the nematode worm. The methods are used for identifying and developing compounds that interact with voltage-gated potassium channels of the Kv4 family. The compounds may be used in the development and/or preparation of compositions for pharmaceutical, agrochemical and/or veterinary use. These may be used in preparing compositions for preventing or treating diseases or conditions such as arrhythmia, tachycardia, congestive heart failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia, Alzheimer's disease or Parkinson's disease. The current sequence represents wild-type hKv4.3 cDNA.

XX Sequence 1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;

XX Query Match 92.4%; Score 1960; DB 12; Length 1968;

XX Best Local Similarity 99.7%; Pred. No. 0;

XX Matches 1963; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 ATGGCGCGCGGAGTGGCGGCTGGCTGCTTGGCCGGGCTGGGCGCATCGGTTGATG 132

DB 1 ATGGCGCGCGGAGTGGCGGCTGGCTGCTTGGCCGGGCTGGGCGCATCGGTTGATG 60

QY 133 CCGGTGGCAACTGCCCCCATGCCCCGCGCGCGCAAGAAAGAGCGGAGATGAG 192

DB 61 CCGGTGGCAACTGCCCCCATGCCCCGCGCGCGCAAGAAAGAGCGGAGATGAG 120

QY 193 CTGATTGCTCTCAAGTGAAGTGGCGGAGGTTCCAGACTTGAGAGACGCGTGGAGCGC 252

DB 121 CTGATTGCTCTCAAGTGAAGTGGCGGAGGTTCCAGACTTGAGAGACGCGTGGAGCGC 180

QY 253 TACCCGGAACACCCGCTGGGCGAGACGGAAGAAGATCTTCTTCAACGAGACACCAAG 312

DB 181 TACCCGGAACACCCGCTGGGCGAGACGGAAGAAGATCTTCTTCAACGAGACACCAAG 240

QY 313 GAGTACTTCTCGACCGGAGACCCCGAGTGTTCGCTGCTCACTTCAACCGCAGC 372

DB 241 GAGTACTTCTCGACCGGAGACCCCGAGTGTTCGCTGCTCACTTCAACCGCAGC 300

QY 373 GGGAGACTGCACTACCCCGGCTTACGAGTGCATCTCTGCTTACGACGAGAGCTGCTTC 432

DB 301 GGGAGACTGCACTACCCCGGCTTACGAGTGCATCTCTGCTTACGACGAGAGCTGCTTC 360

QY 433 TACGGATCCTCCCGAGATCATCGGAGATGCTGCTTACGAGAGTACAGAGACCGCAAG 492

DB 361 TACGGATCCTCCCGAGATCATCGGAGATGCTGCTTACGAGAGTACAGAGACCGCAAG 420

QY 493 AGGAGAACGCGAGCGGCTCATGACGAAACAGACTCGGAGAACACAGAGAGTCCATG 552

DB 421 AGGAGAACGCGAGCGGCTCATGACGAAACAGACTCGGAGAACACAGAGAGTCCATG 480

QY 553 CCTCGCTCAGCTTCGCGCAACATGATGCGGAGCTTGAAGAACCCCAACACGACAG 612

DB 481 CCTCGCTCAGCTTCGCGCAACATGATGCGGAGCTTGAAGAACCCCAACACGACAG 540

QY 613 CTGGCCCTGGTCTTACTACGATGATGAGCTTCTGATGCTGCTCGGTCATCAACAC 672

DB 541 CTGGCCCTGGTCTTACTACGATGATGAGCTTCTGATGCTGCTCGGTCATCAACAC 600

QY 673 GTGGTGAAGACGGTGGCGGTCGCGACAGTCCCGGCGAGAGAGAGCTGCGGGGAG 732

DB 601 GTGGTGAAGACGGTGGCGGTCGCGACAGTCCCGGCGAGAGAGAGCTGCGGGGAG 660

QY 733 CGCTACTCGGAGCTTCTTCTGCTGAGACAGGCTGCTGATGATCTTCAACCGTGGAG 792

DB 661 CGCTACTCGGAGCTTCTTCTGCTGAGACAGGCTGCTGATGATCTTCAACCGTGGAG 720

QY 793 TACCTCTGGGCTCTTGGCGGCTCCAGCGGCTACCGCTTCATCGGACGCTCATAGAGC 852

DB 721 TACCTCTGGGCTCTTGGCGGCTCCAGCGGCTACCGCTTCATCGGACGCTCATAGAGC 780

QY 853 ATCATGACGCTGGTGGCATCATGACCTTACTCATGCTGCTGATGACCAACAGAG 912

DB 781 ATCATGACGCTGGTGGCATCATGACCTTACTCATGCTGCTGATGACCAACAGAG 840

QY 913 GAGGTGCGGCGCTTCTGCTGAGCTCGGAGTTCGCGCTTTCAGAGATCTTCAAGTTT 972

DB 841 GAGGTGCGGCGCTTCTGCTGAGCTCGGAGTTCGCGCTTTCAGAGATCTTCAAGTTT 900

QY 973 TCCGCGCACTCCAGAGGCTGCGGATCTGGGCTACACTGAAGAGCTGTGCTCGAA 1032

DB 901 TCCGCGCACTCCAGAGGCTGCGGATCTGGGCTACACTGAAGAGCTGTGCTCGAA 960

QY 1033 CTGGGCTTCTTCTTCTTCTGCTGACCATGAGCATGATCTTTCGACTGTGATGTTT 1092

DB 961 CTGGGCTTCTTCTTCTTCTGCTGACCATGAGCATGATCTTTCGACTGTGATGTTT 1020

QY 1093 TATGCCGAGAGGGCTCTGCGCAGCAAGTTCAGCAAGATCCCTGCTGTTTGTATC 1152

DB 1021 TATGCCGAGAGGGCTCTGCGCAGCAAGTTCAGCAAGATCCCTGCTGTTTGTATC 1080

QY 1153 ACCATTGTACATGACACACTGAGATGCGAGATGCGGATGCTTGAAGAGATGTCAGGG 1212

DB 1081 ACCATTGTACATGACACACTGAGATGCGGATGCGGATGCTTGAAGAGATGTCAGGG 1140

QY 1213 AAGATCTTGGCTCATCTGCTCTTGAAGTGGCTGCTGATGCTTCCCTGCGAGTCCCT 1272

DB 1141 AAGATCTTGGCTCATCTGCTCTTGAAGTGGCTGCTGATGCTTCCCTGCGAGTCCCT 1200

QY 1273 GTGATTGTTTCCAACTTTAGCGGATTTTACACAGAAATCAGAGACTGATTAACGAGG 1332

DB 1201 GTGATTGTTTCCAACTTTAGCGGATTTTACACAGAAATCAGAGACTGATTAACGAGG 1260

QY 1333 GCACAAAAGAGGCGCGCTTGGCAGAGTCCGTTGAGCCAAACAGGAGATTTGAAATGCA 1392

DB 1261 GCACAAAAGAGGCGCGCTTGGCAGAGTCCGTTGAGCCAAACAGGAGATTTGAAATGCA 1320

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OY 1393 TACCTGACAGCAGGAGGAGGCTCCTCAACGAGGCGCTGAGGTGACGAGCCCA 1452
    |||
DB 1321 TACCTGACAGCAGGAGGAGGCTCCTCAACGAGGCGCTGAGGTGACGAGCCCA 1380
OY 1453 GAGGAGGAGCAGTGGGAGAGCACTCTCATCTGAGAGGCGAGCATCATCTGTCTG 1512
    |||
DB 1381 GAGGAGGAGCAGTGGGAGAGCACTCTCATCTGAGAGGCGAGCATCATCTGTCTG 1440
OY 1513 CACTGCTCGGAAAAAACCACTGGGTTTCTTCTTGTGTGATGATCCCTGTATTCTGTA 1572
    |||
DB 1441 CACTGCTCGGAAAAAACCACTGGGTTTCTTCTTGTGTGATGATCCCTGTATTCTGTA 1500
OY 1573 GGAACCTCCACCATCAAGAACCAAGATTATTGATGAGCAGATGTTTGTGAGAGAACTGC 1632
    |||
DB 1501 GGAACCTCCACCATCAAGAACCAAGATTATTGATGAGCAGATGTTTGTGAGAGAACTGC 1560
OY 1633 ATGGAGAGTTCAATGACAGAACTACCATCCACAGAGAGTCCCTCACTGTCCAGCAGCCA 1692
    |||
DB 1561 ATGGAGAGTTCAATGACAGAACTACCATCCACAGAGAGTCCCTCACTGTCCAGCAGCCA 1620
OY 1693 GGCCTCACTACCACTCTGCTCCCTGCTGTGTGTGTAAGAGACCAACACTGCTCCAACTCT 1752
    |||
DB 1621 GGCCTCACTACCACTCTGCTCCCTGCTGTGTGTGTAAGAGACCAACACTGCTCCAACTCT 1680
OY 1753 AACCTGCAGGCTACTGCGCTGGAGAGAGTCAAGAGGCTCAGACGATCCACTCCAGGAGC 1812
    |||
DB 1681 AACCTGCAGGCTACTGCGCTGGAGAGAGTCAAGAGGCTCAGACGATCCACTCCAGGAGC 1740
OY 1813 AGTGGAGAGCCTCTCCCTCAACACGAGTCCCTCAAGCTTTAATTGAAAGAGACAGCAGGA 1872
    |||
DB 1741 AGTGGAGAGCCTCTCCCTCAACACGAGTCCCTCAAGCTTTAATTGAAAGAGACAGCAGGA 1800
OY 1873 CTGAGACCAAACTGCAAAATCCCAATACCAACAGCCATCATGAGATCCCACTGCC 1932
    |||
DB 1801 CTGAGACCAAACTGCAAAATCCCAATACCAACAGCCATCATGAGATCCCACTGCC 1860
OY 1933 CCAGGCGTAAACCCGAGAGGAGGAGTGGGCGACCCCTGCGAGCCAGGCGCCCAACAG 1992
    |||
DB 1861 CCAGGCGTAAACCCGAGAGGAGGAGTGGGCGACCCCTGCGAGCCAGGCGCCCAACAG 1920
OY 1993 AACATTCCTTCATTAACGAGATGTTGTCAAGTCTCTGTCTTGTAA 2040
    |||
DB 1921 AACATTCCTTCATTAACGAGATGTTGTCAAGTCTCTGTCTTGTAA 1968

RESULT 5
AAV61571
ID AAV61571 standard; cDNA; 2104 BP.
XX
AC AAV61571;
XX
XX 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.
XX
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
XX
XX therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX CDS 1..1908
    /*tag= a
XX
XX MO9842833-A2.
XX
XX 01-OCT-1998.
XX
XX 23-MAR-1998; 98MO-EP001901.
XX
XX 27-MAR-1997; 97GB-00006377.
XX
XX 09-DEC-1997; 97EP-00402971.
XX
XX 11-DEC-1997; 97EP-00403007.

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XX (SMK ) SMITHKLINE BEECHAM LAB PHARM.
PA Brill AWA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
XX WPI; 1998-54227/46.
XX P-Psdb; AAW79589.
DR
XX
XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
XX Claim 2; Page 24; 47pp; English.
XX
XX This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3.
CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated
CC from human heart cDNA by PCR amplification (see AAV61574-77). Another
CC claimed polynucleotide (see AAV61572) encodes an isoform (see AAW79590)
CC of hKv4.3 having an additional 19 amino acids. The invention relates to
CC these hKv4.3 polynucleotides and polypeptides and to methods for
CC producing such polypeptides by recombinant techniques. Also claimed are
CC methods for utilizing the hKv4.3 polynucleotides for the treatment of
CC subjects in need of enhanced or reduced activity or expression of hKv4.3
CC polypeptide. These include the treatment of cardiac arrhythmias and
CC Alzheimer's disease. The invention can also be used to identify agonists
CC and antagonists of hKv4.3, and to detect disease associated with
CC inappropriate hKv4.3 expression or activity
SQ
Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other;
Query Match 86.7%; Score 1838; DB 2; Length 2104;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;
OY 73 ATGGGCGCGGAGAGTTGCGGCGCTTTTGGCCCGGAGTGGCGGAGTGGAGT 132
    |||
DB 1 ATGGGCGCGGAGAGTTGCGGCGCTTTTGGCCCGGAGTGGCGGAGTGGAGT 60
OY 133 CCGGTGGCAACCTGCCCATGCCCCCTGTGGCCCGGCGCAAGAACAGGCGAGATGAG 192
    |||
DB 61 CCGGTGGCAACCTGCCCATGCCCCCTGTGGCCCGGCGCAAGAACAGGCGAGATGAG 120
OY 193 CTGATGTCTTCAACGTGAGTGGGCGGAGTTTCCAGACTTGAAGACCAAGCTGAGAGCG 252
    |||
DB 121 CTGATGTCTTCAACGTGAGTGGGCGGAGTTTCCAGACTTGAAGACCAAGCTGAGAGCG 180
OY 253 TACCGGAGACCCCTGCTGGGAGCAGCAGGAGAGGATCTTCTTCAACGAGACCAAG 312
    |||
DB 181 TACCGGAGACCCCTGCTGGGAGCAGCAGGAGAGGATCTTCTTCAACGAGACCAAG 240
OY 313 GAGTACTTCTTCAACGTGAGTGGGCGGAGTTTCCAGACTTGAAGACCAAGCTGAGAGCG 372
    |||
DB 241 GAGTACTTCTTCAACGTGAGTGGGCGGAGTTTCCAGACTTGAAGACCAAGCTGAGAGCG 300
OY 373 GGGAAAGTGCATACCGGCGCTACGAGTGCATCTGTGCTTCAACGAGAGCTGGCTTC 432
    |||
DB 301 GGGAAAGTGCATACCGGCGCTACGAGTGCATCTGTGCTTCAACGAGAGCTGGCTTC 360
OY 433 TACGGCATCTCCCGGAGATCATGAGGAGACGCTGCTTCAACGAGAGCTGGAG 492
    |||
DB 361 TACGGCATCTCCCGGAGATCATGAGGAGACGCTGCTTCAACGAGAGCTGGAG 420
OY 493 AGGAGAAACGCGGAGGCTCATGAGACGACCAACTCGAGAAACAACAGAGTCCATG 552
    |||
DB 421 AGGAGAAACGCGGAGGCTCATGAGACGACCAACTCGAGAAACAACAGAGTCCATG 480
OY 553 CCTTCGCTCAGCTTCCGCGCAGACCAATGTGGGGCTTTCCAGAACCCCGACACAGCAG 612
    |||
DB 481 CCTTCGCTCAGCTTCCGCGCAGACCAATGTGGGGCTTTCCAGAACCCCGACACAGCAG 540
    |||
OY 613 CTGGCCCTGGCTCTTCAAGTACGATGAGCTTCTTCAATCGCTGCTCGTATCATCAAC 672
    |||

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Db	541	TTGGCCCTGCTTCTACTAGTACTGAGTACCTGCTTCTTCAATCGCTGTCTGTGCATACCAAC	600
OY	673	GTGGTGAAGACGGGTGCGGTGCGGACCGGTCCCGGGACAAAGAGCTGCGTGGGGAG	732
Db	601	GTGGTGGAGACGGGTGCGGTGCGGACCGGTCCCGGGACAAAGAGCTGCGTGGGGAG	660
OY	733	CGCTACTCGGGGCGCTTCTTGCGCTGGACACGGCGTGGCGTACGATCTTCAACGTTGAG	792
Db	661	CGCTACTCGGGGCGCTTCTTGCGCTGGACACGGCGTGGCGTACGATCTTCAACGTTGAG	720
OY	793	TACCTCTGCGAGGCTTTCGCGGCTCCAGCGGCTACCGGCTCATCTCGAGGTCATGAGC	852
Db	721	TACCTCTGCGAGGCTTTCGCGGCTCCAGCGGCTACCGGCTCATCTCGAGGTCATGAGC	780
OY	853	ATCATCGACGTGTGTGGCCATATGCTCCTACTACATCGGTCTGTGTCATGACCAACAGAG	912
Db	781	ATCATCGACGTGTGTGGCCATATGCTCCTACTACATCGGTCTGTGTCATGACCAACAGAG	840
OY	913	GACGTATCCGGGCGCTTGTGTACAGTCCGGGCTTTCCGCGTCTTCAAGATCTTCAAGTTT	972
Db	841	GACGTATCCGGGCGCTTGTGTACAGTCCGGGCTTTCCGCGTCTTCAAGATCTTCAAGTTT	900
OY	973	TCCGCGCACTCCAGAGGCGCTGCGGATCTCGGGACTACACACTGAAAGGTGCGCTCCGAA	1032
Db	901	TCCGCGCACTCCAGAGGCGCTGCGGATCTCGGGACTACACACTGAAAGGTGCGCTCCGAA	960
OY	1033	CTGGGCTTCTTCTTCTTCTCCCTCAACCAATGGCCATCATCTTTCGCACTGTGATGTTT	1092
Db	961	CTGGGCTTCTTCTTCTTCTCCCTCAACCAATGGCCATCATCTTTCGCACTGTGATGTTT	1020
OY	1093	TATGCCGGAAGGGGCTCTCGGCGCAGCAATTACACAGCATCTCTGCTCGTTTGGTAC	1152
Db	1021	TATGCCGGAAGGGGCTCTCGGCGCAGCAATTACACAGCATCTCTGCTCGTTTGGTAC	1080
OY	1153	ACCATTTGCACATATGACCACTGGGATATGCGGATATGCGTCAAGACATTTGCAAGG	1212
Db	1081	ACCATTTGCACATATGACCACTGGGATATGCGGATATGCGTCAAGACATTTGCAAGG	1140
OY	1213	AAGATCTTCGGCTCCATCTGCTCTTGAAGTGGCGCTCGTGTCAATTCCTCGACAGTCCCT	1272
Db	1141	AAGATCTTCGGCTCCATCTGCTCTTGAAGTGGCGCTCGTGTCAATTCCTCGACAGTCCCT	1200
OY	1273	GTGATTTGTTTCCAACTTTAGCCGGAATTTACCAACGGAATCGAGAGCTGATTAACGCAAG	1332
Db	1201	GTGATTTGTTTCCAACTTTAGCCGGAATTTACCAACGGAATCGAGAGCTGATTAACGCAAG	1260
OY	1333	GCACAAAAGAAAGGCCGCTTGCCAGATCCGTGTGGCCAAACAGGCAAGTTCGAATGCA	1392
Db	1261	GCACAAAAGAAAGGCCGCTTGCCAGATCCGTGTGGCCAAACAGGCAAGTTCGAATGCA	1320
OY	1393	TACCTGCAAGCAAGCGGAGCGGCTCTTCAACAGGCGCTGAGCTGACGGGACCCCA	1452
Db	1321	TACCTGCAAGCAAGCGGAGCGGCTCTTCAACAGGCGCTGAGCTGACGGGACCCCA	1380
OY	1453	GAAGAGAGCACATGGGCAAGACCACTCTCATCGAGGCGAGCATCATCACTGCTG	1512
Db	1381	GAAGAGAGCACATGGGCAAGACCACTCTCATCGAGGCGAGCATCATCACTGCTG	1440
OY	1513	CACGTCCGGAAGAAAAACAATGGGTTGCTCATCTTGTGGATGATCCCTGTTATCTGTA	1572
Db	1441	CACGTCCGGAAGAAAAACAAT-----	1461
OY	1573	CGAACCCTCCACCATCAAGAACCAACAGAGTTTATGATGAGAGATGTTTGAACAGACTGC	1632
Db	1462	-----AACCAAGAGTTTATGATGAGAGATGTTTGAACAGACTGC	1503
OY	1633	ATGAGAGTTCAATGCAAGACTTACCCATATCAACAGAAATCCCTCACTGTCCAGCCACCCA	1692
Db	1504	ATGAGAGTTCAATGCAAGACTTACCCATATCAACAGAAATCCCTCACTGTCCAGCCACCCA	1563
OY	1693	GGCTCATATCACCTGTGCTCCGTGTGTAGTAAAGAGACACACACTGCTCCAAATCTT	1752
Db	1564	GGCTCATATCACCTGTGCTCCGTGTGTAGTAAAGAGACACACACTGCTCCAAATCTT	1623

Oy		1755	AACCTGCAGGTATCTCGCTGCGGAGCATGCAAGAAGCTCAGCAGATCCATCATCCAGGGC	1812
Dd		1624	AACCTGCAGTACTCTGCTGCGGAGCATGCAAGAAGCTCAGCAGATCCATCATCCAGGGC	1683
Oy		1813	AGTAGAGCAGCCCTCCCTCACAAACCAGTCGCTCCAGCTTTAATTGGAAGCAGACGCGA	1872
Dd		1684	AGTAGAGCAGCCCTCCCTCCACAAACCAGTCGCTCCAGCTTTAATTGGAAGCAGACGCGA	1743
Oy		1873	CTTGAGACCAAACTGCMAAACATGCCAGATCACACAGCCATCATCAGATCCCCACTCCC	1933
Dd		1744	CTTGAGACCAAACTGCMAAACATGCCAGATCACACAGCCATCATCAGATCCCCACTCCC	1803
Oy		1933	CCAGGCGCTTAACCCGAGGGGGGAAAAGTCGCGCACCCCTGCGCAGCCGAGGCCCAACAG	1992
Dd		1804	CCAGGCGCTTAACCCGAGGGGGGAAAAGTCGCGCACCCCTGCGCAGCCGAGGCCCAACAG	1863
Oy		1993	AACATTCCTTCATTAACCCAGCAATGTTGTCAAAGTCTCTGTTGTAAAAATCCCGCGGC	2052
Dd		1864	AACATTCCTTCATTAACCCAGCAATGTTGTCAAAGTCTCTGTTGTAAAAATCCCGCGGC	1922
Oy		2053	CATGGC 2058	
Dd		1924	GAGGCG 1929	
RESULT 6				
ID	AAV61573			
XX	AAV61573 standard; cDNA; 2104 BP.			
AC	AAV61573;			
XX				
DT	11-JAN-1999 (first entry)			
XX				
DE	Human Kv potassium channel hKv4.3 cDNA.			
KX	Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;			
KM	therapy; diagnosis; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..1911		
FT		/*tag= a		
PN	W09842833-A2.			
XX				
PD	01-OCT-1998.			
XX				
PF	23-MAR-1998; 98WO-EP001901.			
XX				
PR	27-MAR-1997; 97GB-00006377.			
FR	09-DEC-1997; 97EP-00402971.			
PR	11-DEC-1997; 97EP-00403007.			
XX				
PA	(SMIK ) SWITKLIN BEECHAM LAB PHARM.			
XX				
PI	Bril AMA, Calmeis TPG, Faivre JSP, Jayre J, Rouanet S;			
XX				
DR	WPI; 1998-542277/46.			
XX	P-PsDB; AAW79591.			
PT	New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding			
PT	poly:nucleotide(s) useful in the treatment of disorders including cardiac			
PT	arrhythmias and Alzheimer's disease.			
XX				
PS	Claim 18; Page 27; 47pp; English.			
XX				
CC	This cDNA sequence codes for human Kv potassium channel hKv4.3 (see			
CC	AAW79591). It was isolated using expressed sequence tag analysis. The			
CC	sequence has about 91% identity in 1914 nucleotide residues with rat			
CC	Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAV61571-72)			
CC	are also claimed. The invention relates to hKv4.3 polynucleotides and			

CC polypeptides and to methods for producing such polypeptides by  
CC recombinant techniques. Also claimed are methods for utilizing hkv4.3  
CC polynucleotides for the treatment of subjects in need of enhanced or  
CC reduced activity or expression of hkv4.3 polypeptide. These include the  
CC treatment of cardiac arrhythmias and Alzheimer's disease. The invention  
CC can also be used to identify agonists and antagonists of hkv4.3, and to  
CC detect disease associated with inappropriate hkv4.3 expression or  
CC activity

XX Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;

Query Match 86.3%; Score 1830; DB 2; Length 2104;  
Best Local Similarity 96.1%; Pred. No. 0;

Matches 1909; Conservative 0; Mismatches 20; Indels 57; Gaps 1;

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Oy 73 ATGGCGCCGAGAGTGGCGCTGCTGCTTTTGGCCCGGGCTGCGGCATCGGGTGGATG 132
Db 1 ATGGCGCGAGAGTGGAGCTGCTGCTGCTTTTGGCCCGGGCTGCGGCATCGGGTGGATG 60

Oy 133 CCGGTGGCAACTGCGCCCATGCTGGCCCGGCGGACAAAGAGGCGAGATGAG 192
Db 61 CCGGTGGCAACTGCGCCCATGCTGGCCCGGCGGACAAAGAGGCGAGATGAG 120

Oy 193 CTGATTGCTCTCAAGTGAAGTGGGCGAGGTTCCAGACTTGGAGGACACGCTGGAGCGC 252
Db 121 CTGATTGCTCTCAAGTGAAGTGGGCGAGGTTCCAGACTTGGAGGACACGCTGGAGCGC 180

Oy 253 TACCCGGAACACCTGCTGGGAGCAACGAGAGAGGTTCTTCAACGAGAGCAACAG 312
Db 181 TACCCGGAACACCTGCTGGGAGCAACGAGAGAGGTTCTTCAACGAGAGCAACAG 240

Oy 313 GAGTACTTCTTGACACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCACTTACCGCAG 372
Db 241 GAGTACTTCTTGACACCGGAGACCCCGAGGTGTTCCGCTGCTGCTCACTTACCGCAG 300

Oy 373 GGGAGGCTGCACTACCGCGCTAGAGAGTCACTGCTTACGAGAGAGTGGCTTC 432
Db 301 GGGAGGCTGCACTACCGCGCTAGAGAGTCACTGCTTACGAGAGAGTGGCTTC 360

Oy 433 TACGCGATCTCTCCGAGATCATCGGGAGCTGCTGCTACGAGAGTACAGAGCCGCAAG 492
Db 361 TACGCGATCTCTCCGAGATCATCGGGAGCTGCTGCTACGAGAGTACAGAGCCGCAAG 420

Oy 493 AGGGAGAACGCCGAGCGGCTCATGAGCAACGAACTGGAGAGCAACAGAGTCCATG 552
Db 421 AGGGAGAACGCCGAGCGGCTCATGAGCAACGAACTGGAGAGCAACAGAGTCCATG 480

Oy 553 CCTCGCTCAGCTTCGCGAGACGATGAGGGGGCTTCGAGAACCCCAACGAGCAG 612
Db 481 CCTCGCTCAGCTTCGCGAGACGATGAGGGGGCTTCGAGAACCCCAACGAGCAG 540

Oy 613 CTGGCCCTGCTTCTTACTACGTGACTGCTTTCATGCTGTCTCGGTATCAACCAAC 672
Db 541 CTGGCCCTGCTTCTTACTACGTGACTGCTTTCATGCTGTCTCGGTATCAACCAAC 600

Oy 673 GTGGTGAAGAGGTCGCGGCGGCAACGCTCCCGGCGAGCAAGAGCTGCGGGAG 732
Db 601 GTGGTGAAGAGGTCGCGGCGGCAACGCTCCCGGCGAGCAAGAGCTGCGGGAG 660

Oy 733 CGCTACCTGGTGGCTTCTTCTGCTGAGCAACGGGCTGCTGATGATCTTCAACCGTGAAG 792
Db 661 CGCTACCTGGTGGCTTCTTCTGCTGAGCAACGGGCTGCTGATGATCTTCAACCGTGAAG 720

Oy 793 TACCTCTGCGGCTTCTTGGCGGCTCCAGCGGCTACCGCTTATCCGAGCTCATGAGC 852
Db 721 TACCTCTGCGGCTTCTTGGCGGCTCCAGCGGCTACCGCTTATCCGAGCTCATGAGC 780

Oy 853 ATCATGACAGTGGTGGCTCATATGCTCTTAATCATGCTGCTGATGACCAACAGAG 912
Db 781 ATCATGACAGTGGTGGCTCATATGCTCTTAATCATGCTGCTGATGACCAACAGAG 840

Oy 913 GACGTGTCGGGCGCTTGTGTCAGGCTCCGGGCTTCCGGGCTTTCAGAGATCTTCAAGTTT 972
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Db 841 GACGTGTCGGGCGCTTGTGTCAGGCTCCGGGCTTCCGGTCTTCAGAGATCTTCAAGTTT 900
Oy 973 TCCCGCACTCCAGAGGCTTGGGATCTCTGGGCTTACACTGGAAGAGCTGTGCTCCGAA 1032
Db 901 TCCCGCACTCCAGAGGCTTGGGATCTCTGGGCTTACACTGGAAGAGCTGTGCTCCGAA 960

Oy 1093 CTGGGCTTCTTCTTCTTCTTCCCTACAGATGGCAATCATCTTTGCAAGTGTGTTT 1092
Db 961 CTGGGCTTCTTCTTCTTCTTCTTCCCTACAGATGGCAATCATCTTTGCAAGTGTGTTT 1020

Oy 1093 TATGCGAGAGAGGCTCTCTCGGCGAGCAAGTTTCAACAGATCTCTGCTTGTGTTATC 1152
Db 1021 TATGCGAGAGAGGCTCTCTCGGCGAGCAAGTTTCAACAGATCTCTGCTTGTGTTATC 1080

Oy 1153 ACCATTGTACCATGACCAACTGGGATACGAGACATGTGCTTAAGACATTCAGAGG 1212
Db 1081 ACCATTGTACCATGACCAACTGGGATACGAGACATGTGCTTAAGACATTCAGAGG 1140

Oy 1213 AAGATCTTGGCTCATGTGCTCTTGAAGTGGCGCTCGGTGATTTGACCTGCACTGCT 1272
Db 1141 AAGATCTTGGCTCATGTGCTCTTGAAGTGGCGCTCGGTGATTTGACCTGCACTGCT 1200

Oy 1273 GTGATTGTTTCCAACTTTAGCGGATTTACCAACAGATCCAGAGCTGATTAACGACAG 1332
Db 1201 GTGATTGTTTCCAACTTTAGCGGATTTACCAACAGAGCTGATTAACGACAG 1260

Oy 1333 GCACAAAGAGAGGCGGCTTGCAGAGATCCGTGTGSCCAAAACAGGAGTTGATGCA 1392
Db 1261 GCACAAAGAGAGGCGGCTTGCAGAGATCCGTGTGSCCAAAACAGGAGTTGATGCA 1320

Oy 1393 TACCTGCAACAGAGGCAACGCGCTCTTCAACAGAGGCTGAGCTACGCGGACCCCA 1452
Db 1321 TACCTGCAACAGAGGCAACGCGCTCTTCAACAGAGGCTGAGCTACGCGGACCCCA 1380

Oy 1453 GAAAGAGAGCATGAGGCAACCACTCATCTGAGAGCCAGCATCATCACTGCTG 1512
Db 1381 GAAAGAGAGCATGAGGCAACCACTCATCTGAGAGCCAGCATCATCACTGCTG 1440

Oy 1513 CACTGCTTGAAGAAAAACACTGGGTGTCTTATCTTGTGATGCCCTGTATCTGTA 1572
Db 1441 CACTGCTTGAAGAAAAACACT----- 1461

Oy 1573 GGAACCTCACATCATGAAGAACCAAGATTTATGATGAGAGATTTTGAAGAACCTGC 1632
Db 1462 -----AACCAAGATTTATGATGAGAGATTTTGAAGAACCTGC 1503

Oy 1693 ATGAGAGTTCAATGACAGAACTAACCATCCACAAGAGTCCCTCATCTGCCAGCCCA 1692
Db 1504 ATGAGAGTTCAATGACAGAACTAACCATCCACAAGAGTCCCTCATCTGCCAGCCCA 1563

Oy 1693 GGCCTCACTACACCTGTGCTCCGCTGTGTAAGAGAACCAACACTGSCCAATTCT 1752
Db 1564 GGCCTCACTACACCTGTGCTCCGCTGTGTAAGAGAACCAACACTGSCCAATTCT 1623

Oy 1753 AACCTGCCAGTACTCGGCTGCGAGCATGCAAGAGCTCAGACAGATCAATCAAGGGC 1812
Db 1624 AACCTGCCAGTACTCGGCTGCGAGCATGCAAGAGCTCAGACAGATCAATCAAGGGC 1683

Oy 1813 AGTAGAGAGCCCTCCCTCACAACAGATGCTCCAGACCTTAATTTGAAGAGAGAGAGG 1872
Db 1684 AGTAGAGAGCCCTCCCTCACAACAGATGCTCCAGACCTTAATTTGAAGAGAGAGG 1743

Oy 1873 CTGAGACCAAACTGCAAAACATCCAGATCAACAGGCAATCATGAGATCCCACTCC 1932
Db 1744 CTGAGACCAAACTGCAAAACATCCAGATCAACAGGCAATCATGAGATCCCACTCC 1803

Oy 1993 CCAAGGCTAAACCCAGAGGGGAAAGTGGGCAACCCCTGCAAGCCCAAGGCCCAACAG 1992
Db 1804 CCAAGGCTAAACCCAGAGGGGAAAGTGGGCAACCCCTGCAAGCCCAAGGCCCAACAG 1863

Oy 1993 AACATTCCTTCATTAACAGCAATGTTGTCAAGGTCTCTGTGTAAATAATCCCGCGGC 2052
Db 1864 AACATTCCTTCATTAACAGCAATGTTGTCAAGGTCTCTGTGTAAATAATCCCGCGGC 1923
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QY 2053 CATGC 2058  
Db 1924 GAGGC 1929

RESULT 7  
AAH21247  
ID AAH21247 standard; cDNA; 2351 BP.  
XX AAH21247;  
AC  
XX  
XX 13-SBP-2001 (first entry)  
XX DE Human Kv4.2 cDNA.  
XX

Human: Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;  
KW neurodegenerative disease; ischemia; stroke; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;  
KM learning capacity; protein kinase activator; anti-arrhythmic; ss.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 433..2322  
FT /\*tag= a  
FT /product= "Kv4.2 alpha subunit"

DE19963612-A1.  
XX 12-JUL-2001.  
XX 29-DEC-1999; 99DE-01063612.  
XX 29-DEC-1999; 99DE-01063612.  
XX 29-DEC-1999; 99DE-01063612.  
XX (GENI-) FORSCHUNGSEBELSCHAFT GENION MBH.  
XX WPI: 2001-426637/46.  
XX P-PSDB; AAB66319.  
XX  
XX New potassium channel subunit proteins, useful for identifying and  
PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological  
PT agents.  
XX  
XX Claim 11; Page 18-21; 50pp; German.

XX This invention describes a novel potassium channel protein (I) that is  
CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium  
CC channels containing (I) are used to identify and test: (i) compounds for  
CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
CC activators of protein kinases. Host cells that express (I) can identify  
CC agents that do not interact significantly with channels and control I to  
CC (a quickly activated transient current), so lack the side effects of  
CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
CC for testing on organ cultures  
XX

SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Query Match 44.1%; Score 935.4; DB 4; Length 2351;  
Best Local Similarity 70.7%; Pred. No. 8.4e-176;  
Matches 1345; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTCACCATGCGCGCGAGTTGGCGCTGCTTTTCCCGGCGTGGCGCATCGG 125  
Db 423 AGTATCATGGCGCGCGGCGGTGGCAGCGGTGGCTCTTTTTCAGAGGCGCTATCGG 482  
QY 126 GTGATGCGCGTGGCGCGCATGCTCCCTTGGCGCC--GGCCGACAGAAAGCG 182  
Db 483 GTGATGCGCTGTGGCGCTTATGCGCGCTTCCCGGAGGAGAGAAAGGAC 542

QY 183 GCAGATGAGCTGATTTGCTCTCAACGTAGTGGCGGAGGTTCCAGACTGAGACAC 242  
Db 543 CCAAGATGCTCTCATTTGCTGCTGAATGTAGTGGCACCCGCTTCCAGACTGGAGAGAC 602  
QY 243 GCTGGAGCGCTTACCGGAGACACCTGTGGGCGAGCAGAGAAAGAGTTCTTTCAACGA 302  
Db 603 CCTGGAAAGCTTACCGAGACACTTACTGTGGGAGTTTGTAGAGGAGACTTTTTCACACCC 662  
QY 303 GGACACCAAGAGTACTTCTTGCACCGGAGACCCGAGGTTTCCGCTGGGCTCAACTT 362  
Db 663 AGAACTCAGCAGTATTTCTTTGACCGGTGACCCAGACATCTTCCGCAATCTGTAATTT 722  
QY 363 CTACCGCAGCGGAGAGCTGCACTACCGGCTTACAGAGTGCATCTTCTTACAGACGA 422  
Db 723 CTACCGCAGCTGGAGAGCTCCACTATCTCGCAGAGTGCATCTTCTTACAGATAGA 782  
QY 423 GCTGGCTTCTTACGAGTCTCTCCGAGATCATCGGAGCTGCTGTCTAGAGAGTACAA 482  
Db 783 ACTGGCTTCTTGGCTCATCCCGAAATCATCGGAGCTGCTGTATAGAGAGTACAA 842  
QY 483 GGACCGCAAGAGAGAGAGAGCGCGAGGCTCATGAGCAACAAGACTCGGAGAAACAACA 542  
Db 843 GGAATCGCAGCGAGAGAGAGAGCGCGAGGCTCGAGAGAGAGAGAGAGAGAGAGAG 902  
QY 543 GGAG--TCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599  
Db 903 GGAAGAGCGCTTGGCCACCATGACTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 962  
QY 600 CCACACACAG 659  
Db 963 CCACACACAG 1022  
QY 660 GGTATCATCAACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716  
Db 1023 TGTATCGAGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082  
QY 717 GCTGCGGAG 776  
Db 1083 ACTGCGCTGAG 1142  
QY 777 GATCTTACCGTGTGAGTACTCTGCGGCTCTTCCGAGCTCCAGCGCTTCAAT 836  
Db 1143 GATCTTACAGTGTGAGTACTCTGCGGCTCTTCCGAGCTCCAGCGCTTCAAT 1202  
QY 837 CGCAGAGCTATGAGATCATGACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896  
Db 1203 GCGTATGTATGATGATCATGACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262  
QY 897 CATGACCAACAG 956  
Db 1263 GATGACAGACAAATGAG 1322  
QY 957 CAGAGATCTTCAATTTTCCGCGCATCTCCAGAGGCTTGGGATCTGGGCTTACACTGAA 1016  
Db 1323 CAGAGATCTTCAATTTTCCGCGCATCTCCAGAGGCTTGGGATCTGGGCTTACACTGAA 1382  
QY 1017 GAGCTGAGCTCGGAG 1076  
Db 1383 GAGTGTGCTTCAATTTTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1442  
QY 1077 TGCCACTGTGATTTTATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136  
Db 1443 CGCTTACAGTATTTTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1502  
QY 1137 TGCTGTGTTTGTATCACTTGTACCATGACCACTGAGATACGAGAGATGTTGCC 1196  
Db 1503 TGCAGCTTCTGTATATACATCTGTACCATGACCACTGAGATACGAGAGATGTTGCC 1562  
QY 1197 TAAGAGATGAG 1256  
Db 1563 AAAAACCATAGCAG 1622  
QY 1257 TGCCCTGCGAGTCCCTGTGATTTTCAACTTTAGCCGAGATTTACACAGATCAGAG 1316



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Db      1623 TGCTTACTGTGTCGGTGATGTATCCAACTTTCAGTGGCACTTACCAACCAATTCACG 1682
Qy      1317 AGCTGATAAAGCGACGGGCAAAAGAGGCCGCTTGGCAGATCCGTGTGGCCAAAAC 1376
Db      1683 AGCAGACAAACGAAAGGGGCAAAAGAAAGCTAGACTGGGCGAGATCCGGGAGCCAAAAG 1742
Qy      1377 AGGCGTTGGAATGATACCTTGCACAGCAAGGGCAAGGGCTCTTCAACGAGCGCTGGA 1436
Db      1743 CGGAAGCGCAATGCTTACATGCAAGCAAGCAAGATGTTATCTCAGTAATCAGCTGCA 1802
Qy      1437 GCTGACGGGCAACCCGAGAAAGAGACACATGCGGCAAGACCTCACTCATGAGAGCCA 1496
Db      1803 GTTCTCAGAGGA---TGACGAGGCTTTTGTAGCAATCCGGCTCAGCTTTGAAACCCA 1859
Qy      1497 GCATCATCACTGTGCACTGCTGCGTGAAGAAAACCACTGGGTGTCTATCTTGTGATGA 1556
Db      1860 GCACCAACCACTGCTTCACTGCTGGAAGAAAACCACTGCTGCTGGAAGAAAACCACTG 1895
Qy      1557 TCCCTGTATCTGTACGAACCTCCACCATCAAGAACCAAGTTTATGTAGACAGAT 1616
Db      1896 -----GATACGAGTTTGTGAGCAAGT 1922
Qy      1617 GTTGAAGCAAGCTGATGAGAGATTCATGAGAACTACCATCAAGAAAGTCCCTC 1676
Db      1923 CTTTGAAGAAAGCTGATGAGAGATTCATGAGAACTACCATCAAGAAAGTCCCTC 1982
Qy      1677 ACTGTCCAGCAACCGAGGCTCTACCACTGCTGCTCCGTGTGTAGTGAAGAGCCAC 1736
Db      1983 ACTGTCTTCAAGCAAGAGGATCAACCAAGGCTGCTGTGTGTAGAGCAAGCAAGAAACTT 2042
Qy      1737 ACACCTGCCCAATTCTAACCTGCAAGCTACTGCTGCGGAGACATGCAAGAGCTCAGAC 1796
Db      2043 TCGCATCCCAATGCAATGTATGAGAAAGCCATCAAGGTATATACAAAGACTCAGAC 2102
Qy      1797 GATCCACATCCAGGCGAGTGAAGCAGCCCTCCCTCAACCACTGCTGAGCTTAATT 1856
Db      2103 GATTAGATCAAGATGTGTGAGAGAAACACTTGTCTTAACCCAGCTTAATTAAATGC 2162
Qy      1857 GAAAGCAGACGACGACTGAGACCAAACTGCAAAAATCCAGATCACCAAGCCATCAT 1916
Db      2163 CAAATGGAAGAGTGTGTTAACTTAACCTTAAGTGAACAACCTTATGTGACTAGCAATAT 2222
Qy      1917 CAGCATCCCACTCCCGCAGCGCTTAACCCCAAGAGGGGAAAGTCCGCCA 1965
Db      2223 AAGCATCCCAACCTCCAGTAAACCAACAGAGAGAGATAGGCCA 2271

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RESULT 8  
ADM10922  
ID ADM10922 standard; cDNA; 2351 BP.

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XX AC ADM10922;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human O647SgenomicContig3 homologue cDNA #4.
XX
XX KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX   cytostatic; gene therapy; human; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2003206918-A1.
XX
XX PD 06-NOV-2003.
XX
XX PF 05-FEB-2003; 2003US-00361811.
XX
XX PR 10-SEP-1999; 99US-00394374.
XX   01-MAY-2000; 2000US-00561778.
XX   15-AUG-2000; 2000US-00640173.
XX   07-SEP-2000; 2000US-00656668.

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PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
XX (CORI-) CORIXA CORP.
XX
XX PI Fanger GR, Fling SP;
XX
XX DR WPI; 2003-901037/82.
XX   P-Psdb; ADM10928.
XX
XX PT New polynucleotides encoding tumor proteins, treating or inhibiting the
XX   development of cancer, particularly ovarian cancer, and for stimulating
XX   and/or expanding T cells specific for a tumor protein.
XX
XX Example 12; SEQ ID NO 253; 221bp; English.
XX
XX CC This invention describes a novel ovarian tumour protein which can be used
XX   to detecting the presence of an ovarian cancer in a patient by
XX   stimulating and/or expanding T cells specific for the tumour protein. The
XX   products of the invention can also be used in a method to inhibit the
XX   development of a cancer in a patient comprising (a) incubating CD4+
XX   and/or CD8+ T cells isolated from a patient with at least one ovarian
XX   tumour protein, such that T cell proliferate and (b) administering to the
XX   patient the proliferated T cells. The cytostatic polynucleotides or
XX   polypeptides described in the invention are useful for treating or
XX   inhibiting the development of cancer, particularly ovarian cancer and for
XX   stimulating and/or expanding T cells specific for a tumour protein or for
XX   gene therapy.
XX
XX SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
XX
XX Query Match 44.1%; Score 935.4; DB 11; Length 2351;
XX   Best Local Similarity 70.7%; Pred. No. 8.4e-176;
XX   Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
XX
Qy 66 AGTCAACATGCGGCGCGAGTGGCGGCTGCTGCTTTTCCGGGCTGCGGCATCGG 125
Db 423 AGTATCATGTGCGGGGCGGAGTGGCAGCTGCTGCTTTTCAAGGGAGGCGGTATGG 482
Qy 126 GTGATGCGGATGCGCAACGCGCCCATGCGCCCTGCGCCCG---GGCCGCAAGAAACG 182
Db 483 GTGATGCTGTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
Qy 183 GCAGATAGCTGATTTGCTTCAACGTGAGTGGCGAGAGTTCACAGCTGAGAGCAC 242
Db 543 CCAAGATGCTCTCATTTGCTGAGATGAGTGGACCCGCTTCCAGAGCTGGAGAGCAC 602
Qy 243 GCTGAGGCTTACCCGAGACACCTGCTGCGGAGCAGCAGAGAAAGTCTTCTTCAAGA 302
Db 603 CCGGAAAGTAAACCCAGACCTTACCTGAGGAGTCTTGAAGAGGACTTTTCTTCAACC 662
Qy 303 GAGACCAAGAGATCTTCTTCAACCGGAGACCCGAGAGTCTGCTGCTGCTCAACTT 362
Db 663 AGAACTCAGCAATTTCTTGAACCGTGAACCCAGACATCTTCCGCAATCTGAATTT 722
Qy 363 CTACCGCAAGGAGAGTGCATACCTCCGCGCTTACAGATGATCTTCTGCTTACAGAGA 422
Db 723 CTACCGCACTGGAAAGCTCCACTATCTCTGCGCAGAGAGTGAATCTCTGTTAGATGA 782
Qy 423 GCTGCGCTTCTTACGAGCATCTCTCCGAGATATGAGGAGCTGCTGCTTCAAGAGTACA 482
Db 783 ACTGCGCTTCTTGTGCTTCTTCACTCCGGAATATGAGGAGCTGCTTATGAGGATACA 842
Qy 483 GAGCGCAAGAGAGAGAGAGCGCGAGCGCTCATGAGAGCAAGACATGAGAGAACCA 542
Db 843 GATGCGAGGAGAGAGAGAGCGCGAGCGCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 902
Qy 543 GAG---TCCATGCTTGTGCTCAGCTTCCGCAAGACATGAGAGAGAGAGAGAGAGAG 599
Db 903 GAGAGGCGCTTGTCCCAACATGATGCAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 962

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OY	600	CAACACGAGCAGCGTGGGCCCTGGTCTTCTACTATGATGATGAGGCTCTTCAATGCGTGC	659
Db	963	CCAAACACGACGAGATGGCCCTGGTGTCTTACTATGATCAAGGAGTTCATATGCGCTGC	1022
OY	660	GGTCATCAACCAACGCTGTGTGAGACGCTGCGCTGGCGACCGGTCCCGGG--CAGCAAGA	716
Db	1023	TGTATCGCGGAATGTGGTGAAGACATGTGCGGTGGGATCAAGCCAGGTGCATTAAGA	1082
OY	717	GCTGCGGTGCGGGAGCGCTACTGCGTGGCTTCTTCTGCTGGACACCGCGTGTGCAT	776
Db	1083	ACTGCCCCGTGTGAAGCGGTATGCTGTGGCCCTTCTTCTGCTTGGACACCGCGCTGCTCAT	1142
OY	777	GATCTCAACGCTGAGATACCTCCGCGGCTCTTGCGGCTCCGACCGCTACCGCTCAT	836
Db	1143	GATCTCAACATTAATTAATTTTGTCTTCCGTGGCTGACAGCCGCTATGTATCCGTTTGT	1202
OY	837	CCGACGCTCATGAGCATCATCGACGCTGTGGCCATCATGCTCCCTACTACATCGCTCTGT	896
Db	1203	GCGTATGTCTATGATGATCATCGACGCTGTGGCCATCCTGCTTATTAACATTTGGGCTGT	1262
OY	897	CATGACCAACACGAGACGCTGTCCGCGCTTCTGTCACGTCCGGGTCTTTCGCGTCTT	956
Db	1263	GATGACAGACATATGAGACGTCACGCGGAGCCTTTGTCACTCCGAGCTTCCGCGTCTT	1322
OY	957	CAGGATCTTCAAGTTTTCCGCGCATCCACAGGCGTGGATCCGCGGCTTCAACATGAA	1016
Db	1323	CAGGATCTTAAATTTTCCGCGCATCTCAAGCGCTGGCATCTTGGGATCAACATGAA	1382
OY	1017	GAGCTGTGCTCCGAACTGGGCTTCTTCTTCTCTCCCTCAACATTTGGCATCATCTT	1076
Db	1383	GAGTTGTGCTCAGAAATTTGGGCTTCTTCTTCTCGTCAACATTTGGCATCATCTT	1442
OY	1077	TGCCACTGTGATGTTTTATGCCAGAGAGGCTCCTCGGCCAGCAATTCACAGCATCC	1136
Db	1443	CGTCAAGATTAATTTCTACGACAGAGAGGGCTTTCGCTAGCAAGTTCAACACATCC	1502
OY	1137	TGCGCTCGTTTTGATACCACTTGTACCATGACATGAGATCCGAGATCGAGCATGTGGC	1196
Db	1503	TGCAAGCTTCTGTATATCATGTCATCCATACAACTAAGGATGTGTGACATGTGCC	1562
OY	1197	TAAAGCATTCAGAGGAGATCTTCGCTCATCTGCTCTTGTAGTGGCGTCTGTGCAT	1256
Db	1563	AAAAACCATAGCAGGAGAAATTTTGGTCTATCTGTTCGCTGATGGGGCTTGGTCTAT	1622
OY	1257	TGCCCTGCGAGTCCCTGTGATTTTCCACTTAAAGCCGATTTTACACAGAAATCAAG	1316
Db	1623	TGCTCTACTGTGTCGGTATTTGTATCACTTGACGTGACATTAACACAGAAATCAAG	1682
OY	1317	AGCTGATTAAGCAGAGGACAAAGAGAGCCCGCTTCCAGAGATCCGTGTGGCCAAAC	1376
Db	1683	AGCAGACAAACGAGAGGACAAAGAAAGCTGACGTGACAGGATCCCGGACGCCAAAG	1742
OY	1377	AGGCACTTCGATGCTACCTGTGACAGGAGGCAAGGGCTCCCTCAACGAGGCGCTGGA	1436
Db	1743	CGAAGCGCAAAATGCTTACATGACAGCAAAACGAAATGTTTACTCAATATCAAGCTGCA	1802
OY	1437	GCTGACGGGACCCCGAAGAGAGACATGGGCAAGCACTTCATCTCATCGAGAGCCA	1496
Db	1803	GTCTCAAGAGGA---TGAAGAGGCTTTTGTATAGCAAAATCCGGCTCCAGCTTTGAAACCA	1859
OY	1497	GCAATATCACTGCTGTCACTGCTGTGAAAAAACCACTGGGTTGTCTTATCTTGTGATGA	1556
Db	1860	GCAACCAACCTGCTTCACTGCTGTGAAAAAACCA-----	1895
OY	1557	TCCCTGTTATCTGAAGAACTTCACCATCAAGAACACGAGTTTATGTAGAGAGAT	1616
Db	1896	-----GATATCAAGATTTTGTGAGCAAGT	1922
OY	1617	GTTTGAGCAGAACTGCATGAGAGTTCAATGCAAGAACTTACCATTCACAAAGTCCCTC	1676
Db	1923	CTTTAAGAAAGCTCATGAGAAAGTTGCAACTGTTAATGTCTTCAATCAACAGTCCCTC	1982
OY	1677	ACTGTTCACCAACCCAGGCTCTCACTACACTGCTGCTCCGCTGTGATTAAGAAAGCAAC	1736

Accession	Sequence	Position
D8	ACTGCTTTCAACAACAAAGATGCACGACACTGCTGTTCCAGACGACAAAAAACTTT	2042
QY	ACACCTGGCCCAATTCTTAACCTGGCAGCTACTCGCTCTGGAGCATGTGAAGGCTCAGAC	1796
D8	TCCGATCCCAATGCCAATGTATATGAGAACCATCAAGTATGTTTACAGAACTCAGCAC	2102
QY	GATCCACATCCAGGGCAGTGAAGCCCTCCCTCACAACCATGTCTCCACGCTTAATTT	1856
D8	GATTCAATCATGATGTGTGAGAGAAACCTCTGTCTTAACAGCCGATTCAGTTTAAATGC	2162
QY	GAAGCAGACGACGGACTGAGACCAACCTGCAAAATCCAGATCAACACGACCATCAT	1916
D8	CAAAATGAGAAAGTGTGTAACTTAACTGGAACAACCTTATATGACTACACGAATATAT	2222
QY	CAGATATCCCACTCCGCCAGCGCTTAACCCGAGAGGGGAAAAAGTGGGCA	1965
D8	AAGCATCCCAACACTCTCATGTAACCAACCAAGAGGAGACGATAGGCCA	2271

RESULT 9  
 ADJ11252  
 ID ADJ11252 standard; DNA; 2351 BP.  
 XX  
 AC ADJ11252;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human ovarian tumour antigen DNA SeqID 253.  
 XX  
 KW human; dg; ovarian cancer; immunogenic; antibody;  
 KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;  
 KW cyostatic; gene.  
 XX  
 OS Homo sapiens.  
 PN US2003232056-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PE 14-FEB-2003; 2003US-00369186.  
 XX  
 PR 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825284.  
 PR 02-OCT-2001; 2001US-00970366.  
 PR 02-AUG-2002; 2002US-00212677.  
 PR 05-FEB-2003; 2003US-00361811.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Fanger GR, Fling SP;  
 XX  
 DR WPI; 2004-178717/17.  
 DR P-PSDB; ADJ11258.  
 XX  
 XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor  
 PT polypeptide, useful as probes or primers for detecting presence of cancer  
 PT in a patient.  
 XX  
 PS Example 12; SEQ ID NO 253; 222bp; English.  
 XX  
 CC This invention relates to novel isolated polynucleotides and methods for  
 CC the therapy and diagnosis of cancer, particularly ovarian cancer.  
 CC Specifically, it refers to these polynucleotides and the encoded  
 CC polypeptides thereof, as well as immunogenic peptides, antibodies,  
 CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)  
 CC that are targeted to those cells expressing the proteins of interest. The  
 CC present invention describes methods that are useful for stimulating and/  
 CC or expanding T cells specific for a tumourigenic protein (i.e. T cell







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QY 897 CATGACCAACAGAGACGTCGCGGCGCTTCGACGCTCCGGGCTTCCGCGCTT 956
D 1799 GATGACGACAAATGAGAGACGTCAGCGGACCTTGTGACATCCGAGTCTTCGGGCTT 1858
QY 957 CAGGATTTCAAGTTTCCCGGCACTCCAGGCGCTCGGGATCTGGGGTCAACACTGAA 1016
D 1859 CAGGATCTTAAAGTTTCCCGGCACTCTCAAGGCTCGCGATCTGGGGTCAACACTGAA 1918
QY 1017 GAGTGTGCTCCGAACTGGGGCTTCTTCTCTCTCCCTCAACATGGGCAATCATCTT 1076
D 1919 GAGTGTGCTCCGAAATGGGCTTCTTCTCTCTCTCCCTCAACATGGGCAATCATCTT 1978
QY 1077 TGCCTGTGATGTTTATGCGGAGAGGCGCTCCGCGGCAAGTTCAACAGCATCCC 1136
D 1979 CGGTACAGTTATGTTTACGAGAGAGAGGGGTCTTGGCTAGAGAACTTCAACAGCATCCC 2038
QY 1137 TGCCTGTTTGTGTAACCATTTGTCACATGACCACTGGGATACGGAATCATGTGCC 1196
D 2039 TGCAGCTCTGTGATACCATCTGTCACATGACCACTAGGGATGATGACATGTGCC 2098
QY 1197 TAAGACATTTGAGGAGAGATCTTGGGCTCATCTGCTCTGATGGGCGTCTGTCAT 1256
D 2099 AAAAACAATGACAGGAGAAATTTTGTGTTCTATCTGTTGCTGAGTGGGCTTGTGTCAT 2158
QY 1257 TGCCTGCGAGTCCCTGTGATGTTTTCCACTTTAGCGGATTTACCAAGATCATGAG 1316
D 2159 TGCCTGCTGTTTCCGGTGAATGATCAACTTCACTGATGATCAACACAGATCAACG 2218
QY 1317 AGCTGATMAACGACGGGCAAAAAGAGCGGCTGTCAGGATCCGTGTGGCAAAAC 1376
D 2219 AGCAGACAAACGAGGGGCAAAAAGAGCTAGACTGCGGATCCGGGCAAGCAAAAG 2278
QY 1377 AGGAGTTGCAATGATACCTGCAAGAGCGGAGCGGCTCTCAACGAGGCGTGA 1436
D 2279 CGGAAGCGCAATGCTTACATGACAGAGAAAGGATTTACTCACTAATCATGCTGCA 2338
QY 1437 GCTGACGGGCAACCCAGAGAGAGACATGGGAGAGACCACTCATCTCAAGAGCCA 1496
D 2339 GTCCTCAGAGGA---TGAGGAGGCTTTGTTAGAAATTCGGGCTCAAGCTTTGAAACCA 2395
QY 1497 GCATCATCACTGCTGCACTGCTGGAAGAAACCACTGGGTTGCTTCTGTGATGA 1556
D 2396 GCACACACACCTGCTTCACTGCTGGAAGAAACCACTGCTGCTGCTGCTGCTGCTG 2431
QY 1557 TCOCCTGTTATCTGTAAGAACCTCCACCATCAAGACGAGTTTATGATGAGCAT 1616
D 2432 -----GAAATCAAGATTTGTAAGCAAGT 2458
QY 1617 GTTTCAGCAGAACTGATGAGAGTTCAATGACAGAACTACCATCAACAGAAAGTCCCTC 1676
D 2459 CTTTGAAGAAAGCTGATGAGAGTTGCACTGTAATGCTCTCAAGTCAACATCTCTTC 2518
QY 1677 ACTGTCAGCCACCCAGGCTCACTACCACTGCTGCTCCGCTGTGTAAGAAAGCAAC 1736
D 2519 ACTGTCCTTCAACAAAGAGATCACACGACCTGCTGTTCAAGAGAACAAAGAAATTTT 2578
QY 1737 ACACCTGCGCAATCTAACCCTGCGAGCTACCTGCGTGGAGAGATGAGAGCTCACAC 1796
D 2579 TCGCATCCCAATGCAATGATATAGAGAGCATCAAGATGATGATCAAGAACTACAGAC 2638
QY 1797 GATTCACATCCAGGAGAGTGAAGAGCCCTCCCTCAACACAGTGCCTCAAGCTTAATTT 1856
D 2639 GATTCAGATGATGATGATGAGAGAAACCTCTGCTAAGAGCGGATCAAGTTAAATGC 2698
QY 1857 GAAAGCAGAGAGAGCTGAGACCAAACTGCAAAATCCAGATCAACACAGCATCAT 1916
D 2699 CAATATGGAAGAGTGTGTTAAACTGAACTGAACTATGATGATGATGATGATGATGAT 2758
QY 1917 CAGATCCCACTCCCAAGCGCTAACCAGAGGGGAGAGTGGGCA 1965
D 2759 AAGATCCCAACACTCCAGTAAACACACAGAAAGAGAGATGAGGCA 2807
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RESULT 12
ADMI0921
ID ADMI0921 standard; cDNA; 5333 BP.
XX
AC ADMI0921;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue cDNA #3.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytoskeletal; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
XX 01-MAY-2000; 2000US-00561778.
XX 15-AUG-2000; 2000US-00640173.
XX 07-SBP-2000; 2000US-00656668.
XX 14-NOV-2000; 2000US-00713550.
XX 03-APR-2001; 2001US-00825294.
XX 02-OCT-2001; 2001US-00970966.
XX 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2003-901037/82.
XX
DR P-PSDB; ADMI0927.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
XX development of cancer, particularly ovarian cancer, and for stimulating
XX and/or expanding T cells specific for a tumor protein.
XX
PS Example 12; SEQ ID NO 252; 221bp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
XX to detecting the presence of an ovarian cancer in a patient by
XX stimulating and/or expanding T cells specific for the tumour protein. The
XX products of the invention can also be used in a method to inhibit the
XX development of a cancer in a patient comprising (a) incubating CD4+
XX and/or CD8+ T cells isolated from a patient with at least one ovarian
XX tumour protein, such that T cell proliferate and (b) administering to the
XX patient the proliferated T cells. The cytostatic polynucleotides or
XX polypeptides described in the invention are useful for treating or
XX inhibiting the development of cancer, particularly ovarian cancer and for
XX stimulating and/or expanding T cells specific for a tumour protein or for
XX gene therapy.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
XX
Query Match 44.1%; Score 935.4; DB 11; Length 5333;
Best Local Similarity 70.7%; Pred. No. 9,4e-176;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;
QY 66 AGTCACATGGGGGGGGAGGTTGGCGGCTGGGCTGTTGGCCGGGCTGGGCAATCGG 125
D 959 AGTAATCATGCGCGGGGGTGGCAGGTGGCTGCTTGGCAAGGAGCAAGGCGCTATCGG 1018
QY 126 GTGATGCGCGGTGGCAACTGACCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 182
D 1019 GTGATGCGCGGTGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1078
QY 183 GCAGATGACCTGATGCTCTCAACGTGATGGGCGGAGGTTCCAGACTGAGAGACAC 242
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PR 03-APR-2001; 2001US-00825294.  
PR 02-OCT-2001; 2001US-00970966.  
PR 02-AUG-2002; 2002US-00212677.  
PR 05-FEB-2003; 2003US-00361811.  
XX  
XX (CORI-) CORIXA CORP.  
XX Fanger GR, Fling SP;  
XX WPI; 2004-178717/17.  
XX P-PSDB; ADJ11259.  
XX  
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor  
XX polypeptide, useful as probes of primers for detecting presence of cancer  
XX in a patient.  
XX  
XX Example 12; SEQ ID NO 254; 222pp; English.  
XX  
XX This invention relates to novel isolated polynucleotides and methods for  
XX the therapy and diagnosis of cancer, particularly ovarian cancer.  
XX Specifically, it refers to these polynucleotides and the encoded  
XX polypeptides thereof, as well as immunogenic peptides, antibodies,  
XX antigen presenting cells (APCs) and immune system cells (e.g. T cells)  
XX that are targeted to those cells expressing the proteins of interest. The  
XX present invention describes methods that are useful for stimulating and/  
XX or expanding T cells specific for a tumourigenic protein (i.e. T cell  
XX therapy). Furthermore, compositions can be used for the diagnosis,  
XX treatment and/or prevention of ovarian cancer by stimulating an immune  
XX response in a patient. Accordingly, these compositions exhibit cytostatic  
XX activity. This polynucleotide is a human ovarian tumour antigen DNA  
XX sequence given in an exemplification of the invention.  
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
Query Match 44.1%; Score 935.4; DB 12; Length 5333;  
Best Local Similarity 70.7%; Pred. No. 9,4e-176;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;  
QY 66 AGTACCATGAGCGCGAGAGTGGCGGCTGCTCTTTGCGCGGCTGCGGCATCGG 125  
DB 959 AGTATATATGCGCGCGGCGGAGTGGCGAGCTGCTGCTTTTGCAGAGGCAACGCTATCGG 1018  
QY 126 GTGGATCCGCTGCGCACTGCGCCCATGCCCCCTGGCCCC--GGCCGACAAAGCAAGCG 182  
DB 1019 GTGGATCCTGTGGCTCGGCGGCTATGCGGCTCCCGGAGGAGAGAAAGAGAC 1078  
QY 183 GCGAGATGAGCTGATTTCTCTCAACGTGAGTGGCGGAGTTCCAGACCTGGAGAGCAC 242  
DB 1079 CCAAGATGCTCTATTTGTGTGATGTGATGGGACCCCGCTTCAGACGTGGCAGGACAC 1138  
QY 243 GGTGAGACGCTACCCGAGACACCTGTGGGAGCAGCAGAGAGAGTTCTTCTTCAACGA 302  
DB 1139 CTTGGAACGTTTACCAACACTCTACTGGGCACTTCTTGAGAGGACCTTTTCTTACACC 1198  
QY 303 GAGACCAAGAGATCTTCTTTCGACCGGAGACCCGAGGTGTTCCGTGCTGCTCAACTT 362  
DB 1199 AGAAATCTACGACGATTTCTTTCGACCGTACCCAGACATCTTCGCGACATCTGAAATT 1258  
QY 363 CTACCGGAGCGGAGAGCTGACACTACCCGCTTACGATGATCTCTCTCTTACAGACGAG 422  
DB 1259 CTACCGGAGCTGGAGAGCTCACTATCTCTGCGCAGATGATCTCTCTTACGATGAGA 1318  
QY 423 GGTGAGCTTCTTACGAGCATCTCCCGAGATCATCGGAGAGCTGTGCTACGAGAGTCAAA 482  
DB 1319 ACTTGCTTTCTTTGGCTCTATCCCGAATATATGGGAGCTGCTGTTTATGAGAGTCAAA 1378  
QY 483 GAGCCGCAAGAGGAGAGACCGCGAGCGCTCATGAGACAGACACTCGAGAGAAACAACA 542  
DB 1379 GAGTCGAGGAGAGAGACCGCGAGCGCTGCGAGAGAGAGCGGATACCGAGACCGCTGG 1438  
QY 543 GAGG---TTCATGCTCTGCTGCTGCTTCCGCAACATGTGGGCGCTTTCGAGAACCC 599  
DB 1439 GAGAGGCGCTTTCACCATGATGCTGCAAGGAGAGGCTTGGAGGCGCTTTCGAGAACCC 1498

QY 600 CCACACACAGACGCTGGCCCTGTGCTTCTTCAACGTAAGTGGCTTCTTATGCTGCTTC 659  
DB 1499 CCACACACAGACGATGGCCCTGTGCTTCTTCAACGTAAGTGGCTTCTTATGCTGCTTC 1558  
QY 660 GGTATCATCAACAGTGTGTGAGAGACGCTGCGGCGCAAGGCTCCCGG---CAGCAAGA 716  
DB 1559 TGTCACTGGGAATGTGTGTGAAAACAGTGTGCGGAGTCAAGCCCGAGTCACTTAAAGA 1618  
QY 717 GGTGCGGTGCGGAGAGCGCTACCTGCGTGGCTCTTCTCTCTCTGACACAGCGGCTCAT 776  
DB 1619 ACTGCGCTGTGAGAGCGGTATGCTGTGGCTCTTCTCTCTGACACAGCGGCTCAT 1678  
QY 777 GATCTTACCGTGGAGTACCTCTGCGGCTCTTTCGCGGCTCCAGCGCTTACGCTTCAT 836  
DB 1679 GATCTTACAGTGAATATTGCTTGGCTGCGTGGCGAGGCTTACGCTTACGCTTTCAT 1738  
QY 837 CCGCAGCGCTTACGATCATGACGCTGTGGCGCATCATGCTTACTATCATGCTGTGCT 896  
DB 1739 GCGTATGTCTATGATGATCATGACGCTGTGGCGCATCTGCTTATTAATGAGGCTGAT 1798  
QY 897 CATGACCAACAGAGAGAGTGTCCGCGCTTCTGACAGCTCCGCGCTTCCGCGCTT 956  
DB 1799 GATGACAGACATGAGAGAGTCAAGCGAGCTTGTGACACTCCGAGCTTCCGCGCTT 1858  
QY 957 CAGATCTTCAAGTTTCCCGCCTCCAGGCGCTGCGAGTCTTGGGCTTACACACTGAA 1016  
DB 1859 CAGATCTTCAAGTTTCCCGCCTCCAGGCGCTGCGAGTCTTGGGCTTACACACTGAA 1918  
QY 1017 GAGCTGTGCTCGGACAGTGGGCTTCTTCTTCTTCCCTTCAACATGCGCATCATCTT 1076  
DB 1919 GAGTGTGCTCGGACAGTGGGCTTCTTCTTCTTCCCTTCAACATGCGCATCATCTT 1978  
QY 1077 TGGCAGTGTGATGTTTATGCGAGAGAGGCTCTGCGCAGCAGTTCACAGATCC 1136  
DB 1979 CGCTTACGTTATGTTTCTTACGAGAGAGAGGCTTGGCTAGCAAGTTTACAGCATCC 2038  
QY 1137 TGGCTGTGTTTGTATACCACTTGTCACTGACACACTGAGTATGAGAGAGATGTC 1196  
DB 2039 TGCAGCTTGTGTATATACATGCTACATGACACACTAGGGTATGATGACATGTC 2098  
QY 1197 TAAAGATTTGACGAGGAAGATCTTGGCTTCATGCTCTCTTGAAGTGGCTCTGTCAT 1256  
DB 2099 AAAAACCATAGCAGGAGAGATTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2158  
QY 1257 TGGCCTGCAAGTCTGTGATGTTTCAACTTACCGGATTTTACACAGATCAGAG 1316  
DB 2159 TGTCTTACCTGTTCCGATGATTTTATCACTTCACTGCTGATTTACACAGATCAGAG 2218  
QY 1317 AGCTGATTAACGAGGAGCAAAAAGAGGCGCTTGGCAGGATCGTGTGGCAAAAC 1376  
DB 2219 AGCAGCAAAAGAGGAGCAAAAAGAGGCTTACAGTGGCAGGATCGGAGCAACAAAG 2278  
QY 1377 AGCAGTGTGATGATCTTCTGACAGCAAGAGCGGCTCTTCAAGAGGCGCTGGA 1436  
DB 2279 CGGAAGGCGAAATGCTTACATGACAGAGCAAAAGGATGTTTACTAGTAAATAGCTGCA 2338  
QY 1437 GGTGAGGAGGACCCAGAGAGAGGACATGGGCAAGACCACTCATCTGATGAGAGCCA 1496  
DB 2339 GTTCTGAGAGGA---TGAAGAGGCTTTTGTACCAAAATCGGCTTCAAGCTTTTAAACCA 2395  
QY 1497 GCATCATCACTGCTGCTGCTGCTGAGAAAAAACCACTGGGTTGCTCTATCTTGTGATGA 1556  
DB 2396 GACACACACCTGCTTCACTGCTGAGAAAAAACCACTGCTGCTGCTGCTGCTGCTGCT 2431  
QY 1557 TCCCTGTATTCTGTACGAACCTTCAACATCAAGAACACAGAGTTTATGATGACAGAT 1616  
DB 2432 -----GAAATCAAGAGTTTGTGAGCAAAAGAT 2458  
QY 1617 GTTTGAGAGAACTGATGAGAGTTCAATGCAAGACTACCATCCACAAAGAGTCCCTC 1676  
DB 2459 CTTTGAAGAAAGCTGATGAGAGTTGCACTGTTAATCGTCTTCAAGTCAAGTCTTTC 2518

QY 1677 ACTGTCAGACCCAGGCGCTCACTACCACTGCTGCTCCGTCGTAAGAGACCAAC 1736  
DB 2519 ACTGCTTCACACAGAGAGTACACAGACCTGCTGTTACAGACACACAAAACCTTT 2578  
QY 1737 ACACCTGCCCAATTCTTAACCTGCGACTACTGCTGCGGACATGACAGACTGACAC 1796  
DB 2579 TCGCATCCCAATGCGCAATGATTCAGGAAGCATCAAGGTATATACAAAGACTGAGC 2638  
QY 1797 GATCCACATCCAGGGCAGTGAAGACCCCTCCCTCAACACAGTCCGCTCAAGCTTAATTT 1856  
DB 2639 GATTAGATCAAGATGTGTGAGAGAAACCTCTGTCTTAACACCCATCCAGTTTAAATGC 2698  
QY 1857 GAAGCAGACGACGAGACTGAGACCAACCTGCAAAACATCCGATCACACAGCATAT 1916  
DB 2659 CAAATGGAAGAGTGTGTTAACTTAACCTGTAACCACTTATGTGACTACAGCAATAT 2758  
QY 1917 CAGCATCCCACTCCCGCCTTAACCCAGAGGAGGAAAGTCCGCCA 1965  
DB 2759 AAGCATCCCAACACTCCAGTAAACCAACGAGAGAGCATAGGCCA 2807  
RESULT 14  
ADJ11251  
ID ADJ11251 standard; DNA; 5333 BP.  
XX  
AC ADJ11251;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Human ovarian tumour antigen DNA Seqid 252.  
XX  
KM human, ds; ovarian cancer; immunogenic; antibody;  
KM antigen presenting cell; APC; immune system cell; T cell; tumourigenic;  
KM cytosolic; gene.  
XX  
OS Homo sapiens.  
XX  
PN US2003232056-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 14-FEB-2003; 2003US-00369186.  
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CC polypeptides thereof, as well as immunogenic peptides, antibodies,  
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CC that are targeted to those cells expressing the proteins of interest. The  
CC present invention describes methods that are useful for stimulating and/

CC or expanding T cells specific for a tumourigenic protein (i.e. T cell  
CC therapy). Furthermore, compositions can be used for the diagnosis,  
CC treatment and/or prevention of ovarian cancer by stimulating an immune  
CC response in a patient. Accordingly, these compositions exhibit cytostatic  
CC activity. This polynucleotide is a human ovarian tumour antigen DNA  
CC sequence given in an exemplification of the invention.  
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
Query Match 44.1%; Score 935.4; DB 12; Length 5333;  
Best Local Similarity 70.7%; Pred. No. 9.4e-176;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;  
QY 66 AGTACCAATGCGCGCCGAGATTGGGCGCTGCTGCTTTTCCCGGCGTCCATCGG 125  
DB 959 AGTATCATGCGCGCGGAGGAGGAGCGCTGCTGCTTTTCCAAAGGAGCGCTATCGG 1018  
QY 126 GTGATGCGGCTGCGCAACTGCCCATGCGCCCTGAGCCCTCC--GGCCGACAAAGACG 182  
DB 1019 GTGATGCTGTGCTGCTGCGGCTTATGCGGCTCCCGAGGCGAGAGAGAAAGAC 1078  
QY 183 GCAGATGAGCTGATTGTCTCAACGTGATGCGGCGAGGTTCCAGACTGAGAGACAC 242  
DB 1079 CCAAGATGCTCTCATTTGCTGAATGTGAGTGACACCGCTTCCAGAGTGGACAGAC 1138  
QY 243 GCTGAGGCTTACCCGACACCTGCTGGGACAGACGAGAGAGTCTTCTTCAACGA 302  
DB 1139 CCGGAGGTTACCCAGACACTTACTGAGGAGTGTGAGAGGACCTTTTCTACACCC 1198  
QY 303 GACACCAAGAGATGCTTCTTGAACCGGAGCCCGAGGTTTCCGCTGCTCAACTT 362  
DB 1199 AGAATCTAGCATATTTCTTTGACCGTGAACCGACATCTTCCGACATCTGAAATT 1258  
QY 363 CTACGCAACGGGAAAGCTGACCTACCGCGCTACGATGATCTCTGCTACGACGAG 422  
DB 1259 CTACGCACTGGGAAGCTCACTATCTCGCCAGAGATGATCTCTGCTTACGATGAAG 1318  
QY 423 GCTGCTCTTCAACGCACTCTCCCGAGATATATGGGAGCTGCTGCTACGAGATCA 482  
DB 1319 ACTGCTCTTCTTGTGCTCATCTCCGGAATATCATGGGACATCTGTTATGAGAGTAA 1378  
QY 483 GACCGCAAGAGGAGGAGAACCGCGAGCGCTCATGAGACGACATCGAGAAACCA 542  
DB 1379 GATGCGAGCGGAGAGAACCGCGAGCGCTCATGAGACGAGATACGACACCGCTGG 1438  
QY 543 GGAG---TCATGCTCTGCTCACTGCTTCCGCAAGACATGTCGGGCTTTCGAAACCC 599  
DB 1439 GGAAGGCGCTTGGCCACATGATCGCAAGGACAGGGCTTGGAGGCTTTCGAAACCC 1498  
QY 600 CCAACACGACGCTGCGCTGCTTCTTACTAGTGACTGCGCTTTCATCGCTGTCTC 659  
DB 1499 CCACACGACGACGATGCGCTGCTGCTTCTACTAGTGACTGCGGAGTCTTTCATGCTG 1558  
QY 660 GGTATCAACCAAGTGTGAGAGCGGTGCGGTGCGGACGCTTCCCGG--CAGCAAGGA 716  
DB 1559 TGTATGCGGAATGTGTGAGAAACATGCGGTGCGGATCAAGCCAGCTCATTTAAAGA 1618  
QY 717 GCTGCGGTGCGGAGCGCTACTGCTGCGCTTCTTCTGCTGACACGCGTGGCTAT 776  
DB 1619 ACTGCGCTGTGAGAGGCGGTATGCTGCGCTTCTTCTGCTTGGACACGCGCTGGCTAT 1678  
QY 777 GATCTTACCGTGAATCTCTGCGGCTTTCGCGGCTTCCAGCGCTTACCGCTTAT 836  
DB 1679 GATCTTACAGTTGATGATTTGCTTCCGCTGCGTGAAGCGCTTGTGCTTACCGTTTGT 1738  
QY 837 CCGAGCGCTATGAGCATCACTGAGTGTGAGGAGCATATGCGCTTACTCATCGCTGTGT 896  
DB 1739 GCGTATGTATGATATCATGACGTGTGTGCGATCTGCTTATTTATTTGGGCTGT 1798  
QY 897 CATGACCAACAGAGAGCTGTCCGCGCTTGTGACGCTTCCGAGTCTTTCGCGCTT 956  
DB 1799 GATGACAGACATGAGAGCTGACGCGGCTTGTGTACACTCGAGTCTTCCGAGTCTT 1858

QY	957	CAGATCTCTCAAGTTTTCGCGCACTCCACAGGGCTGGATTCGCGGGCTTACAACATGAA	1016
Dp	1859	CAGAGTCTTTAAGTATTTCCCGCACTCTCAAGGGCTGGCATCTCGGGGTACACACTGAA	1918
QY	1017	GAGCTGTGCTCCCAACTGGGCTTCTTCTCTCTCCCTCAACATGGCCATCATCATCTT	1076
Dp	1919	GAGTTGTGGCTCAGAAATTGGGCTTCTTGCTTTTCTCGCTCAACATGGCTATCATCATCTT	1978
QY	1077	TGCCACTGTGATGTTTATATGCCGAGAAAGGCTCCTCGGCCAGCAATTACACAGATCCC	1136
Dp	1979	CGCTACAGTTATGTTCTACGCAAGAAAGGGGTCTTCGGCTGACAAATTACACACATCCC	2038
QY	1137	TGCTTCGTTTGGTATACCAATTGTCACCATATACCACTGGGATATCGGAGATATGTGCC	1196
Dp	2039	TGCAGCCTTCTGTGATACATATGTCACATATACAACACTAGGGATATGTGACATGTGCC	2098
QY	1197	TAAAGCATTTGCAGGGAAAGATCTTCCGCTCATCTGCTCTTGAATGGCGTCTGTGAT	1256
Dp	2099	AAAAACCATACAGAGGAAGATTTTGTGTTATCTGTTCCGTATGGAGGGGCTTGATCAT	2158
QY	1257	TGCCCTGCGCACTCCCTGTGATTTGTTTCCACTTTAAGCCGGAATTTACCCAGATTCAGAG	1316
Dp	2159	TGCTCTACGTTCCTCGGATTTGATTCMACTTCAAGTCGATCTTACACACCAAGATTCACG	2218
QY	1317	AGCTGATTAACGACAGGGCAAAAAGAGGCGCGCTTGCCAGAGATCCGTGGGCAAAAC	1376
Dp	2219	AGCAGACAAAGAGGGGACAAAAGAAAGTACATGACTGGCCACAGATCCGGGACGCAAAAG	2278
QY	1377	AGGCAATTGCAATGCATCTCTGCAACGACAGCGCAACGGGCTCCTCAACGAGGCGCTGGA	1436
Dp	2279	CGGAAGCGCAATGCTTATCATGACAGAGCAAAACGAATGGTTTACTAGTATACAGCTGCA	2338
QY	1437	GCTGACGGGGACCCCAAGAGAGGAGCAATGGGCAAGACCTTCATCTCATCGAGAGCCA	1496
Dp	2339	GTCTCTCAGAGCA---TGAGCAGGCTTTTGTTAGCAAAATCCGGCTTCAGCTTTGAACCA	2395
QY	1497	GCATCATCACCTGCTGCACTCCTCGAGAAAAACAACCATGGGTTGTCTTATCTTGTGATGA	1556
Dp	2396	GCACCAACACCTGCTTCACTGCTGGAAAAAACAC-----	2431
QY	1557	TCCCTGTTATCTGTAGCAACCTCCACCATCAAGAACCAAGCATTTATGTAGACAGAT	1616
Dp	2432	-----GATTCACAGATTTGGAGCGAAACAGT	2458
QY	1617	GTTTGAGCAGAACTGCATGAGAGAGTTCAATGACAGAACTAACCATCCACAAGAGCTCCTC	1676
Dp	2459	CTTTGAAAGAAAGCTGCATGAGAAATTGCAACTGTTATATGTCTCTTCAAGTCAAGTCTTC	2518
QY	1677	ACTGTCCAGCAACCCAGGCTCTCACTTACCACCTGTGCTCCCGTGTAGTAAAGAACCAAC	1736
Dp	2519	ACTGTCTTCAACAACAAAGGAGTCCACAGCACTGCTGTTCAAGACACAAAAAAAATCTT	2578
QY	1737	ACACTGCTCCCAATTCTAACCTGCCAGGTACTTCGCTGGGAGCATGCAAGAGCTTCAGAC	1796
Dp	2579	TTCGATCCCAATGTCCAAATGTATCAGGAAGGCATCTCAAGATGTATACAAAGAACTCAGAC	2638
QY	1797	GATCCCACTTCAGGGCAGTGAAGAGCCTCCTCTCAACCAAGTCGCTCAGCCTTAATTT	1856
Dp	2639	GATTCAGTTCAGATGTGTGAGAGAAACACTCTGTCTTACAGCCGATTCAGTTTAAATGC	2698
QY	1857	GAAGACAGACGACGGACTGAGACCAAACTGCAAAAATCCACAGATCACACAGCCATCAT	1916
Dp	2699	CAAAATGMAAGTGTGTTAAACTTAACTGTGAACAACTTATGTGACTACAGCAATATAT	2758
QY	1917	CAGATATCCCACTCCCCAGGCGTTTACCCCAAGAGGGGAAAGTCGGCCA	1965
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Db 1319 ACTGCGCTTCTTGGCGCTCATCCGGAAATCATCGGCGACTGCTGTATGAGAGTACAA 1378  
Qy 483 GGAACCGCAAGAGGAAAGCCGAGCGGTCAATGACGACAAAGACTGGAGAACACCA 542  
Db 1379 GGATGGCAGGGGAGAAAGCGGAGCGGCTTCGACGACGACGCGATATCCGACCGCTGG 1438  
Qy 543 GGAG---TCGATGCGCTCGCTCAGCTTCGCGCAGCAATGCGGGGCTTCGAGAACCC 599  
Db 1439 GAGAGCGCGCTTGGCCACCATATGACGAAAGGAGGCTGGAGAGGCTTCGAGAACCC 1498  
Qy 600 CCACACGACGACGCTGCGCTGCTGCTTCTACTACGCTGAGCTTCTTATCGCTGCTC 659  
Db 1499 CCAACGACGACGAGAGCGCTGCTGCTTCTACTATGACGAGGCTTTCATGCGCTC 1558  
Qy 660 GGTATCATCAACGCTGTGGAGACGCTGCGCTGCGGACGCTCCGGG---CAGCAAGA 716  
Db 1559 TGTCACTCCGAAATGGTGGAAACAGTCCGCGGATCAAGCCACGAGTCATTAAGA 1618  
Qy 717 GCTGCGGCGGGGAGCGCTACTCGGTCGCTTCTTTCGCTGAGACAGCGCTGGCTAT 776  
Db 1619 ACTGCGCTGTGAGAGCGGTATGCTGTGCGCTTCTTCTGTGACAGCGCTGCGTAT 1678  
Qy 777 GATCTTCAACGCTGAGTACTCTGCGGCTCTTCCGCGCTCCACCGCTACCGCTGAT 836  
Db 1679 GATCTTCAACGCTGAGTACTCTGCGCTGCTGCGAGCGCTACGCTTACCGCTTGT 1738  
Qy 837 CCGAGCGCTCATGACATCATGACGCTGGGCGCATATGCCCTACTACATCGCTGAT 896  
Db 1739 GCGTGTGCTCATGATATCATGACGCTGGGCGCATATGCCCTACTACATCGCTGAT 1798  
Qy 897 CATGACCAACAGAGAGCGTGTCCGGCGCTTCCGTCACGCTCCGGGCTTCGCGCTCT 956  
Db 1799 GATGACAGACATGAGAGCGTACGAGCGCTTCTTCTACACCTCCAGTCTTCGCGCTCT 1858  
Qy 957 CAGGATCTTCAAGTTTCCCGCACTCCACGGGCTGCGGATCTGGGCTACACACTGAA 1016  
Db 1859 CAGGATCTTCAAGTTTCCCGCACTCTCAGAGCGCTGCGGATCTGGGCTACACACTGAA 1918  
Qy 1017 GAGCTGTGCTCGAAGCTGGGCTTCTTCTTCTTCTCCCTCACCATGGCCATCATCTT 1076  
Db 1919 GAGTGTGCTCGAAGTGGGCTTCTTCTTCTTCTTCTCCTCACCATGGCTATCATCTT 1978  
Qy 1077 TGCCATGTGATGTTTATGCGAGAGAGGCTCTCGGCGACAGTTTCAAGCATCCC 1136  
Db 1979 CGTACAGTATGTTTCTACGAGAGAGAGGCTTCTCGCTAGCAAGTTTCAAGCATCCC 2038  
Qy 1137 TGCCCTGTTTGTACACATTTGTACCATGACACACTGGGATACGAGACATGATGCC 1196  
Db 2039 TGCAAGCTTCTGTATACATGTGTACCATGACACACTGGGATACGAGATGATGCC 2098  
Qy 1197 TAAAGCATGTCAGGGAAGATCTTCGGCTCCATCTGCTCTTGAAGTGGGCTCTGATCAT 1256  
Db 2099 AAAAACATAGCAGGGAAGATTTTGGTTCTATCTGTTGCTGAGTGGGCTCTGATCAT 2158  
Qy 1257 TGCCCTGCGAGTCTCTGTGATGTTTCCAATTATGCGGATTTACACAGATCAAGAG 1316  
Db 2159 TGCTCTACTCTGTTCCGATGATGTTTCAACTTCAGTGCATCTACACAGAAATCAACG 2218  
Qy 1317 AGCTGATTAACGACAGGACAAAGAGGCGCGCTTGCAGAGATCCGTTGCGCAAAAC 1376  
Db 2219 AGCAGACAAAGAGAGGACAAAGAAAGCTTGAATGAGCTGGCAGAGATCCAGCAAAAG 2278  
Qy 1377 AGGCAATTGCAATGATACCTGACAGACAGGCAAGCGGCTCTCAAGAGAGCGCTGGA 1436  
Db 2279 CGAAGCGCAATGCTTACATGACAGCAAGGATGTTTACTCAATATCAGCTGCA 2338  
Qy 1437 GCTGACGGGACCCCGAAGAGAGACATGGGCAAGACCACTCATCATGAGAGCA 1496  
Db 2339 GTCTCTAAGAGA---TGAGCAGGCTTTTGTATGCAAAATCGGCTCAGCTTTGAACCCA 2395  
Qy 1497 GCATCATCACTGCTGACACTGCGGAAAAACCACTGGGTTGTCTTATCTTGTGATGA 1556  
Db 2396 GCACACACACCTGCTTCACTGCTGAAAAAACAC----- 2431

Qy 1557 TCCCTGTATCTGTAGAACCTCCACCATGACAAAGACGAGTTTATGAGACAT 1616  
Db 2432 -----GATCAGAGTTTGTGAGCAAGT 2458  
Qy 1617 GTTGGAGAGACTGATGAGAGATTCAATGACAGAACTAACCATTCACAAAGTCCCTC 1676  
Db 2459 CTTTGAAGAAAGCTGATGAGAGTTGCAACTGTATATGCTCTTCAAGTCAAGTCTTC 2518  
Qy 1677 ACTGTCCAGCAACCGAGGCTCACTACCACTGTGCTCCGCTGTAGTAAAGACAC 1736  
Db 2519 ACTGCTTCAACAAAGAGTCAACAGCAGCTGTGTTCAAGACGACAAAGAACTTT 2578  
Qy 1737 ACACCTGCCAATTTTAACTGCGAGCTACTGCTGCGGACGATGCAAGCTACAGAC 1796  
Db 2579 TCGATCCCAATGCAATGTATCAGAGGCGATCTAGATGTATTAAGAACTCAGAC 2638  
Qy 1797 GATCCACATCCAGGCAAGTGAAGAGCGCTCCCTCAACACAGTGCCTCAGCTTAATT 1856  
Db 2639 GATTCAGATCAGATGTGTGAGAGAACCTCTGTCTTAACAGCGATCAGTTTAAATG 2698  
Qy 1857 GAAGCAGACGACGACTGAGACCAAACTGCAAAATCCAGATCACACAGCCATCAT 1916  
Db 2699 CAAGTGAAGAGTGTAACTTAACTTAACTGTAACAACTTATGTGACTACAGCAATAT 2758  
Qy 1917 CAGCATCCCACTCCCGCAGCGCTAACCCGAGAGGGGAAAGTGGCCA 1965  
Db 2759 AAGATCCCAACCTCCAGTAAACCAACAGAGAGAGAGATAGGCCA 2807

Search completed: April 5, 2005, 15:08:35  
Job time : 2517.09 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2121	100.2	2121	13	US-10-062-879-1	Sequence 1, April
2	1997	94.2	2064	13	US-10-062-879-3	Sequence 1, April
3	935.4	44.1	2351	15	US-10-212-677-253	Sequence 253, April
4	935.4	44.1	2351	17	US-10-361-811-253	Sequence 253, April
5	935.4	44.1	2351	17	US-10-369-186-253	Sequence 253, April
6	935.4	44.1	5333	15	US-10-212-677-252	Sequence 252, April
7	935.4	44.1	5333	15	US-10-212-677-254	Sequence 252, April
8	935.4	44.1	5333	17	US-10-361-811-252	Sequence 252, April
9	935.4	44.1	5333	17	US-10-361-811-254	Sequence 254, April
10	935.4	44.1	5333	17	US-10-369-186-252	Sequence 252, April
11	935.4	44.1	5333	17	US-10-369-186-254	Sequence 254, April

12	798.2	37.6	2528	14	US-10-121-746-9	Sequence 9, Appl1
13	795.4	37.5	3474	17	US-10-296-115-373	Sequence 373, Appl1
14	679	32.0	5404	15	US-10-312-677-255	Sequence 255, Appl1
15	679	32.0	5404	17	US-10-361-811-1255	Sequence 255, Appl1
16	679	32.0	5404	17	US-10-369-186-255	Sequence 255, Appl1
17	634.2	29.9	11121	16	US-10-029-386-24777	Sequence 24777, A
18	354.4	16.7	1597	15	US-10-312-677-256	Sequence 256, Appl1
19	354.4	16.7	1597	17	US-10-361-811-256	Sequence 256, Appl1
20	354.4	16.7	1597	17	US-10-369-186-256	Sequence 256, Appl1
21	338	15.9	612	9	US-09-864-761-26304	Sequence 26304, A
22	266	12.5	2882	18	US-10-317-139-19	Sequence 19, Appl1
23	259.2	12.2	3254	15	US-10-312-677-251	Sequence 251, Appl1
24	259.2	12.2	3254	17	US-10-361-811-1251	Sequence 251, Appl1
25	259.2	12.2	3254	17	US-10-369-186-251	Sequence 251, Appl1
26	240	11.3	3304	18	US-10-322-281-95	Sequence 95, Appl1
27	240	11.3	3303	18	US-10-322-281-94	Sequence 94, Appl1
28	240	11.3	3305	18	US-10-322-281-94	Sequence 94, Appl1
29	230	10.8	1408	16	US-10-029-395-10	Sequence 20260, A
30	221.2	10.4	2565	17	US-10-435-935-10	Sequence 10, Appl1
31	221.2	10.4	3765	18	US-10-377-139-18	Sequence 18, Appl1
32	216	10.2	2483	13	US-10-325-891-3	Sequence 3, Appl1
33	216	10.2	2483	14	US-10-325-891-3	Sequence 3, Appl1
34	215.6	10.2	1747	9	US-09-804-0114-7	Sequence 7, Appl1
35	214.6	10.1	1371	9	US-09-974-712-1	Sequence 1, Appl1
36	214.6	10.1	1792	9	US-09-974-712-3	Sequence 3, Appl1
37	213	10.0	1341	10	US-09-875-321-7	Sequence 7, Appl1
38	213	10.0	1341	14	US-10-162-012-7	Sequence 7, Appl1
39	213	10.0	1341	17	US-10-162-012-7	Sequence 7, Appl1
40	213	10.0	1341	19	US-10-316-061-7	Sequence 7, Appl1
41	213	10.0	6823	9	US-09-989-920-16	Sequence 16, Appl1
42	211.4	10.0	4372	9	US-09-993-811-1	Sequence 1, Appl1
43	211.4	10.0	4372	15	US-10-254-010-3	Sequence 3, Appl1
44	207.6	9.8	1587	18	US-10-322-281-92	Sequence 92, Appl1
45	207.6	9.8	21587	18	US-10-322-281-91	Sequence 91, Appl1

## ALIGNMENTS

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RESULT 1
US-10-062-879-1
: Sequence 1, Application US/10062879
: Publication NO. US20020127649A1
: GENERAL INFORMATION:
: APPLICANT: Cockett, Mark I.
: APPLICANT: Dिल्s, Daniel W.
: APPLICANT: Chang Ling, Hsui-Ping
: APPLICANT: Sokol, Patricia T.
: TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
: FILE OF INVENTION: Polypeptides and Uses Therefor
: FILE REFERENCE: ahp-98089
: CURRENT APPLICATION NUMBER: US/10/062,879
: PRIOR FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: US/09/178,109
: PRIOR FILING DATE: 1998-10-23
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2121
: TYPE: DNA
: ORGANISM: human
US-10-062-879-1

Query Match          100.0%; Score 2121; DB 13; Length 2121;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1  GATTGCTGAAGTAACTCCAGCTGTGTGCTTACAGTCCGCGCGGCTGCGCGCCCAAGA 60
DB      1  GATTTCCTGAAGTAACTCCAGCTGTGTGTGCTAGCGTCCGCGGCGTGCAGCCCAAGA 60
OY      61  GCTGAGTAGCACCATGGCGCGCGCGAGTTGCGGCTTGAGCCTTTTGGCCCGGCGTGCAGCC 120
DB      61  GCTGAGTAGCACCATGGCGCGCGCGAGTTGCGGCTTGAGCCTTTTGGCCCGGCGTGCAGCC 120

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Db	61	GCCTGGAGTCAACATGAGGAGGCGCGAGTTGGCGGCTGCGCTTTTGTGCGCGAGCTGGGCGC	120
QY	121	ATCGGATGATGTCGGGTGAGCCACTGCCCCATGCTGCTGGCTGGCCCGCCGACAGAAACAAG	180
Db	121	ATCGGATGATGTCGGGTGAGCCACTGCCCCATGCTGCTGGCTGGCCCGCCGACAGAAACAAG	180
QY	181	CGGACGAGTGAAGCTGATTTGTCTCAACGTTGATGATGGGAGAGTTCCAGACTCGTAGGAGAC	240
Db	181	CGGACGAGTGAAGCTGATTTGTCTCAACGTTGATGATGGGAGAGTTCCAGACTCGTAGGAGAC	240
QY	241	ACGCTGAGGCGCTACCCGAGCACCTCTGAGGAGCAGCAGAGAAAGAGTTCTTTCTTAAC	300
Db	241	ACGCTGAGGCGCTACCCGAGCACCTCTGAGGAGCAGCAGAGAAAGAGTTCTTTCTTAAC	300
QY	301	GAGGACACCAAGAGATCTTTCTGACCGGAGCCCCAGAGTGTTCCTGCTGCTCAAC	360
Db	301	GAGGACACCAAGAGATCTTTCTGACCGGAGCCCCAGAGTGTTCCTGCTGCTCAAC	360
QY	361	TTCTAACGCAAGGGGAAAGCTGCACTTACCCGGCTACAGATGCACTTCTGCTTAAGACGAC	420
Db	361	TTCTAACGCAAGGGGAAAGCTGCACTTACCCGGCTACAGATGCACTTCTGCTTAAGACGAC	420
QY	421	GAGCTGAGCTCTACAGGACTCTCCCGGAGATCACTCGGAGACTGCTGCTACAGAGATAC	480
Db	421	GAGCTGAGCTCTACAGGACTCTCCCGGAGATCACTCGGAGACTGCTGCTACAGAGATAC	480
QY	481	AAGGACCGCAAGAGGAGAAAGCCGAGCGGCTCAAGCAACAGACTGAGAAACAAC	540
Db	481	AAGGACCGCAAGAGGAGAAAGCCGAGCGGCTCAAGCAACAGACTGAGAAACAAC	540
QY	541	CAGAGATTCATAGCCCTCGCTCAGCTTCGGCAGACCATATGGCGGGCTTTCAGAAACCC	600
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QY	601	CACACAGACAGCTGAGCCTGATCTTCTTCACTACAGACTGGCTTCTTCACTGCTGCTCG	660
Db	601	CACACAGACAGCTGAGCCTGATCTTCTTCACTACAGACTGGCTTCTTCACTGCTGCTCG	660
QY	661	GTCATACCAACGATGATGAGAACGAGTGCAGTGCAGACGATCCGGGACGAAAGAGCTG	720
Db	661	GTCATACCAACGATGATGAGAACGAGTGCAGTGCAGACGATCCGGGACGAAAGAGCTG	720
QY	721	CCGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGAGCAAGGGCTGCTCATATC	780
Db	721	CCGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGAGCAAGGGCTGCTCATATC	780
QY	781	TTCAACCGTGAATACCTCTGCGGCTTTCGCGGCTCCCAACCGCTACCGCTTATCGGC	840
Db	781	TTCAACCGTGAATACCTCTGCGGCTTTCGCGGCTCCCAACCGCTACCGCTTATCGGC	840
QY	841	AGCTCATAGACATCATCGATGTGAGCATCATATGCCCTTACATCGATCTGTGATG	900
Db	841	AGCTCATAGACATCATCGATGTGAGCATCATATGCCCTTACATCGATCTGTGATG	900
QY	901	ACCAACAACGAGACGTGTCCGCGGCTTTCGTACAGCTCCGAGTCTTCCGCTTACAG	960
Db	901	ACCAACAACGAGACGTGTCCGCGGCTTTCGTACAGCTCCGAGTCTTCCGCTTACAG	960
QY	961	ATCTTCAAGTTTCCCGGCACTCCCAAGGGGCTCGGAGATCCGAGGCTTACACTAAGAGC	1020
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QY	1021	TGTGCTCTCGAAGCTGGGCTTCTTCTCTCTTCCCTCAACATGAGCATCATCTTTGCC	1080
Db	1021	TGTGCTCTCGAAGCTGGGCTTCTTCTCTCTTCCCTCAACATGAGCATCATCTTTGCC	1080
QY	1081	ACTGTGATGTTTATGCCGAGAAAGGCTCTTCGAGCAGCAAGTTCAACAGCATCCCTGCC	1140
Db	1081	ACTGTGATGTTTATGCCGAGAAAGGCTCTTCGAGCAGCAAGTTCAACAGCATCCCTGCC	1140
QY	1141	TGCTTTTGTATCAACATATGTACCACTGACCACTGGAGATACGAGACATGATGCTTAAG	1200
Db	1141	TGCTTTTGTATCAACATATGTACCACTGACCACTGGAGATACGAGACATGATGCTTAAG	1200

QY	1201	ACGATTGACAGGGAAGATCTTCGGCTCCATCTGCTCTCTTGAGTGGCGCTCTGGTCAATTGGC	1280
Db	1201	ACGATTGACAGGGAAGATCTTCGGCTCCATCTGCTCTCTTGAGTGGCGCTCTGGTCAATTGGC	1280
QY	1261	CTGCACAGTCCCTGTGATTGTTTCCACTTTAAGCCGGAATTTAACCAACAGAAATCAGAGACT	1320
Db	1261	CTGCACAGTCCCTGTGATTGTTTCCACTTTAAGCCGGAATTTAACCAACAGAAATCAGAGACT	1320
QY	1321	GATTAACGCAAGGCACAAAAGAGAGCCCGCTTGCACAGATCCGTGTGGCCAAACAGGC	1380
Db	1321	GATTAACGCAAGGCACAAAAGAGAGCCCGCTTGCACAGATCCGTGTGGCCAAACAGGC	1380
QY	1381	AGTTTGGAAATGATACCTGACACAGAACGCAACGGGCTCTCTCAACAGAGCGCTGACCTG	1440
Db	1381	AGTTTGGAAATGATACCTGACACAGAACGCAACGGGCTCTCTCAACAGAGCGCTGACCTG	1440
QY	1441	ACGGGCAACCCCAAGAGAGAGCAATGAGGCAAGACACTTCACTCATCGAGAGCCAGCAT	1500
Db	1441	ACGGGCAACCCCAAGAGAGAGCAATGAGGCAAGACACTTCACTCATCGAGAGCCAGCAT	1500
QY	1501	CATCACTGTGTGCACTGTCTGGAAAAAACCACTGGGTTGTCTTATCTTTGTGATGATCC	1560
Db	1501	CATCACTGTGTGCACTGTCTGGAAAAAACCACTGGGTTGTCTTATCTTTGTGATGATCC	1560
QY	1561	CTGTTATCTGTACGAACCTCCACCATAGAACACACAGATTATTTGATGACACATGTTT	1620
Db	1561	CTGTTATCTGTACGAACCTCCACCATAGAACACACAGATTATTTGATGACACATGTTT	1620
QY	1621	GAGCAGAACTGCATGAGAGAGTTTCAATGCAGAACCTAACCCATCCACAGAAAGTCCCTCACTG	1680
Db	1621	GAGCAGAACTGCATGAGAGAGTTTCAATGCAGAACCTAACCCATCCACAGAAAGTCCCTCACTG	1680
QY	1681	TCACAGCACCCAGGCTCTCATACCACTGTGCTCCGTCCGTAGTAAAGAACCAACAC	1740
Db	1681	TCACAGCACCCAGGCTCTCATACCACTGTGCTCCGTCCGTAGTAAAGAACCAACAC	1740
QY	1741	CTGGCCAAATTTCAACTCCGACGACTACTCGCTGGGACAGTACAGAAAGCTCAGACGATC	1800
Db	1741	CTGGCCAAATTTCAACTCCGACGACTACTCGCTGGGACAGTACAGAAAGCTCAGACGATC	1800
QY	1801	CACATCCACGAGCAGTGAAGCAGCCCTCCCTCAACACAGTCCGCTCAGCCTTAATTTGAAA	1860
Db	1801	CACATCCACGAGCAGTGAAGCAGCCCTCCCTCAACACAGTCCGCTCAGCCTTAATTTGAAA	1860
QY	1861	GCAGACGACGAGCTGAGACCAAACTGCAAAACATCCAGATACCAACGACATCATCAGC	1920
Db	1861	GCAGACGACGAGCTGAGACCAAACTGCAAAACATCCAGATACCAACGACATCATCAGC	1920
QY	1921	ATCCCACTCCCCCAGCGCTTAACCCCAAGGGGGGAAAGTGGGCAACCCCTCCAGGCCCA	1980
Db	1921	ATCCCACTCCCCCAGCGCTTAACCCCAAGGGGGGAAAGTGGGCAACCCCTCCAGGCCCA	1980
QY	1981	GAGCCCAACAGAACATCTCTTCCATAACAGCAATGTTTCAAGAGTCTCTGTCTTGAAA	2040
Db	1981	GAGCCCAACAGAACATCTCTTCCATAACAGCAATGTTTCAAGAGTCTCTGTCTTGAAA	2040
QY	2041	AAATCCCGCGGCATGTGGCGGCGGGAGCATCGACGTGGGGCCCAATTGGCCCTTAACTG	2100
Db	2041	AAATCCCGCGGCATGTGGCGGCGGGAGCATCGACGTGGGGCCCAATTGGCCCTTAACTG	2100
QY	2101	AGTCGATATTAAGCCGAATTC	2121
Db	2101	AGTCGATATTAAGCCGAATTC	2121

RESULT 2  
US-10-062-879-3  
; Sequence 3, Application US/10062879  
; Publication No. US20020127649A1  
; GENERAL INFORMATION:  
; APPLICANT: Cockett, Mark I.  
; APPLICANT: Dilks, Daniel W.



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; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-10-062-879-3

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Best Local Similarity	97.3%	Pred. No. 0		
Matches 2064	Conservative	0	Mismatches	0
			Indels	57
			Gaps	1

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Db	1	GAATTTGCGAACTAACTCCAGAGTGGTGGCTTAGGGTTCGCGGGTGGCGGGCCCAAGA	60
QY	61	GCTGAGTCAACCATGCGCGCGGAGTGTGGCGCTGCGCTTTTGGCCCGGGCTGGCGGC	120
Db	61	GCTGAGTCAACCATGCGCGCGGAGTGTGGCGCTGCGCTTTTGGCCCGGGCTGGCGGC	120
QY	121	ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCAGCAAG	180
Db	121	ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCAGCAAG	180
QY	181	CGGCAAGATGAGCTGATGTTGCTTCAACGTGAGTGGGCGGAGGTTTCCAGACTGAGAGCC	240
Db	181	CGGCAAGATGAGCTGATGTTGCTTCAACGTGAGTGGGCGGAGGTTTCCAGACTGAGAGCC	240
QY	241	ACGCTGAGACGCTTACCCGAGCAACCTGCTGGGCGAGACGGAAGAGTCTTCTTCAAC	300
Db	241	ACGCTGAGACGCTTACCCGAGCAACCTGCTGGGCGAGACGGAAGAGTCTTCTTCAAC	300
QY	301	GAGGACACCAAGAGTACTTCTTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTCAAC	360
Db	301	GAGGACACCAAGAGTACTTCTTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTCAAC	360
QY	361	TTCTACCGGACGGGGAGTGCATACCCGCGCTACAGATGCATCTCTGCTTACAGAC	420
Db	361	TTCTACCGGACGGGGAGTGCATACCCGCGCTACAGATGCATCTCTGCTTACAGAC	420
QY	421	GAGCTGGGCTTCTAGCGGACATCCGCCGGAGATCATCGGGGACGTGCTACGAGAGTAC	480
Db	421	GAGCTGGGCTTCTAGCGGACATCCGCCGGAGATCATCGGGGACGTGCTACGAGAGTAC	480
QY	481	AAGGACCGCAAGAGGGAGACGCCGAGCGGCTCATGAGCAACACGACTCGAGAACAC	540
Db	481	AAGGACCGCAAGAGGGAGACGCCGAGCGGCTCATGAGCAACACGACTCGAGAACAC	540
QY	541	CAGGATCCATGCTTCGCTACGCTTCGCGACAGCCATGTGGCGGGCTTTCGAAACCCC	600
Db	541	CAGGATCCATGCTTCGCTACGCTTCGCGACAGCCATGTGGCGGGCTTTCGAAACCCC	600
QY	601	CACACACGACGCTGGGCCCTGGATCTTCTACTAGTACGTGGCTTCTTCAATCGGTGCTCG	660
Db	601	CACACACGACGCTGGGCCCTGGATCTTCTACTAGTACGTGGCTTCTTCAATCGGTGCTCG	660
QY	661	GTCATCACCAACGTGGTGGAGACGATGCCGTGGCGACGATCCCGGGACAGCAAGAGCTG	720
Db	661	GTCATCACCAACGTGGTGGAGACGATGCCGTGGCGACGATCCCGGGACAGCAAGAGCTG	720
QY	721	CCGTGCGGGGAGCGTACTCGGTGGGCTTCTTCTGCTTGGACACGGCGTGCATGATC	780
Db	721	CCGTGCGGGGAGCGTACTCGGTGGGCTTCTTCTGCTTGGACACGGCGTGCATGATC	780

QY	781	TTCAACCGTGAAGTAACTCTCTCGGCTCTTCGGGGGTCTCCAGCCGTACCGCTTCAATCCGC	840
Db	781	TTCAACCGTGAAGTAACTCTCTCGGCTCTTCGGGGGTCTCCAGCCGTACCGCTTCAATCCGC	840
QY	841	AGCGTCATGAGCATCATGACGTGGTGGCAATCAATGACCTTACTACATCGCTGGTCAATG	900
Db	841	AGCGTCATGAGCATCATGACGTGGTGGCAATCATGCTCTTACTACATCGCTGGTCAATG	900
QY	901	ACCAACAAAGAGACGTGTCCGGCGCTTCGTCAAGCTCCGGGTCTTCGGGTCTTCAGG	960
Db	901	ACCAACAAAGAGACGTGTCCGGCGCTTCGTCAAGCTCCGGGTCTTCGGGTCTTCAGG	960
QY	961	ATCTTCAAGTTTTTCCCGCACTCCAGGGGCTCGGGATCTTGGGCTTACAACCTGAAGGC	1020
Db	961	ATCTTCAAGTTTTTCCCGCACTCCAGGGGCTCGGGATCTTGGGCTTACAACCTGAAGGC	1020
QY	1021	TGTGCTCCGAACATGGGGCTTCTCTCTCTCTCCCTCAACATGAGGCATCATCTCTTGGC	1080
Db	1021	TGTGCTCCGAACATGGGGCTTCTCTCTCTCTCCCTCAACATGAGGCATCATCTCTTGGC	1080
QY	1081	ACTGTGATGTTTTATGCGAAGAGGGCTCTCGGCGACAGAACTTCAACAGCATCCCTGCC	1140
Db	1081	ACTGTGATGTTTTATGCGAAGAGGGCTCTCGGCGACAGAACTTCAACAGCATCCCTGCC	1140
QY	1141	TCGTTTTGGTACACCATTTGTCAACATGACCAACTGSGATACGAGACATGGTGTCTAAG	1200
Db	1141	TCGTTTTGGTACACCATTTGTCAACATGACCAACTGSGATACGAGACATGGTGTCTAAG	1200
QY	1201	ACGATTTGAGAGGAAGATCTTGGGCTCCATCTGCTCTCTGTAATGGCGTCTGTCTAATGCC	1260
Db	1201	ACGATTTGAGAGGAAGATCTTGGGCTCCATCTGCTCTCTGTAATGGCGTCTGTCTAATGCC	1260
QY	1261	CTGCCAGTCCCTGTGATGATTGTTTCCAACTTTAGCCGGAATTTTACCAACAGAACTCAGAGACT	1320
Db	1261	CTGCCAGTCCCTGTGATGATTGTTTCCAACTTTAGCCGGAATTTTACCAACAGAACTCAGAGACT	1320
QY	1321	GATTAACGACAGGGACAAAGAAGAGCCCGCTTGTCCAGAGATCCGTGTGGCCAAAACAGGC	1380
Db	1321	GATTAACGACAGGGACAAAGAAGAGCCCGCTTGTCCAGAGATCCGTGTGGCCAAAACAGGC	1380
QY	1381	AGTTGGAATGCAATCTGSCACAGCAAGGCGCAACGGGCTCTTCAACAGAGGCGCTGAGCTG	1440
Db	1381	AGTTGGAATGCAATCTGSCACAGCAAGGCGCAACGGGCTCTTCAACAGAGGCGCTGAGCTG	1440
QY	1441	ACGGGCAACCCGAAAGAGAGACATATGGGGCAAGACCACTCACTCATATGAGAGCGACAT	1500
Db	1441	ACGGGCAACCCGAAAGAGAGACATATGGGGCAAGACCACTCACTCATATGAGAGCGACAT	1500
QY	1501	CATCAACCTGTGCACTGCTGGAAAAAACACTGGGGTTTGTCTATCTTTGGATGATGCC	1560
Db	1501	CATCAACCTGTGCACTGCTGGAAAAAACACT-----	1533
QY	1561	CTGTTATCTGTAGCAACTCCACATCAAGAACCAAGATTATGATGAGCAAGTGT	1620
Db	1534	-----AACACAGATTATGATGAGCAAGTGT	1563
QY	1621	GAGGAGAACTGCAATGAGAGATTCAATGAGAACTAACCAATCCACAAGAAAGTCCCTCACTG	1680
Db	1621	GAGGAGAACTGCAATGAGAGATTCAATGAGAACTAACCAATCCACAAGAAAGTCCCTCACTG	1623
QY	1681	TCCAGGCCACCCAGGCGCTCACTACCACTGTGCTCCGTCGTATGAAAGAACCAACAC	1740
Db	1684	TCCAGGCCACCCAGGCGCTCACTACCACTGTGCTCCGTCGTATGAAAGAACCAACAC	1683
QY	1741	CTGCCCAATTTTAACTGTCCAGCTACTGCGCTGCGCAGCATGCAAGACTCAGCACGATC	1800
Db	1684	CTGCCCAATTTTAACTGTCCAGCTACTGCGCTGCGCAGCATGCAAGACTCAGCACGATC	1743
QY	1801	CACATTCAGGGCAGTGAAGAGCCCTCCCTCAACACAGTGCCTCAGGCTTAAATTTGAAA	1866
Db	1744	CACATTCAGGGCAGTGAAGAGCCCTCCCTCAACACAGTGCCTCAGGCTTAAATTTGAAA	1803
QY	1861	GCAAGCGACGACTGAGACCAAACTGCAAAAATCCAGATCAACACAGCCATCATGAC	1920



QY 1557 TCCCTGTTATCTGTAGCAACCTCCACCATCAAGAACACAGAGTTTATGTAGACAT 1616  
Db 1896 -----GATACGAGTTTGTGAGAACTAAGT 1922  
QY 1617 GTTTGAGAGAGACTGATGAGAGTTTCAATGACAGAACTAACCCATCCAGAAAGTCCCTC 1676  
Db 1923 CTTTGAAAGAAAGCTGATGAGAGTTTCAATGAGTTTAACTGCTTCAAGTCAAGTCTTC 1982  
QY 1677 ACTGTCAGCAACCCAGGCTTCATCAACCTGCTGCTCCGCTGTAGTAAAGAACAC 1736  
Db 1983 ACTGCTTCAACAAAGAGATCACAGACCTGCTGTTCAAGACACAAACAACTTT 2042  
QY 1737 ACACCTGCCAATTTCTAATCTGCGAGCTAATCGCTGGGAGACATGCAAGACTAGAC 1796  
Db 2043 TCGATCTCCAAATGCAATGATATCAGAAAGCCATTAAGTATATCAAGAACTAGAC 2102  
QY 1797 GATCCACATCCAGGAGCACTGAGACAGCCCTCCCTCAACAACAGTCCGCTCAAGCTTAATTT 1856  
Db 2103 GATTCAGATCAGATGTGTGAGAGAAACCTCTGTCTAACAGCCGATCCAGTTTAAATGC 2162  
QY 1857 GAAAGCAGACGAGACTGAGACCAAACTGCAAAATCCAGATCACACAGCCATCAT 1916  
Db 2163 CAAATGGAAGAGTGTGTTAACTTAACTGTGAACAACCTTATGTAGCTAAGCAATAT 2222  
QY 1917 CAGCATCCCACTCCCGCAGCGCTTAAACCCAGAGGGGAAAGTCCGCCA 1965  
Db 2223 AAGATCCCAACACTTCCAGTAAACCAACAGAAAGAGCATAGGCCA 2271

RESULT 4  
US-10-361-811-253  
; Sequence 253, Application US/10361811  
; Publication No. US20030206918A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C8  
; CURRENT APPLICATION NUMBER: US/10/361,811  
; CURRENT FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 253  
; LENGTH: 2351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-361-811-253

Query Match 44.1%; Score 935.4; DB 17; Length 2351;  
Best Local Similarity 70.7%; Pred. No. 2.6e-248;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 363 CTACCCGACCGGGGAAGCTGCACTAACCCGCGCTACGAGTGCATCTCTGCTACGACGAGA 422  
Db 723 CTACCGACCTGGGAAGCTCCACTATCTGCGACAGATGATCTCTGCTTACGATGAAGA 782  
QY 423 GCTGGCTTTTACGAGCATCTCCGAGATCATCGGGAGCTGCTGCTACGAGAGTACAA 482  
Db 783 ACTGGCTTTTGGCCCTCATCCGGAATATATCGGCACTGCTGTTATGAGAGTACAA 842  
QY 483 GACCCGAAAGAGAAAGCCGAGCGGCTCATGAGACAAACGACTCGAAGAACCA 542  
Db 843 GATGCGAGGAGAGAAAGCCGAGCGGCTCAAGACAGCCGATACCGAACCCGCTGG 902  
QY 543 GAG---TTCATGCTTCTGCTACGCTCCGCAACATATGAGGGGCTTGAAGACCC 599  
Db 903 GAAAGCGCCCTTGGCCACCATAGCTGCAAGGAGGCTGAGAGGGCTTGAAGACCC 962  
QY 600 CCACACGAGCAGCGCTGGCCCTGATCTTCTAATAAGCTGAGCTGCTTCTTATGCTGCTC 659  
Db 963 CCAACCGACGAGATGGCCCTGGTGTCTATATGTACAGGGTTTTCATTTGCCGTCTC 1022  
QY 660 GGTATCAACAAAGTGTGAGAACGATGCGGTGCGGCAAGGTCCGAG--CAAGCAAGA 716  
Db 1023 TGTATGCGAATGAGTGGTGAAGAACATGTCGATCAAGCCAGGTCATTAAGA 1082  
QY 717 GCTGCGTGGCGGGAGCGCTACTGCTGCTCTTCTGCTGACAGAGGCTGCTCAT 776  
Db 1083 ACTGCGCTGTGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGAACAGGGCTGTGAT 1142  
QY 777 GATCTTACCGGTGAGTAACTCTGCGGCTTCTGCGGCTCCAGCGCTACCGCTTAT 836  
Db 1143 GATCTTACAGTATGATTTTCTTCTGCTGCGGCTTCTGCTTACCTTACCTTTTGT 1202  
QY 837 CCGAGCGTCAATGAGCATCATGAGTGTGAGGATCATGAGCTTATCATATGAGTGTGT 896  
Db 1203 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262  
QY 897 CATGACCAACAGAGAGCTGTCCGCGGCTTGTGTCACGCTCCGGGCTTCCGCTTT 956  
Db 1263 GATGACAGACATAGAGAGCTGACAGGAGCTTTGTGTCACGCTCCGAGCTTCCGCTTT 1322  
QY 957 CAGATCTTCAAGTTTCCCGGCACTCCAGGCGCTGAGATCCGAGGCTACACATGAA 1016  
Db 1323 CAGATCTTCAAGTTTCCCGGCACTCCAGGCGCTGAGATCCGAGGCTACACATGAA 1382  
QY 1017 GAGCTGTGCTCCGAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1076  
Db 1383 GAGTTGTGCTCCGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1442  
QY 1077 TGCACTGTGATGTTTATGCGAGAAAGGCTCTCCGCGCAGCAATTCACAGATCCC 1136  
Db 1443 CGCTACAGTATGTTTATGCGAGAAAGGCTCTTCCGCTGAGCAATTCACAGATCCC 1502  
QY 1137 TGCTCGTTTGTGATCAACATGTCACATGACCACTGGGATACGAGACATGTGTC 1196  
Db 1503 TGACGCTTCTGTGATCAACATGTCACATGACCACTGGGATACGAGACATGTGTC 1562  
QY 1197 TAAACATTTGACAGGAAGATCTTCCGCTCCATGCTGCTTGAAGGCTGCTGATCAT 1256  
Db 1563 AAAAACATGACAGGAAGATTTTGGTTCATCTGTTCTGAGTGGGCTTGGTTCAT 1622  
QY 1257 TGCCCTGCAAGTCCCTGTGATGTTTTCOAATTTAGCCGATTTTACCAAGATTCAGAG 1316  
Db 1623 TGCTCTACCTGTGCTGAGATGATCCAACTTCAAGTCCGATTCACCAAGATTCAGAG 1682  
QY 1317 AGCTGATTAAGCGAGGACAAAGAGGCGGCTTGCAGAGATCCGTGTGGCAAAAC 1376  
Db 1683 AGCAGACAAAGAGGAGCAAAAGAGAGCTAGAGCTGACAGATCCGAGGACCAAGAG 1742  
QY 1377 AGGAGTTGAAATCATCTGACAGCAAGCGGAGCGGCTCTCAAGAGGCGTGA 1436  
Db 1743 CGAAGGCAAAATGCTTATCATGACAGCAAAAGGAGTTTACTAGTATTCAGCTGCA 1802

QY	1437	GCTACGGGACCCCGAAGAGGAGGACATGAGGACAGCACCTCATTGATCGAGAGCCA	1439
Db	1803	GTCTCTCAGAGA---TGAGAGGCGCTTTTGTATGACAAATCCGGCTTCAGCTTTGAAACCA	1859
QY	1497	GCATCATCACTCTGTGCACTGCTGAGAAAAAACCACTGGGTTGTCTTATCTTGTGATGA	1556
Db	1860	GCACACACCACTGCTTCACTGCTGAAAAAACAC-----	1895
QY	1557	TCGCCCTGTATCTGTAGCAACCTCCACCATCAAGACCAAGATTATATGATGACAGAT	1616
Db	1896	-----GATACCAAGTTTGTGACGACCAAGT	1922
QY	1617	GTTTGTAGCAGAACTGCATGAGAGAGTTCAATGACAGAACTTACCATTCCACMAAGTCCCTC	1676
Db	1923	CTTTGAAGAAAGCTGCATGAGAAAGTTGCACATGTTAATATGTCCTTCAATCACAAGTCCTTC	1982
QY	1677	ACTGTCCAGCACCACCGAGCCCTCTACTACCACTGCTGCTCCCTGTTAGTAAGAACCAAC	1736
Db	1983	ACTGTCTTTCACAAACAAAGAGTCCACGACACTGTGCTTTCACAGACACCAAAAAAATT	2042
QY	1737	ACACCTGCGCCAAATTCTAACTGCACAGTACTGCGCTGCGGACGATGCAAGAGCTCAGAC	1796
Db	2043	TCGCATCCCAATGCAATGATATGATGAGAAAGCATCAAGTAGTATACAAAGAACTCAGAC	2102
QY	1797	GATCCACATCCAGGCGAGTGAACGAGCCTCCCTCAACAACAGTGGCTCCAGCCTTAATT	1856
Db	2103	GATTTCAGTTCAGATGTGTGAGAGAAACCTCTGTCTTAAAGCGGATCCAGTTTAAATGC	2162
QY	1857	GAAAGCAGACGACGAGTGAAGACCAAACTGCAAAAAATCCAGATCACCAAGCCATCAT	1916
Db	2163	CAAAATGGAAGAGTGTGTTAAACTTAAATGTGAGACAACTTATGTGACTACAGCAATAT	2222
QY	1917	CAGCATCCCACTCTCCCAAGCGCTTAACCCAGAGGGGAAAAGTCGACCA	1965
Db	2223	AAGCATCCCAACACTCTCCAGTAAACCAACAGAGAGACGATAGCA	2271
RESULT 5			
US-10-369-186-253			
Sequence 253, Application US/10369186			
Publication No. US20030232056A1			
GENERAL INFORMATION:			
APPLICANT: Fanger, Gary R.			
APPLICANT: Fling, Steven P.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER			
FILE REFERENCE: 210121.484C9			
CURRENT APPLICATION NUMBER: US/10/369,186			
NUMBER OF SEQ ID NOS: 293			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 253			
LENGTH: 2351			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-369-186-253			

Query Match	44.1%	Score 935.4	DB 17	Length 2351
Best Local Similarity	70.7%	Pred. No. 2.6e-248		
Matches 1349		0	Mismatches 491	Indels 69
				Gaps 5

QY	66	AGTACCACTGGCGGCGGAGTTGGCGGCCTGGCTGCTTTTGGCCGGGCTGGCGCATGG	125
Db	423	AGTAAATACATGGCGGGGGGGTGGGACGCTGGCTGCTTTTGGAAAGGCGAGGGCGTATGG	482
QY	126	GTGATAGCCGGTGGGCACTGCCCATCCTCCCTGGCCCC---GGCCCAACAAGAACG	182
Db	483	GTGATAGCTGTGGCTCTGGGGGCTTATCCCGGCTCCCGCAGAGCAGAGAGGAAAGAAC	542
QY	183	GCAGATAGCTGATTGTCTCAACGTAGTGGGCGAGGTTCCAGACTTGGAGGACAC	242
Db	543	CCAAAGATCTCTCATTTGTGCTGAATGTAAGTGGACACCGCTTCCAGAGTGGCAGGAC	602

QY	243	GCCTGAGACCGCTACCCCGGACACCCCTGCTGGGACACACGAGAAAGAGTTCTTCTTAAACGA	302
Db	603	CTGTGAACCTGTACCACAGACACTCTACCTGGGCAAGTCTGAAGAGGAACTTTTCTAACACCC	662
QY	303	GGACACCAAGAGACTCTTCTTCGACCGGAGACCCCGAGAGTTCCTCGCTGCTGTCAACTT	362
Db	663	AGAAACCTCACAGATTTTCTTTGACCTGTACCCAGACATCTTCCGCCACATCTCTGAATTT	722
QY	423	GCTGGCCTTTCTACGGCATCTCTCCCGAGATCATCTGGGGAATCTGTCTGCTACAGAGATTCAA	482
Db	723	CTACCGCACTGGGAAGCTCCACTATCTCTCCACACAGATGATCTGTCTTACATGTAAGA	782
QY	783	ACTGGCCTTTTGGCTCTCATCCCGAAATCATCTGGGAGCTGTGTTATGAGAGTTCAA	842
Db	483	GGACCGCAAGGGGAGAAAGCCCGAGCGGCTCATGGACGACAAACGAATCTGGAGAACAAACA	542
QY	843	GGATTCGAGCGGAGAGAACCCCGAGCCCTCTGACAGACGACGCGATTCGACACCCGCTGG	902
Db	903	GGAGAGCGCCTTGGCCACCATGACTGCAAGGAGAGAGGTCTTGGAGGGCCTTTCAGAAACC	962
QY	543	GGAG---TCCATGCGCTCGCTCACTTCGCGACAGACCATGTGGCGGGCCTTTCAGAAACC	599
Db	903	GGAGAGCGCCTTGGCCACCATGACTGCAAGGAGAGGTCTTGGAGGGCCTTTCAGAAACC	962
QY	600	CCACACCAAGCAGCTGGGCGCTGTCTTCTACTAGATCTGGCTTCTTCACTGCTGTCTC	659
Db	963	CCACACCAAGCAGCTGGGCGCTGTCTTCTACTAGATCTGGCTTCTTCACTGCTGTCTC	1022
QY	660	GGTCATCACCAAGTGTGTGAGACCGGTCGCGTGCAGGACCGTCCCGGG---CAGCAAGGA	716
Db	1023	TGTCTATGCGAAATGTGTGAGAAACAGTCCGTGCGATCAAGCCGAGGTACATTTAAAGA	1082
QY	717	GCTGCGGTGCGGGAGCGCTACTCGGTGCGCTTCTTCTGCTGTGACAACGCGCTGCTCAT	776
Db	1083	ACTGCGCTGTGGAGAGGGTATGCTGTGGCTTCTTCTGCTTGTGACAACGCGCTGCGCTCAT	1142
QY	777	GATCTTACCGGTGAGTACCTCTCTGGGCGCTTCTTGGGCGCTCCAGCGGCTACCGCTTCAT	836
Db	1143	GATCTTACAGTGTGAGATTTGTGCTTCCCTGCGGTGACGCGCTCATGTGTTACGGTTTGT	1202
QY	837	CCGCAAGGCTATGAGCATATCGACGATGCGGCGCATATGACCCCTCATATATCGGTCTGT	896
Db	1203	GCGTATGTCTATGATATCATATCGACGATGTGGCCATCTCTCTTATTAATTTGGCTGT	1262
QY	897	CATGACCAACAAGAGGACGTGTCCGGCGCCTTCGTACACCTCCGGGCTCTTCCGCGTCTT	956
Db	1263	GATGACAGACATATGAGGACGTCAAGCGGAGGCTTTGTCACTCCGAGTCTTCCGGGCTT	1322
QY	957	CAGGATCTTCAAGTTTCCCGCACCTCTCAAGGCGTGGCATCTTGGGGTATCACACTGAA	1382
Db	1323	CAGGATCTTCAAGTTTCCCGCACCTCTCAAGGCGTGGCATCTTGGGGTATCACACTGAA	1382
QY	1017	GAGCTGTGGCTCCGAACTGGGCTTCTTCTTCTCCCTCATGACATGGCCATATCATCTT	1076
Db	1383	GAGTTGTGCTCAGAAATTTGAGCTTCTTCTTCTGCTCATCAATGGCTATATCATCTT	1442
QY	1077	TGCCACTGTATGTTTATGCTCCGAGAAAGGCTCTCGGCGAGCAAGTTTCAACAAGCATCCC	1136
Db	1443	CGCTACAGTATATGTCTACGCAAGAAAGGGGTCTTGGGCTAGCAAGTTTACACAGCATCCC	1502
QY	1137	TGCTGTGTTTGTATCCATTTGTCACTATGACCAACTGGGATACGAGACATGTGTCC	1196
Db	1503	TGCAGCCTTCTGGTATACATCTGTCACATGACAAACTATGGGATATGTATGATATGTGGCC	1562
QY	1197	TAAAGCATTTGCAGGGAAGATCTTGGGCTCATCTGTCTCTTAGTGTGGGTCTCTGTGCAT	1256
Db	1563	AAAAACATATGCAAGGGAAGATTTTGTGTCTATCTGTCTGTAGTGGGTCTTGTGCAT	1622
QY	1257	TGCCCTCAGTCCCTGTGATTTGTTTCCAACTTTAGCGGATTTACACCAAGATTCAGAG	1316
Db	1623	TGCTCTACTGTTTCCGTGATTTGTATCTCAACTTCATGTCGATCTTACACACAGATTCACG	1682
QY	1317	AGCTGATTAACGCAAGGCAAAAAAGAGGCCCGCTTGCAGGATTCGTGTGGCAAAAC	1376

Db	1663	AGCAGACAAAGGAGGGGCAAAAGAAAGCTTGAAGTGGCCAGAAATCCGGGCAAGCCAAAG	1742
Qy	1377	AGGCAGTTTGAATGATATCTTGACAGGAAAGGCAACGGGCTCTTCAAAGAGCCGTGGA	1436
Db	1743	CGAAGGCCCAATGCTTACATGACAGCAAAACGAAATGTTTACTCAGTAATCAGCTGCA	1802
Qy	1437	GCTACGGGGCAACCCAGAAAGAGGACATGGGCAAGACACCTCACTCATTCGAGAGCA	1496
Db	1803	GTCTCTCAGAGA---TGACAGGCTTTTGTGTAGCAAAATCCGGCTCAGCTTTGAAACCA	1858
Qy	1497	GCATCATCACTGCTGCACTGCTGTGAAAAAACAATGGGTGTCTCTTGTGATGA	1556
Db	1860	GCACCACCACTGCTTCACTCACTGGAAAAACAC	1899
Qy	1557	TCCCTGTATTCTGTAGAACCTCCACATCAAGAACACAGATTATGTAGACAGAT	1616
Db	1896	-----GATATCAAGATTGTGAGCAACAACT	1922
Qy	1617	GTTTGAGCAGAACTGCATGAGAGAGTTCAATGCAGAACTTAACTTCAACAAGAGTCCCTC	1676
Db	1923	CTTTGAAGAAAGCTGCATGAGAAAGTTGCAACTGTATTAATGCTTCAATGTCACAGCTTTC	1982
Qy	1677	ACTGTCCAGCAACCAAGGCTCTCACTACCACTGCTGCTCCGCTGTATTAAGAACCAAC	1736
Db	1983	ACTGCTTTCAACAACAAGAGTGCACAGACCTGCTGTTCAGACCAACAAAAAACTTT	2042
Qy	1737	ACACTTGTCCAAATTTCTTAACCTGCGACGTAATCGCTGTGCGAGCATGCAAGAGCTCAGCAC	1796
Db	2043	TCCGATCCCAATGTGCATGTATATGACGAAGGCATCAAGSTATGTAACAAGAACTCAGCAC	2102
Qy	1797	GATCCACATCCAGGGCAATGAGCAGCCCTCCCTCACAACAAGTGGCTCCAGCTTAATTT	1856
Db	2103	GATTTCAGTTCAGATGTGTGAGAGAACCTCTGTCTTCAACAGCCGATCAATTTAAATGC	2162
Qy	1857	GAAAGCAGACCAAGCATGAGACCAAACTGCAAAAACATCCAGATCAACAAGCATCAT	1916
Db	2163	CAAAATGGAAGATGTGTTAAACTTAATCTTGAAACAACTTATGTGATCAAGCAATAT	2222
Qy	1917	CAGATATCCCATCTCCCAAGGCTTAACCCCAAGGGGGAAGTGGGCCA	1965
Db	2223	AAGATATCCCAACCTTCCAGTAAACCAACCAAGAAAGAACAGTATGGCCA	2271

RESULT 6  
US-10-212-677-252  
; Sequence 252, Application US/10212677  
; Publication No. US20030129192A1

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1  APPLICANT: Chenault, Ruth A.
2  APPLICANT: Xu, Jiangchun
3  APPLICANT: Fanger, Gary R.
4  APPLICANT: Harlocker, Susan L.
5  APPLICANT: McNeill, Patricia D.
6  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
7  TREATMENT OF OVARIAN CANCER
8  FILE REFERENCE: 210121.484C7
9  CURRENT APPLICATION NUMBER: US/10/212,677
10 CURRENT FILING DATE: 2002-08-02
11 NUMBER OF SEQ ID NOS: 288
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 252
14 LENGTH: 5333
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 OS-10-212-677-252

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Query Match	44.1%	Score 935.4	DB 15	Length 5333
Best Local Similarity	70.7%	Pred. No. 3.2e-248		
Matches 1349	Conservative 0	Mismatches 491	Indels 69	Gaps 5
QY	66	AGTCACTATGGCGGCGGAGTTGGCGGCTTGCGCTTTTGGCCGGGCTGGCGGCATATGG	125	

Db	959	AGTATATATGCGCGCGGGGGTGGCAGCGCTGGCTGCCTTTTTCGAAGGGCAGCGGCTATCG	1018
Qy	126	GTGATGCGCGGTGGCCAACTGCCCCCATATGCCCTTGGCCCC---GGCCGACAAAGAACAGCG	182
Db	1019	GTGGATGCTGTGGGCTCGGGGCGTATAGCCGGCTCCCCGAGGCGAGGAGAAAGAAC	1078
Qy	183	GCAGATGATGCTGATTGTCTCTCAACGTGATGGGCGAGAGTTCCAGACTTGGAGACAC	242
Db	1079	CCAAGATGCTCTCATTTGGCTGGAATGTGATGGGCAACCGCTTCCAGAGTGGCAGGACAC	1138
Qy	243	GCTGGAGGCGTACCCCGGACACCCGCTGGGGCAGACCGGAGAAAGAGTCTTCTTCAACGA	302
Db	1139	CTGGAAAGTTTACCAAGACACTCTTATGGGCAAGTTCTGAGAGGGACCTTTTTCTACACCC	1198
Qy	303	GGACACCAAGAGTACTTCTTCGACCGGGACCCCGAGGTGTTTCGCTGCGCTCAACTT	362
Db	1199	AGAAAGCTGAGAGTATTTCTTTGACCGTGAACCAAGACATCTTCCGCCACATCTGAATTT	1255
Qy	363	CTACCCGACGGGGAGCTGCATACCCGCGCTACGATGCATCTCTGCTTACAGACGACGA	422
Db	1259	CTACCCGACTGGGAAGCTCCACTATCCCTCGCAAGAGTGCATCTCTGCTTACGATGAAGA	1318
Qy	423	GCTGGCCCTTCAACGGCAATCCTCCCGGAGATCATGGGGGACGCTGCTACAGGAGTCAAA	482
Db	1319	ACTGGCCCTTCTTGGCTCATCTCCGGAATATCGGCGGACTGCTGTATGAGGAGTACAA	1378
Qy	483	GGACCGCAAGGGGAGAACCGCGACGGCTCATGACGACACACGACTCGAGAACACCA	542
Db	1379	GGATTCGACGGCGAGAGAACCCCGAGCCCTCGACAGACGACCGGATACGACACCGCTGC	1438
Qy	543	GGAG---TCATGCTCTGCTCAGCTTCCGACACCATGTGCGGGCTTTCGAAACC	599
Db	1439	GGAGAGCGCTTGGCCCACTGACTGCAAGGCAAGAGGTCTGGAGGGCTTTCGAAACC	1498
Qy	600	CCAAACCAACGACCGCTGGCCCTTGTCTTACTAGTACTGTGGCTTCTTCACTGGTGTCTC	659
Db	1499	CCAAACCAACGACGATGGGACCCCTGGGTCTACTAGTACAGGGAGTTTTTCAATGGCGTCTC	1558
Qy	660	GGTGATCAACCAACCTGGTGGAGACGGTGCCTGGGGCAGCGGTCCCGG---CAGCAAGAA	716
Db	1559	TGTATGCGCAATGTGTGGAAACAGTGGCCGTGGGATCAAGCCAGGTCACTTAAAGA	1618
Qy	717	GCTGCGGTGGGGAGGCGTACTCGATGGCTTCTTCTGCTGGACAGCGGTGGCTCAT	776
Db	1619	ACTGCCCTGGAGAGGCGGTATGCTGTGGCTTCTTCTGCTTGGACACGGGCTCGTCAT	1678
Qy	777	GATTTTCAACCGTGAATCTCTCTGCGGCTCTTGGCGGCTCCAGCGGCTACCGCTTCAT	836
Db	1679	GATTTTCAACCGTGAATTTGCTTCCGCTGGCTGACCGCGCTAGTGTGTTACCTTTTGT	1738
Qy	837	CCGCAAGGTATGAGCATTCGACCGTGGTGGCCATCATGCGCCACTACATCGGCTGTGT	896
Db	1739	GCGTAGTGTATGATATCTGACCGTGGTGGCCATCTGCTTTATTAATTTGGGCTGTGT	1798
Qy	897	CATGACCAACACAGAGCGTGTCCGCGCTTCGTGTCAGCTCCGGTCTTTCGCGTCTT	956
Db	1799	GATGACGACAAATGAGGACGTGACGCGGACCTTTGTCACTCGGATCTTTCGGGTCTT	1858
Qy	957	CAGGATCTTCAAGTTTCCCGGCACTCCAGGGCTGCGGATCTCTGGGCTTACACACTGAA	1016
Db	1859	CAGGATCTTCAAGTTTCCCGCACTTCAAGGCTGGCGATCTCTGGGCTTACACACTGAA	1918
Qy	1017	GAGGTGGCGTCCGAACTGGGCTTCTTCTCTCCCTCACAATGGCCATCATCTT	1076
Db	1919	GAGTTGGCTCAGAAATTTGGGCTTCTTGTCTTCTGCTCAACATGGCTATCATCATCTT	1978
Qy	1077	TGCACTGTGATGTTTATGCGGAGAGGCTCTCGGCGACGAAAGTTTCAACAAGCATCCC	1136
Db	1979	CGTACAGTATATGTTTACGCAAGAGAGGGGTCTTGGCTTAGCAAGTTTCAACGATCCC	2038
Qy	1137	TGCTCGCTTTTGGTACCAATTCACACATGACACACTGGGATACGGAAACATGTGTCC	1196
Db	2039	TGCAAGCTTCTGGTATACATGTCACATGACACACTGAGGGATGTGTACATGTGTCC	2098

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QY 1197 TAAGACATTCAGGAGAAAGATCTTCGCTCCATCTGCTCTTGATGAGCGCTCTGATCAT 1256
Db 2099 AAAAAACATATGACGAGGAAAGATTTTGGTTCTATCTGTGCTAGTGGGGTCTTGATCAT 2158
QY 1257 TGGCCCTGCAAGTCCCTGTGATTTGTTTCAACTTTAGCCGATTTTACCACCAATCAGAG 1316
Db 2159 TGTCTACCTGTTCCGGTGTATGTATCTCACTTCAAGTCGATCTACACCAAGATCAACG 2218
QY 1317 AGCTGATTAACGAGGAGCAACAAAGAGGCGCTTGCCAGGATCCGTGTGAGCAAAAC 1376
Db 2219 AGAGACAAACGAGGAGCAACAAAGAGGAGTAAAGTAACTGAGTCCGAGTCCGAGCAAAAG 2278
QY 1377 AGGCACTGCAATGATGATCTGTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1436
Db 2279 CGGAAACGCAAAATGCTTACATGACAGACAAACGAAATGTTTACTGATTAATCAGCTGCA 2338
QY 1437 GCTGACGGGACACCCAGAGAGAGACATGAGGACCACTCACTCACTCACTCACTCACTCA 1496
Db 2339 GTCCCTAGAGGA---TGAGCAGAGCTTTTGTAGCAATCCGAGTCCAGCTTTGAAACCCA 2395
QY 1497 GCATCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
Db 2396 GCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2431
QY 1557 TCCCTGTTATCTGTAGCAACCTCCACATCAACCAACGAGTTTATTTAGTACAGAT 1616
Db 2432 -----GAAATCAGAGTTGTGAGCAAGT 2458
QY 1617 GTTTGACGAAATCTGATGAGAGTTCATGACGAAGTACCTCCATCCACAAAGAGTCCCTC 1676
Db 2459 CTTTGAAGAAAGTGTGATGAGAGTTCATGCTTAAATGCTTCAAGTCAAGTCAAGTCCCTC 2518
QY 1677 ACTGTCAGGACACCCAGGAGGCTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
Db 2519 ACTGTTTCAACAAAGAGTTCACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2578
QY 1737 ACACTGCTCAATTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
Db 2579 TCGCATCCCAATATGCAATGATATCAGAAAGCATCAAGATGATATCAAAATCACTGAGCAC 2638
QY 1797 GATTCATCTCAGGAGGAGTGAAGAGGCTTCCCTCAACACAGTGTGCTTCACTTAAATTT 1856
Db 2639 GATTTCATCTGATGTGTGAGAGAAACCTCTGTCTTAAACGCGATCCAGTTTAAATGC 2698
QY 1857 GAAAGCAGACGAGAGCTGAGCAAACTGCAAAACATCCAGATCCAGACGATCAT 1916
Db 2699 CAAAATGGAAGAGTGTGTTAACTTAACTGTAACCTTATGTGACTACAGCAATAT 2758
QY 1917 CAGCATCCCACTCCCAAGGCTTAACTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1965
Db 2759 AAGCATCCCAACACTCCAGTAACTCAACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2807

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## RESULT 7

```

US-10-212-677-254
: Sequence 254, Application US/10212677
: Publication No. US2003012912A1
: GENERAL INFORMATION:
: APPLICANT: Chenault, Ruth A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C7
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 254
: LENGTH: 5333

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: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-212-677-254
Query Match 44.1%; Score 935.4; DB 15; Length 5333;
Best Local Similarity 70.7%; Pred. No. 3.2e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTCACATGAGCGGCGGAGGATTCGGGCTGCGCTGCTTTCGCGGAGTTCGCGGAGTTCGCG 125
Db 959 AGTATCATGAGCGGCGGAGGATTCGGGCTGCGCTGCGCTTTCGCGGAGTTCGCGGAGTTCGCG 1018
QY 126 GTGATGCGGAGGAGGATTCGGGCTGCGCTGCGCTTTCGCGGAGTTCGCGGAGTTCGCG 182
Db 1019 GTGATGCGGAGGAGGATTCGGGCTGCGCTGCGCTTTCGCGGAGTTCGCGGAGTTCGCG 1078
QY 183 GCAGATGAGTGTATGCTTCAACTGATGAGGAGGAGTTCGCGGAGTTCGCGGAGTTCGCG 242
Db 1079 CCAAGATGCTTCAATGTGTGATGAGGAGGAGTTCGCGGAGTTCGCGGAGTTCGCG 1138
QY 243 GCTGAGCGGCTACCGGAGACCCCTGCTGCGGAGGAGGAGGAGTTCGCGGAGTTCGCG 302
Db 1139 CCGGAGACCTTACCGGAGACCCCTGCTGCGGAGGAGGAGTTCGCGGAGTTCGCG 1198
QY 303 GGAACCAAGAGATCTTTCGAGCCGAGACCCGAGGAGTTCGCTGCTGCTGCTGCTGCTGCT 362
Db 1199 AGAAATCAGAGATATTTCTTTGACCGTACCGAGATCTTTCGCGGAGTTCGCG 1258
QY 363 CTACCGGAGGAGGAGTTCGATACCCGCTGAGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 1259 CTACCGGAGGAGGAGTTCGATACCCGCTGAGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCT 1318
QY 423 GCTGCGCTTCTACGCGGATCTCCGAGATTCATCGGAGGAGTTCGCTGCTGCTGCTGCTGCT 482
Db 1319 ACTGCGCTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1378
QY 483 GGAACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
Db 1379 GGAATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1438
QY 543 GGAAG---TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db 1439 GGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1498
QY 600 CCACACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
Db 1499 CCACACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558
QY 660 GGTGATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
Db 1559 TGTGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1618
QY 717 GCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 776
Db 1619 ACTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1678
QY 777 GATCTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 836
Db 1679 GATCTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1738
QY 837 CCGAGCGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 896
Db 1739 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1798
QY 897 CATGACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 956
Db 1799 GATGACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1858
QY 957 CAGGATCTTCAAGTTTTCGAGCACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016
Db 1859 CAGGATCTTCAAGTTTTCGAGCACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1918
QY 1017 GAGCTGTGCTCGAAGCTGAGGCTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1076

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Db	1919	GAGTGTGCTCAGAAATTGGGCTTCTTGCTTTTCTCGCTCAACCAAGGCTATCATCTT	1978
Oy	1077	TGCCACTGTGATGTTTATATGCGAGAAAGGCTCTCGGCGACGAAGTTTCAACAGCATCCC	1136
Db	1979	CGCTACATATATGTTCTAAGCAGAGAAAGGGCTTTCGGCTAGCAAGTTTACACAGATCCC	2038
Oy	1137	TGCTCGTTTTGATACACATTTGTCCATGACACACACTGGGATACGAGACATGTTGCC	1196
Db	2039	TGCAGCCTTCTGTATATCATCGTCAACATGACACACTAAGGGATATGGATCATGTGTC	2098
Oy	1197	TAAACCATTCGAGGGAAGATCTTCGGCTCATCTGCTCTCTTGAATGGGCTCTGTAT	1258
Db	2099	AAAAACCATACAGGGAAGATTTTGGTTCTATCTGTTCTCGAGATGGGGCTTGTGAT	2158
Oy	1257	TGCCCCGACAGCCCTGTGATTTGTTTCCACTTTAGCCGGATTTACCAACCAAGATCAAG	1316
Db	2159	TGCTCTACCTGTTCCGGTGAATGTATCCAACTTCAGTGCATCTACACCAAGATCAAG	2218
Oy	1317	AGCTGATTAACGCAAGGGCAAAAGAAAGGCGCGCTTCCAGAGTCCGTGTGGCCAAAC	1376
Db	2219	AGCAGACAAACGAAGGGCACAAAGAAAGCTAGACTGGCCAGGATCTCGGGCAGCCAAAG	2278
Oy	1377	AGGCAGTTGCAATGATACCTTGACAGAGAGCGCAACGGGCTCTTCAAAGAGCGCTGGA	1436
Db	2279	CGAAGCGCAATGCTTCAATGACAGAGAAACGAATGGTTTACTCAGTAATCAGCTCA	2338
Oy	1437	GCTACGGGCAACCCAGAGAGAGACATGGGCAAGACCACTCATCTGAGAGCCA	1496
Db	2339	GTCCTCAAGGA---TGAAGAGGCTTTTGTATGACAAATCCGGCTTCAGCTTTGAAACCA	2399
Oy	1497	GCATCATACCGTCTGCACTGCTGTGAAAAACCACTGGGTTGTCTATCTTGTGATGA	1558
Db	2396	GCAACCAACCTGCTTCACTGCTGTGAAAAACCA-----	2431
Oy	1557	TCGCCCTTATCTGTACGAACCTCCACCATCAAGAACACGAGTTATTTGAGCAGAT	1618
Db	2432	-----GATACACAGTTTGTGAGCAACAGT	2458
Oy	1617	GTTTGAGCAGAACTGCTATGAGAGTTCAATGCAAGACTAACCCATCACAGAGTCCCTC	1676
Db	2459	CTTTGAAGAAAGCTGACATGAAAGTTGCAACGTGTATGTCCTTCAAGTACACAGCTTTC	2518
Oy	1677	ACTGTCCAGCAACCAGGCTTCACTACCAACTGCTGCTCCGTCGTAGTAAGAACCAAC	1736
Db	2519	ACTGCTTTCACAAACAGGAGTCAACGAGACCTGCTGTTCACGACCAACAAAAACCTT	2578
Oy	1737	ACACCTGCCCAATTCTAACCTGCGCAAGTACTGCGCTGCGACATGACAAAGCTCAGAC	1796
Db	2579	TGCGATCCCAATGTCCAAATGATATCGAAGGCAATCAAGTATGATTAACAGAACTCAGAC	2638
Oy	1797	GATCCACATCCAGGGCAGTGTGACAGGCGCTCTCCTCAACACAGTCCCTCAGCCTTAATT	1856
Db	2639	GATTCAGATCAGATGTGTGAGAGAACACCTCTGTCTAACAGCGCATCCAGTTTAATGC	2698
Oy	1857	GAAGACAGACGACGACTGTGAACCAAACTGCAAAAATCCAGATCACACAGCCATAT	1916
Db	2699	CAAAATGAAAGTGTGTTAACTTAATCTGTGAACACTTATATGACTACAGCAATAT	2758
Oy	1917	CAGATATCCCATCCCCCAGCGCTTATCCCAAGGGGGAAAGTGGGCA	1965
Db	2759	AAGATATCCCAACCTTCAGTAAACCAACCAAGAGAGACGATTAAGGCA	2807

RESULT 8  
 US-10-361-811-252  
 : Sequence 252 Application US/10361811  
 : Publication No US20030206918A1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Fanger, Gary R.  
 : APPLICANT: Fling, Steven P.  
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 : TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

```

; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361.811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-252

Query Match      44.1%; Score 935.4; DB 17; Length 5333;
Best Local Similarity 70.7%; Pred. No. 3.2e-248;
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5

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QY	66	GTGACCAATGCGCGGCCGAGATTGGCGGCGCTGGCTGCTTTTCCGCGCGGTGGCGGCATCG	125
Db	959	AGTATATCATGCGCGCGGGGATGGGACGCGTGGCTGCTTTTTCAMGGGACGCGGCTATCG	10116
QY	126	GTGATGCGCGGTGGCCAACTGCCCCATGCGCCCTGGCCCC---GGCCGACAAAGAACAGCG	182
Db	1019	GTGATGCTCTGTGGCTCGGGGCGCTATGCGGCTCCCCCGAGGCGAGGAGAGAAAAGGAC	10786
QY	183	GCAGGATGAGCTGATTGTCTCTCAACGTGATGGGCGAGGTTCCAGACTTGGAGGACAC	242
Db	1079	CCAAGATGCTCTCATTTGTGCTGAATGTGATGGGACCGCTTCCAGAGTGGGACAGAC	11386
QY	243	GCTGGAGGCGTACCCCGGACCCCTGCTGGGCGAGCACGGAGAAAGGAGTCTTCTTCAACGA	302
Db	1139	CTTGGAACGTTTACCGAGACACTCTACGTGGGAGTTCTGAGAGGGACTTTTCTACACCC	11996
QY	303	GGACACCAAGAGTACTTCTTCGACCGGGACCCCGAGGTGTCTCGCTGCGTCAACTT	362
Db	1199	AGAAACTAGGAGATTTCTTTGACCGTGAACCAAGACATCTTCCGCCACATCTGAATTT	12556
QY	363	CTACCGCACGGGGAACTGCACTAACCCGCGCTACGATGTCATCTGTGCTTACGACGACA	422
Db	1259	CTACCGCACTGGGAAGCTCCACTATCTCGCCACGAGTGCATCTCTGCTTACGATGAAGA	13186
QY	423	GCTGGCCCTTTCAGCGGACCTCTCCCGGAGATCATGGGGGACGCTGCTACGAGGAGTACAA	482
Db	1319	ACTGGCCCTTCTTTGCTCTCATCTCCGAAATATGCGGCGACTGCTGTATGAGAGATACAA	13786
QY	483	GGACCGCAAGGGAGAAAGCGCGGAGCGGCTCATGAGACGACACGACTTGGAGAAACAACA	542
Db	1379	GGATGCGACGGGAGAGAAAGCGCGAGCGCTGACAGAGGACGCGGATACGACACCGCTGG	14386
QY	543	GGAG--TCCATGCGCTGCTCAGCTTCCGCAACATGTGGCGGCGCTTTCGAGAACCC	599
Db	1439	GGAAGCGCCCTTGGCCCCACATGACTGCAAGGCAAGGAGTCTGAGAGGCGCTTTCGAGAACCC	14986
QY	600	CCACACACGACGCGTGGCGCTGCTTCTACTAGTGACTGGGCTTCTTCACTGCGTGTGTC	659
Db	1499	CCACACACGACGATGGCGCTGCTGCTTCTACTAGTCACGGGGATTTTTCATTTGCGCTGTC	15586
QY	660	GGTCAATCAACAACCTGTGTGAGACGCTGCCCTGGCGGACGCTGCCGGG---CAGCAAGGA	716
Db	1559	TGTCAATCCGGAATGTGTGTGAAGAACGTGCCGTGGAGATCAAGCCAGGTCAATTAAAGA	16186
QY	717	GCTGCCGTGGCGGAGCGCTACTCGGTGGCTTCTTCTGCTGGAACACGCGGTGCTCAT	776
Db	1619	ACTGCCCTGTGGAAGCGGATATGCTGTGGCTTCTTCTGCTTGGACACGCGCTCGTCAAT	16786
QY	777	GATCTTCAACGCTGAGATACCTCCGCGGGCTTTCGGCGGCTCCGACGCGTACCGCTTCAT	836
Db	1679	GATCTTCAACGCTGAGATATTTGCTTCCGCTGGCTGCAAGCGCTCATGTGTGTTACCGTTTGT	17386
QY	837	CCGACGCGTCAATGACATCATCGACGTGTGGCCATATGCGCTTACTACTACATCGGCTGTGT	896
Db	1739	GCGATGTGATATGATATCATTCAGCGTGTGGCCATCTTGCTTATTAACATTTGGGCTGTGT	17986
QY	897	CATGACCAACACAGAGACGTGTCCGGCGCTTGTCAAGTCCGCGGCTTTCGCGCTT	956



Db 1799 GATGACAGCAATGAGAGAGCTGACGGAGCCTTTGTCACTCCGAGTCTTCGGGCTCT 1858  
Qy 957 CAGGATCTTCAAGTTTCCCGCCACTCCAGGAGCTGCGGATCTTGAGGCTACACATGAA 1016  
Db 1859 CAGGATCTTCAAGTTTCCCGCCACTCCAGGAGCTGCGGATCTTGAGGCTACACATGAA 1918  
Qy 1017 GAGCTGTGCTCCGAACTGGGCTTTCTTCTTCTCCCTCAGGAGGAGGATCATCTT 1076  
Db 1919 GAGTTGTGCTCAGAAATGGGCTTTCTTCTTCTGCTTCTGCTCAGCATGGCTATCATCTT 1978  
Qy 1077 TGGCAGTGTGATTTTATGCGAAGAAAGGCTCTGCGGAGGAGAGTTCACAGCATCC 1136  
Db 1979 CGCTACAGTTATTTCTACGCAAGAAAGGAGCTTGGCTAGGAGTTCAACGAGATCCC 2038  
Qy 1137 TGGCTGTTTGGTACACCATGTGACCATGACCAACTGGAGATACGAGAGATGGTGC 1196  
Db 2039 TGGAGCTTCTGTATATCCATCTGTCACATGACCAACTGGAGATGGTATGGTGC 2098  
Qy 1197 TAAAGCATTTGAGGAGAAAGTCTGCGCTCATCTGCTCTTGAAGTGGCTGCTGAT 1256  
Db 2099 AAAACCATGACAGGAAAGATTTTGGTCTATCTGTTCTGAGTGGGCTTGGTCTAT 2158  
Qy 1257 TGGCTTCCAGTGTGCTGTGATTTGTTTCCACTTGAAGGATTTTACCAAGATCAGAG 1316  
Db 2159 TGTCTACCTGTTCCGGTGTATGATTCACATTCAGTGTGATTCACCAAGATCAGAG 2218  
Qy 1317 AGCTGATTAAGCAGAGGCACAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1376  
Db 2219 AGCAGACAAACGAAAGGAGCAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2278  
Qy 1377 AGGCACTTGAATGATGATCTGTCAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1436  
Db 2279 CGGAGAGGCAAAATGCTTACATGACAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2338  
Qy 1437 GCTGAGCGGAGACCCCAAG 1496  
Db 2339 GTCCTCAGAGAG--TGAGAGAGGCTTTTGTAGAAATTCGGGCTCCAGCTTTGAAACCA 2395  
Qy 1497 GCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1556  
Db 2396 GCACACACACCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2431  
Qy 1557 TCCCTGTTTCTGTGAGAACTTCCACCATCAAGAACACGAGTTTATGATGAGCAGAT 1616  
Db 2432 -----GAATCAAGAGTTTGTGAGCAAGAT 2458  
Qy 1617 GTTTGAGCAGAACTGCAATGAGAGTTCAATGACAGAACTACCAAGAGTCCCTC 1676  
Db 2459 CTTTGAAGAAAGCTGCAATGAGAGTTGCACTGTTAATGCTTCAAGTACAGATCCTTC 2518  
Qy 1677 ACTGTCAGGACCCAGAGGCTCACTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1736  
Db 2519 ACTGTTCTTCAACAGAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2578  
Qy 1737 ACACTGCTCAATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1796  
Db 2579 TCCGATCCCAATGCTGATGATCAGAGAGCATCAAGATGATGATGATGATGATGATGATG 2638  
Qy 1797 GATTCACATCAGAGGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1856  
Db 2639 GATTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2698  
Qy 1857 GAAAGCAG 1916  
Db 2699 CAAAG 2758  
Qy 1917 CAGCATCCCACTTCCCAAGGCTTAACTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1965  
Db 2759 AAGCATCCCAAGCTCCAGTAAACACACAGAGAGAGAGAGAGAGATGGCCA 2807

RESULT 9  
US-10-361-811-254

Sequence 254, Application US/10361811  
Publication No. US20030206918A1  
GENERAL INFORMATION:  
APPLICANT: Fanger, Gary R.  
APPLICANT: Filing, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C8  
CURRENT APPLICATION NUMBER: US/10/361,811  
CURRENT FILING DATE: 2003-02-05  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 254  
LENGTH: 5333  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-361-811-254

Query Match 44.1%; Score 935.4; DB 17; Length 5333;  
Best Local Similarity 70.7%; Pred. No. 3,2e-248;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

Qy 66 AGTCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 125  
Db 959 AGTATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1018  
Qy 126 GTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 182  
Db 1019 GTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078  
Qy 183 GCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 242  
Db 1079 CCAAGATGCTCATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1138  
Qy 243 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302  
Db 1139 CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1198  
Qy 303 GAGACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362  
Db 1199 AGAAATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1258  
Qy 363 CTACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 422  
Db 1259 CTACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318  
Qy 423 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 482  
Db 1319 ACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378  
Qy 483 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542  
Db 1379 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1438  
Qy 543 GAGG--TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599  
Db 1439 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1498  
Qy 600 CCAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659  
Db 1499 CCAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558  
Qy 660 GATCATCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716  
Db 1559 TGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1618  
Qy 717 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 776  
Db 1619 ACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1678  
Qy 777 GATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 836  
Db 1679 GATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1738

QY 837 CCGAGCGTCATGAGCATCATGACGTGTGGCCATATGCCCTACTATCGGTCTGT 896  
DB 1739 GCGTGTGTCTATGATCATGACGTGTGGCCATCTGCTTATATCATTTGGGCTGT 1798  
QY 897 CATGACCAACAACGAGAGAGTGTCCGGGCTTCTGTCAGCTCCGGGTCTTCCGGCTT 956  
DB 1799 GATGACAGACATATAGAGAGCTCAGGGAGCTTTGTACACTCCGAGTCTTCCGGGTCTT 1858  
QY 957 CAGATCTTCAAGTTTCCCGCCACTCCAGGGCTCTGGGATCTGGGCTACACACTGAA 1016  
DB 1859 CAGATCTTCAAGTTTCCCGCCACTCTCAAGGCTCTGGGATCTGGGATCTGGGATGAA 1918  
QY 1017 GAGGTGGCTCCCAAGCTGGGCTTCTCTCTCCCTCAACATGGCCATCATATCTT 1076  
DB 1919 GAGTGTGCTCAGATGATGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1978  
QY 1077 TGCCACTGTGATGTTTATGCGGAGAGGGCTCTCCGGCCAGCAAGTTCAACAGCATCCC 1136  
DB 1979 CGCTACAGTTATGTTCTACGAGAGAGGGGTCTTCCGGCTACAGATTCACAGCATCCC 2038  
QY 1137 TGCCCTGTTTGTATACACATGTCACATGACCACTGGGATACGAGACATGGTCC 1196  
DB 2039 TGCAAGCTTCTGTATACATGTCACATGACCACTAGGGATATGGTACATGGTCC 2098  
QY 1197 TAAAGCATTTGAGGAGAGATCTTGGGCTCATCTGCTCTTGAAGTGGCTCTGTAT 1256  
DB 2099 AAAAAACATACAGGAGAGATTTTGTATCTGTTCTGCTGAGTGGGCTCTGTAT 2158  
QY 1257 TGCCCTGCGAGTCTCCGTGATGTTTTCACCTTATGCGGATTTTACCAAGAAATCAGAG 1316  
DB 2159 TGCTCTACTCTTTCGGGATGTTATCTCACTTCACTGCTCATCTACCAAGAAATCAGAG 2218  
QY 1317 AGCTGATTAACGAGGAGGAGCAAAAGAGGCGCTTCCAGATCCGTGTGGCCAAAC 1376  
DB 2219 AGCAGACAAAGAGAGGAGCAAAAGAGGAGTACAGTGGCCAGAGATCCGGGAGCCAAAG 2278  
QY 1377 AGGAGATTTGAGATCATCTGTCACAGAGAGGAGGCTCTCTCAACAGAGGCTTGA 1436  
DB 2279 CGGAAGGCAATATCTTATCATGACAGAGAGAAAGATGTTTATCTCAGTAACTCAGCTGCA 2338  
QY 1437 GCTGACGGGAGCAACCCAGAGAGAGAGACATGAGGAGAGCACTCATCTCATGAGGCA 1496  
DB 2339 GTCTCTAGAGAGA---TGAGAGGCTTTTGTATGCAAAATCCGGCTCAGCTTTGAACCA 2395  
QY 1497 GCATCATCACTGTGTGACCTGAGAAAAAACCACTGAGTGTCTTATCTTGTGTATGA 1556  
DB 2396 GCACACACACCTGCTTCACTGCTGAAAAAACCACTGAGTGTCTTATCTTGTGTATGA 2431  
QY 1557 TCCCTCTTATCTGATGAGACCTCCACCATCAAGAACCACTGAGTGTATGATGAGCAT 1616  
DB 2432 -----GATACAGAGTTTGTGAGCAAGAT 2458  
QY 1617 GTTTGAGAGAACTGATGAGAGTTTCAATGAGAACTAACCATCAACAAAGTCCCTC 1676  
DB 2459 CTTTGAAGAAAGCTGATGAGAAAGTTGCACTGTTATGTTCTTCAATCAACAGTCCCTC 2518  
QY 1677 ACTGTCCAGCAACCCAGGCTCTCACTACCACTGTGTCTCCGTGTATGAGAAAGCAAC 1736  
DB 2519 ACTGTCTTCAACAAGAGAGTCAACAGCACTGTGTCTTCAAGAGCACAAAAAAATCTT 2578  
QY 1737 ACACCTGCCCCAATTTTAACTGTGCAAGTACTGTGCTGGGAGCATGAGAGCTCAGAC 1796  
DB 2579 TCGCATCCCAATATCCATATGATCAGAGAGGATCAAGAGTATGATACAAAGATCTAGAC 2638  
QY 1797 GATCCACATCCAGGAGAGTGAAGAGCTTCCCTCAACAGAGTGGCTCAGCTTAATTT 1856  
DB 2639 GATTCAGATCAGATGTGTGAGAGAGACCTCTGTCTTAAAGCCGATCAAGTTTAAATTC 2698  
QY 1857 GAAAGCAGACGAGCTGAGACCAAACTGCAAAACATCCAGATCACACAGCCATCAT 1916  
DB 2699 CAAATGGAAGAGTGTGTTAACTAACTGAAACAACTTATGTGATGATGAGCAATAT 2758

QY 1917 CAGATCCCACTCCCGGAGGCTAACCCAGAGGAGGAGAAAGTCCGCA 1965  
DB 2759 AAGCATCCCACTCCCGGAGGCTAACCCAGAGGAGGAGAAAGTCCGCA 2807

RESULT 10  
US-10-369-186-252  
; Sequence 252, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.4849  
; CURRENT FILING DATE: US/10/369,186  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 252  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-369-186-252

Query Match 44.1%; Score 935.4; DB 17; Length 5333;  
Best Local Similarity 70.7%; Pred. No. 3.2e-248;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;

QY 66 AGTCACCATGAGCGGCGGAGGAGTGGGCTGAGCTGCTTTTGGCGGGGCTGGGCATGCG 125  
DB 959 AGTATCATGAGCGGCGGAGGAGTGGGCTGAGCTGCTTTTGGCGGGGCTGGGCATGCG 1018  
QY 126 GTGATGCGGCTGAGCACTGCGCCATGCTCCCTGAGCCCTC---GGCCGACAAAGCAAGCG 182  
DB 1019 GTGATGCGCTGAGCACTGCGGCTGAGCTGCGCCATGCTCCCTGAGCCCTC---GGCCGACAAAGCAAGCG 1078  
QY 183 GCAGATGAGCTGATGTTGCTTCAACCTGAGTGGGCGAGAGTTCACAGACTGAGAGACAC 242  
DB 1079 CCAAGATGCTCTCATTTGCTGAGATGAGTGGGAGCCCGCTTCAAGCTGAGAGACAC 1138  
QY 243 GCTGAGGAGCTACCCGAGCACTGCTGAGGAGAGAGAGAGTCTTCTTCAAGCA 302  
DB 1139 CTTGAAAGCTTACCAAGCACTTACTGAGGAGAGTCTGAGAGAGAGCTTTTCTTCAACCC 1198  
QY 303 GGAACCAAGAGATCTTCTTCAACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
DB 1199 AGAAATCAGAGATTTCTTGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1258  
QY 363 CTACCGGAGGAG 422  
DB 1259 CTACCGGAG 1318  
QY 423 GCTGAGGAG 482  
DB 1319 ACTGAGCTTCTTGGCTCTATCCGAAATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1378  
QY 483 GGAACCAAG 542  
DB 1379 GGAAG 1438  
QY 543 GGAAG---TCAAGCTGCTGCTGAGCTTCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
DB 1439 GGAAG 1498  
QY 600 CCAACAG 659  
DB 1499 CCAACAG 1558  
QY 660 GGTATCAACAACTGTGTGAG 716  
DB 1559 TGTATGCGGAAATGTGTGAG 1618

QY 717 GCTGCGGAGGAGCGCTACTCGGTGCGCTTCTTCTGCTGAGACAGGCGTGCAT 776  
DB 1619 ACTGCCCTGTGAGAGAGGAGTATCTGTGCGCTTCTTCTGCTGAGACAGGCGCTGCAT 1678  
QY 777 GATCTTCAACCGTGAAGTACTCTCTGGGCGCTTCTGGGCGCTTCCAGCGCTTCACTCCGCTTCA 836  
DB 1679 GATCTTCAACCGTGAAGTATTTGCTGCGCTGAGCGCTGATGCTTCACTCCGCTTCA 1738  
QY 837 CCGCAGCGCTGAGCATGAGCATGAGCGTGTGCGCATCATGCGCTTCACTCACTCCGCTTCA 896  
DB 1739 GCGTATGTCATGATGATCATCATGAGTGTGCGCATCTGCTTATTTCACTTGGCGTGT 1798  
QY 897 CATGACCAACAGAGAGCGTGTGCGCGCTTCTGTCAGCTCCGCGCTTCTGCGCTT 956  
DB 1799 GATGACAGCAATGAGAGCGTCAAGCGCTTGTTCACACTCCGAGTCTTCCGCGCTT 1858  
QY 957 CAGGATCTTCAATTTTCCCGCACTCCAGGCGCTTCCGATCTCTGGGCTTCACTCACTGAA 1016  
DB 1859 CAGGATCTTCAATTTTCCCGCACTCCAGGCGCTTCCGATCTCTGGGCTTCACTCACTGAA 1918  
QY 1017 GAGCTGTGCGCTGAGAGTGTGCTTCTCTCTCCCTCAGCATGCGCTTCACTCTT 1076  
DB 1919 GAGTGTGCTGAGAGTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1978  
QY 1077 TGGCTGTGATGTTTATGCGAGAGAGGCGCTCTGCGCAGCAAGTTCAAGCATCCC 1136  
DB 1979 CGCTACAGTATGTTCTACAGCAAGAGGCGCTCTGCGCTACAGCAAGTTCAAGCATCCC 2038  
QY 1137 TGGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1196  
DB 2039 TGGAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2098  
QY 1197 TAAGCATGAGAGAGAGTCTTGGCTCATCTGCTCTGAGTGTGCTGCTGCTGCTGCT 1256  
DB 2099 AAAAACAATGAGAGAGAGTCTTGGCTCATCTGCTCTGAGTGTGCTGCTGCTGCTGCT 2158  
QY 1257 TGGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316  
DB 2159 TGGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2218  
QY 1317 AGCTGATTAACGAGAGGCAAAAGAGGCGCTTGGCAGATCTGCTGCTGCTGCTGCTGCT 1376  
DB 2219 AGAGAGCAAAAGAGGCAAAAGAGGCGCTTGGCAGATCTGCTGCTGCTGCTGCTGCT 2278  
QY 1377 AGGCAATGAGATGATGCTGCAAGAGAGGCGCTTGGCAGATCTGCTGCTGCTGCTGCT 1436  
DB 2279 CGAGAGGCAAAAGCTTCACTGAGAGCAAAAGAGGCTTGGCAGATCTGCTGCTGCTGCT 2338  
QY 1437 GCTGACGGGCAAGGAGAGAGGAGCATGAGGCAAGAGGCTTGGCAGATCTGCTGCTGCT 1496  
DB 2339 GCTGACGGGCAAGGAGAGAGGAGCATGAGGCAAGAGGCTTGGCAGATCTGCTGCTGCT 2395  
QY 1497 GATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556  
DB 2396 GATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2431  
QY 1557 TCCCTGTATCTGTAAGAACTTCAACATCAAGAAAGAGGTTTATGATGAGCAT 1616  
DB 2432 -----GATCAAGAGTTTGTGAGCAAAAGT 2458  
QY 1617 GTTGAAGCAAGTGAAGAGTTCATGAGAACTTCACTCAAGAAAGTCTTCC 1676  
DB 2459 CTTTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2518  
QY 1677 ACTGTCAAGCAAGGAGGCTCACTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736  
DB 2519 ACTGTCTTCAAGCAAGAGTTCACAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2578  
QY 1737 AGACCTGCAAGTCTTCACTGCAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796  
DB 2579 TCGCATCCCAAAATGCAATGATATCAAGAGAGCATCAAGAGTATGATCAAGAACTCAGCAC 2638  
QY 1797 GATTCACATCAAGGAGTGAAGAGGCTTCCCTCAACCAAGTGTCTCAGCTTAATTT 1856

DB 2639 GATTCAGATCAAGTGTGAGAGAACTCTGTCTTAACACCGATCCAGTTTAATGC 2698  
QY 1857 GAAAG 1916  
DB 2699 CAATATGAAAGAGTGTGTTAACTTAATCTGTAACAACCTTATGTAAGTCAAGCAATAT 2758  
QY 1917 CAGCATCCCACTCCCGCAGCTTAACCCAGAGGAGGAGAGTTCGCA 1965  
DB 2759 AGCATCCCACTCCCGCAGCTTAACCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807  
  
RESULT 11  
US-10-369-186-254  
; Sequence 254, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Filing, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FaersEQ for Windows Version 4.0  
; SEQ ID NO 254  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-369-186-254  
  
Query Match 44.1%; Score 935.4; DB 17; Length 5333;  
Best Local Similarity 70.7%; Pred. No. 3.2e-248;  
Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;  
  
QY 66 AGTACCATGAGCGGCGAGAGTGTGCGCTGCTGCTTGTGCGGCGTGGCCATCCG 125  
DB 959 AGTATCATGTGCGGCGGAGGAGTGTGCGCTGCTTGTGCGAGGCGAGCGCTATCCG 1018  
QY 126 GTGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182  
DB 1019 GTGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078  
QY 183 GCAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242  
DB 1079 CCAAGTGTCTTCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1138  
QY 243 GCTGAGCGCTACCCGAGACCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302  
DB 1139 CCGTGAAGCTTACCGAGACCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198  
QY 303 GGAACACAGAGTACTTCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
DB 1199 AGAAATTCAGAGTATTTCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258  
QY 363 CTACCGCAGGAG 422  
DB 1259 CTACCGCAGGAG 1318  
QY 423 GCTGAGCTTCTACAGGATCTTCCGAGATCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 482  
DB 1319 ACTGAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1378  
QY 483 GGAACCGAG 542  
DB 1379 GGAATCCAG 1438  
QY 543 GGAG---TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599  
DB 1439 GGAAG 1498  
QY 600 CCAACACAG 659

Db 1499 CCAACACGACGAGATGCGCCCTGCTGTTTACATATGACGGGTTTTCATGTCCTC 1558  
Qy 660 GGTATATCAACAGTGTGTGAGACGGTCCGTCGGACGGTCCCGG--CAGAAAGA 716  
Db 1559 TGTATCCGAGATGTGTGAGAAACAGTCCGGATCAAGCCAGGTCATTAAGA 1618  
Qy 717 GCTCCGCGGGGAGCGCTACTCGTGGCCCTTCTTCTGAGCAGGGGTGGTAT 776  
Db 1619 ACTGCGCTGTGAGAGCGGTATGCTGTGCTTCTTCTGAGCAGGGCTGCTAT 1678  
Qy 777 GATCTTCAACCTGTGAGTACTCTGCGGCTCTTCCGCGCTCCACCGCTACCGTTAT 836  
Db 1679 GATCTTCAACGTTAGTATTTGCTTCCGCTGCTGACAGCGCTAGTCTTACCGTTTGT 1738  
Qy 837 CCGAGCGCTATGAGCATATGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 896  
Db 1739 GCGTAGTGTATGATGATCATGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1798  
Qy 897 CATGACCAACAGAGACGTGTCCGCGCTTGTGATCGCTCCGCGCTTCCGCGCTT 956  
Db 1799 GATACACAGACATAGAGAGCTGAGGAGCTTGTGATCACTCCAGTCTTCCGCGCTT 1858  
Qy 957 CAGGATCTTCAAGTTTCCCGCACTCCAGGCGCTGCGGATCTGCGGCTACACCTGA 1016  
Db 1859 CAGGATCTTCAAGTTTCCCGCACTCTCAAGGCTGCGGATCTGCGGCTACACCTGA 1918  
Qy 1017 GAGCTGTGCTCGAAGTGTGCTTCTTCTTCCCTCAACATGAGCATATCATCTT 1076  
Db 1919 GAGTGTGCTCGAAGTGTGCTTCTTCTTCCCTCAACATGAGCATATCATCTT 1978  
Qy 1077 TGCCATCTGTATGTTTATGCCAGAGAGGCTCTCGGCGCAAGTTTCAACAGATCCC 1136  
Db 1979 CGCTACAGTTATGTTTATGCCAGAGAGGCTCTCGGCGCAAGTTTCAACAGATCCC 2038  
Qy 1137 TGCCGCTGTTTGTATACATGTTGATGATGATGATGATGATGATGATGATGATGATG 1196  
Db 2039 TGCAACCTTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2098  
Qy 1197 TAAAGCATGTCAGGAGAGATCTTCCGCTCATCTGCTCTTGAAGTGTGCTGTAT 1256  
Db 2099 AAAAACATATACAGGAGAGATTTTGTGTTATGCTGCTGAGTGTGAGTGTGAT 2158  
Qy 1257 TGCCCTGCACTCTGCTGTATGTTTGTGATGATGATGATGATGATGATGATGATG 1316  
Db 2159 TGCTCTACTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2218  
Qy 1317 AGCTGATTAAGCGAGGAGCAAAAGAGGCGCGCTTGCAGGATCCGTTGCGCAAAAC 1376  
Db 2219 AGCAGACAAAGAGGAGCAAAAGAGGCTGATGATGATGATGATGATGATGATGATG 2278  
Qy 1377 AGGAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1436  
Db 2279 CGGAAGCGCAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2338  
Qy 1437 GCTGACGGGCAACCCAGAGAGAGACATGAGGCAACCTTCACTCATGAGAGCCA 1496  
Db 2339 GTCCTCAGAGAG--TGAGAGGCTTGTGATGAGAAATCCGCTCAGCTTGAACCCA 2395  
Qy 1497 GCATCATACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1556  
Db 2396 GCACACCACTGCTTCACTGCTGAGAAACCAAC----- 2431  
Qy 1557 TCCCTGTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1616  
Db 2432 -----GATCAGAGGTTTGTGAGCAAGT 2458  
Qy 1617 GTTTGAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1676  
Db 2459 CTTTGAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2518  
Qy 1677 ACTGTCAGACACCGCTCATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1736

Db 2519 ACTGCTTACACAGAGAGTACACAGACCTGCTGTTACAGAGACACAAAACTTT 2578  
Qy 1737 ACACCTGCCCCAATTCTAACCTGACGATCTGCGTGGAGCATGCAAGGCTCAGAC 1796  
Db 2579 TCGATCCCAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2638  
Qy 1797 GATCAGATCCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1856  
Db 2639 GATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2698  
Qy 1857 GAAAGACAGACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1916  
Db 2699 CAATATGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2758  
Qy 1917 CAGATCCCACTCCCGCTTAAACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1965  
Db 2759 AAGATCCCAACCTCCAGTAAACCAACAGAGAGAGAGAGAGAGAGAGAGAGG 2807

RESULT 12  
US-10-121-746-9  
; Sequence 9, Application US/10121746  
; Publication No. US2003003648A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Ruter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. US2003003648A1 Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US/09/336,643A  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 3424  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (257)...(2195)  
; OTHER INFORMATION: K+Hnov12  
US-10-121-746-9

Query March 37.6%; Score 798 2; DB 14; Length 3424;  
Best Local Similarity 72.8%; Pred. No. 2.7e-210; Indels 24; Gaps 3;  
Matches 1079; Conservative 1; Mismatches 379; Indels 24; Gaps 3;

Qy 65 GAGTACACATGCGCGCGAGATTGCGGCTGCTGCTTGTGCGCGGCTGCGGCAATCG 124  
Db 249 GTGGCAAGATGCGCGAGGCTGCGCAAGTGTGCTGCTTGTGCGGCAAGATGCG 308  
Qy 125 GGTGATGCGGAGGCGCAATGCGGCAATGCGGCTGCGGCGGCGGCGCAAGAGGCGC 184  
Db 309 GCTGCTGCGGCGGCGGCGGCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 368  
Qy 185 AGATGAGCTGATGCTGCTCAAGTGTGAGTGTGAGGAGGTTTCAACCGAGAGCAAGC 244  
Db 369 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 428  
Qy 245 TGAAGCGTACCGGAGACCTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304  
Db 429 TGAAGCGTACCGGAGACCTTGTGCGGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 488

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QY 305 ACAACAAAGATGACTTCTTGACCGGAGACCCGAGGTGTTCCGCTGCGTCAACTCTT 364
DB 489 ACTCAGGCGAGTACTTCTTGATCGGACCTGACATGTTCCGCAATGCTGAATCTTCT 548
QY 365 ACCGCAACGGGAGAGTCTGCACTACCCGCGCTACAGATGCACTCTGCTTAAGACAGAGC 424
DB 549 ACCGAAACGGGCGGCTGCACTTGTCCACGCGAGATGCACTCAAGGCTTTCAGAGAAAGC 608
QY 425 TGGCTTTTACGAGCATCTCCCGAGATCATCGGGAGCTGCTGTAAGAGATCAAG 484
DB 609 TGGCTTTTACGAGCATCTGCTTCCGAGCTAGTCGTAATCTGCTTGAAGATTAACGG 668
QY 485 ACCGCAAGAGAGAGAAACCGGAGCGGCTACAGCAACGATCGGAGAACCAACAG 544
DB 669 ACCGAAAGAGAGAGAAATGCGAGCGCTGACAGATGAGAGGACAGACAGCGCGGG 728
QY 545 AGTCATAGCCCTGCG-----TCACTTCCGCGACAGCAATGTGGCGGCTTTCGAGA 595
DB 729 ACCGCGCGAGCGCTGCGACAGGAGCTCCCTGCGGACGCGCTTGGCGGCTTTCGAGA 788
QY 596 ACCCGCACACAGACAGCTGCGCTGCTTCTACTAGTACGATGCTGCTTCTCATCGCTG 655
DB 789 ATTCACACACAGACAGACCGAGCGCTGCTTCTACTAGTACGATGCTTCTCATCGCG 848
QY 656 TCTCGGTCAATACCAACGTGTGAGAGCGGTGCGCGACGCTCCCGGAG----- 710
DB 849 TGTCTGATCGCAATGTGTGAGAGCATCCATGCTCCGCGCTGACAGAGGTCT 908
QY 711 -CAAGAGCTGCGGTGCGGAGAGCGCTACTCGGTGCTTCTTGTGTAACAGCGCT 769
DB 909 CAAGGAGAGCGCTGTGAGAGCGCTTCCACAGGCTTTCGTGATGACAGCGCT 968
QY 770 GCGTCAATGATCTTCAACCGTGAAGTACTCTGCGGCTTTCGCGGCTCCCGAGCGCTACC 829
DB 969 GTGTACTCATATTTACAGGTGAATACCTCTGCGGCTTTCGCGGCTCCCGAGCGCTGCG 1028
QY 830 GCTTCAATCGGAGCGTATGAGATCATGACAGGTGTGACCATATGCTTACTTACATCG 889
DB 1029 GTTCTCGCGAGAGTATGATGAGCTTATCGACGAGGTGCGCATCTGCTTACTTACATG 1088
QY 890 GTTGTGATGACCAACAGAGAGAGTGTCCGCGCTTCTGTCACGCTCCGGGTCTTCC 949
DB 1089 GGTCTTTTGTGACCAAGAGAGAGATGTCTGCGCGCTTGTGACCTCGTGTCTCC 1148
QY 950 GCGTCTTCAAGATCTTCAAGTTCCTCCGCACTCCAGGCGCTGCGGATCTTGGGCTACA 1009
DB 1149 GGGTGTGTGCACTTCAAGTTCCTCCAGGCACTCAAGGCGTGAAGATCTTGGGCTACA 1208
QY 1010 CACTGAAGAGCTGTGCTCGAACTGAGGCTTCTTCTTCTTCTTCCATGAGGCAATCA 1069
DB 1209 CACTGAAGAGCTGTGCTGAGCTGAGGCTTCTTCTTCTTCTTCCATGAGGCAATCA 1268
QY 1070 TCACTTTTGGCACTGTGATGTTTATGCGAGAGGGCTCTCGGCGACAGATTCAGAA 1129
DB 1269 TCACTTTTGGCACTGTGATGTTTATGCGAGAGGGCAACAAACAGACCACTTTACAA 1328
QY 1130 GCATCCCTGCTGCTTGTGTAACATGTCACATGACACAGACACATGAGGATTAAGAGACA 1189
DB 1329 GCATCCCTGCGGCTTGTGTAACATGTCACATGACACAGACACATGAGGATTAAGAGACA 1388
QY 1190 TGGTGTCTGAAGAGATGACAGGAGATCTTGGCTTCATGTGCTTCTTGAAGTGGCTCC 1249
DB 1389 TGGTGTCTGAAGAGATGCTGAGAGATTTTGGGCTCATGTGCTCATGAGTGGCTCT 1448
QY 1250 TGGTCAATGCGCTGCGAGTCCCTGTGATGTTTTCGAACTTTAGCGGATTTACACAGA 1309
DB 1449 TGGTCAATGCGCTGCGAGTCAATGTGTCACTTTAGCGGATTTACACACAGA 1508
QY 1310 ATCAGAGAGCTGAATAACGAGGAGCAAAAGAGGCGGCTTTCAGAGATCGGTGG 1369
DB 1509 ACCAGCGGCTGACAGAGCGCGAGACAGAGAGAGAGGCGGCTTTCAGAGATCGGATGG 1568
QY 1370 CCAAAACAGGCAATTCGATGCAATCTGCAAGCAAGCGCAAGGCGCTCTTCAACGAGG 1429
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DB 1569 CAAAGGTGTGATCAACCAATGCTTCTGCACTACAGAGATGGGCGCTTGA----- 1623
QY 1430 CGGTGAGCTGACGGGCAACCCAGAGAGAGACATAGGAGCAACCACTCATCTATCG 1489
DB 1624 ----GACACGGCGAGGTGGCGAGAGAACAGGCTTGTGTGACAGAACGTTTGCCTTTG 1679
QY 1490 AAGAGCAGCATCATCACTGTGCACTGCTGAGAAAAAACAC 1532
DB 1680 AACAGCAATCATCACTGTGCACTGTCTAGAGAAAGCAAC 1722
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## RESULT 13

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US-10-296-115-373
; Sequence 373, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: HySeq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-373
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Query Match 37.5%; Score 795.4; DB 17; Length 2578;

Best Local Similarity 72.9%; Pred. No. 1.5e-209; Mismatches 376; Indels 24; Gaps 3;

Matches 1075; Conservative 0;

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QY 73 ATGCGCGCGGAGATTGCGGCTGCTGCTTTCGCGGAGCTGCGGCAATCGGATGATG 132
DB 1 ATGCGCGCGGAGCTGCGGCAATGCTGCTTTCGCGGAGCTGCGGCAATCGGATGATG 60
QY 133 CGGTGCGCACTGCGGCAATGCTGCTTTCGCGGAGCTGCGGCAATCGGATGATG 192
DB 61 CGGTGCGCGGAGCAATGCTGCTTTCGCGGAGCTGCGGCAATCGGATGATG 120
QY 193 CGATTTGCTCAAGTGAAGTGGGAGGATTCACAGCTGAGAGCAAGCTGAGCGC 252
DB 121 GTTCTGTGTGAACGTGAGCGGAGCTTGTGAGACTTGAAGATTAAGCTGAGCGC 180
QY 253 TACCGGAGACCTGCTGCGGAGAGAGAGATTTCTTCAACGAGACCAAG 312
DB 181 TACCGGAGACCTGCTGCGGAGAGAGATTTCTTCAACGAGACTGAGCTGAGCGC 240
QY 313 GAGTACTTTTGCACCGGAGACCCGAGGTTCCTGCTGCTCAACTTACGCAAG 372
DB 241 GAGTACTTTTGCATGCGACCTGACATGTTCCGCAATGCTGTAATCTTACCAAG 300
QY 373 GGGAGCTGCACTACCGGCGCTACAGTGCATCTGCTTACGAGAGAGAGCTGCGCTTC 432
DB 301 GGGCGGCTGATGCTTCCAGCGGAGAGTGCATCAAGCTTTCAGCAAGAGCTGCGCTTTC 360
QY 433 TACGCAATCCTCCCGAGATTCATCGGAGAGCTGCTGCTTACAGAGATTAAGAGAGAG 492
DB 361 TACGCAATCCTCCCGAGATTCATCGGAGAGCTGCTGCTTACAGAGATTAAGAGAGAG 420
QY 493 AAGGAGAGCGCGAGCGGCTCATGAGACGACGATCGAGAGACCAAGAGTGCATG 552
DB 421 AAGGAGAGCGCGAGCGGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 553 CCTGCTCT-----CAGCTTCCGCGAGACCATGTGCGGCGGCTTTCAGAGATCCAGC 603
DB 481 GCTCTGCGAGAGAGAGCTTCTGCGGAGCGGCTTTCAGAGATCCAGC 540
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QY 604 ACCAGCAGCTGCGCCCTGATCTTCTACTACGAGCAGGCTTCTGATGCTGCTGCTC 663
DB 541 AGGACACCGCAGCGCCCTGATCTTCTACTACGAGCAGGCTTCTGATGCTGCTGCTC 600
QY 664 ATCAACCAACGTGTGTGAGACCGGTGCGGCAAGCTTCCCGGAG-----CAAGAG 717
DB 601 ATCCGCAATGTGTGTGAGACCGGTGCGGCAAGCTTCCCGGAG-----CAAGAG 660
QY 718 CTGCGGTGCGGAGCGCTACTGCTGCTGCTTCTTCTGCTGTGACACGCGGCTGCTCATG 777
DB 661 CAGCCCTGTGTGCGAGACGCTTCCCAAGGCTTCTTCTGCTGTGACACGCGGCTGCTCATG 720
QY 778 ATCTTCAACGCTGTGAGTACTCTCTGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 837
DB 721 ATATTCAAGGTGATGATCTCTCTGCGGCTTCTTCTGCGGCTTCCAGCGGCTGCTCATG 780
QY 838 CGCAGCGCTGATGAGCATGATGACGCTGTGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 897
DB 781 CGAGGTGTGATGAGCATGATGACGCTGTGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 840
QY 898 ATGACCAACAAAGAGACGTGTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
DB 841 GTGCGCAAGAAAGAGACGTGTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 958 AGGATCTTCAAGTCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 1017
DB 901 CGCATCTTCAAGTCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 960
QY 1018 AGCTGTGCTTCCGAACTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1077
DB 961 AGCTGTGCTTCCGAACTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 1078 GCCACTGTGATGTTTATGCGGAGAGGAGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 1137
DB 1021 GCCACTGTGATGTTTATGCGGAGAGGAGGCTTCCAGCAACAGACTTTCAGCAAGCTTCT 1080
QY 1138 GCGCTGTGTTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
DB 1081 GCGCTGTGTTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1198 AAGACGATTTGAGGAGAAATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
DB 1141 AGCAGCATTTGCTGGAATTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1258 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
DB 1201 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1318 GCTGATTAAGCGCAGGAGCAAAAGAGGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 1377
DB 1261 GCTGATTAAGCGCAGGAGCAAAAGAGGCGGCTTCTGCGGCTTCCAGCGGCTGCTCATG 1320
QY 1378 GCGAGTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
DB 1321 GCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
QY 1438 CTGACGCGGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
DB 1372 AGCGGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 1498 CATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1532
DB 1432 CATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466

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## RESULT 14

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US-10-212-677-255
; Sequence 255, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.

```

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FASTSEQ for Windows Version 4.0
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; LENGTH: 5404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-255

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DB 1422 GTGATGCTGTTGCTGCTGCGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
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DB 1482 CCAAGATGCTTCAATTTGCTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1541
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 08:07:28 ; Search time 6220.08 Seconds  
(without alignments)  
12979.627 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hlc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1761.4	83.0	1911	9	AY419308 Pan trogl
3	1576.8	74.3	1911	9	AY419309 Mus muscu
4	1290.2	60.8	3730	3	AK033962 Mus muscu
5	920.2	43.4	2997	3	AK033268 Mus muscu
6	904.6	42.6	1893	3	AY06812 Homo sapi
7	889.2	41.9	1893	9	AY406814 Mus muscu
8	797	37.6	1944	9	AY408063 Homo sapi
9	759.8	35.8	1956	9	AY408065 Mus muscu
10	664.8	31.3	1893	9	AY406813 Pan trogl
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ALIGNMENTS

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DEFINITION Homo sapiens KCND3 gene, VIRUTAL TRANSCRIPT, partial sequence,  
ACCESSION AY419307  
VERSION AY419307.1 GI:39775264  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
1 (bases 1 to 1911)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
TITLE Direct Submission  
COMMENT Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment.  
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## RESULT 2

AY419308

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AY419308 1911 bp DNA linear GSS 17-DEC-2003  
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 AY419308  
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 1 (bases 1 to 1911)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1911)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
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DEFINITION genomic survey sequence.  
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VERSION AY419309.1 GI:39775266  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1911)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

JOURNAL 14671302  
PUBMED 2 (bases 1 to 1911)  
REFERENCE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
AUTHORS Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
These sequences were made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
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ORIGIN  
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QY 133 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCCGGCCGACAAAGAACGCGAGATGAG 192  
DB 61 CCAATGGCCAACTGCCCATGCCCCCTGGCCCCCGGCCGACAAAGAACGCGAGAG 120  
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LOCUS				
DEFINITION	Mus musculus adult male dienecephalon cDNA, RIKEN full-length enriched library, clone:J930129C02 product:ipotasium voltage-gated channel, Shal-related family, member 3, full insert sequence.			
ACCESSION	AK033962			
VERSION	AK033962.1 GI:26329580			
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SOURCE	Mus musculus (house mouse)			
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REFERENCE				
AUTHORS	Carninci,P. and Hayashizaki,Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			

JOURNAL MEDLINE PUBMED AUTHORS	Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3
JOURNAL MEDLINE PUBMED AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitenuai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4
JOURNAL MEDLINE PUBMED AUTHORS	THE RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5
JOURNAL MEDLINE PUBMED AUTHORS	THE PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 3730) Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Shuho-cho, Tsukuba, Ibaraki, 305-8575, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
JOURNAL MEDLINE PUBMED AUTHORS	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://pantom.gsc.riken.jp/ Location/Qualifiers 1. .3730 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM_DB:9330129C02" /db_xref="taxon:10090" /clone="9330129C02" /sex="male" /tissue_type="neocortex" /clone_id="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 224. .1819 /note="unlabeled protein product; potassium voltage-gated channel, Shal-related family, member 3 [MGDI MG1:1928743, GB NM_019931, evidence: BLASTN, 100%, match=1462] putative"

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LOCUS				
DEFINITION				
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mRNA, full insert sequence.				
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AK032268				
VERSION				
AK032268.1 GI:26328092				
KEYWORDS				
HTC; CAP trapper.				
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Mus musculus				
ORGANISM				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE				
1 Carninci, P. and Hayashizaki, Y.				
High-efficiency full-length cDNA cloning				
Meth. Enzymol. 303, 19-44 (1999)				
2 MEDLINE				
99279253				
PUBMED				
10349636				
REFERENCE				
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
Itoh, M., Kono, H., Okazaki, Y., Muraizumi, M. and Hayashizaki, Y.				

**TITLE**

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL  
MEDLINE

20499374  
11042159

## REFERENCE AUTHORS

Kimura, H., Akiyama, Y., Iizawa, K., Nagatsuma, T., Sasaki, N., Carninci, P., Sumi, N., Ietani, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sekiguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Iizawa, M., Matsui, S., Matsuki, M., Yonejima, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Ohtsuka, E., Watabiki, M., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multiplexed capillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000).

PUBMED

4

## AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

## REFERENCE AUTHORS

Group Ph

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2997)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Haru, A., Hashizhune, W., Hayashida, K., Hayatsu, N., Hiamoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakemura, M., Nishi, K., Nomura, K., Numasaki, R., Onno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Yumetatsu, M., and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9322, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>

**sour**

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mRNA (GB|AF107780, evidence: BLASTn, 100%, match:1893)"

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Db	2102	GCGCATGTATCCAAAAACCAATAGCAGGGAAGATTTTGGGTCCATCTGCTCACTGACGG	2161
OY	1244	GGGTCCGGTATTTGCCCTGCGCAGTCCCTGTGATTTTTCACACTTTTACCGGATTAAC	1303
Db	2162	GAGTCTTGTGTATTCGCTACCCGCTGTGATGTGTCAAACTTCAGTGGAGATCTAAC	2221
OY	1304	ACCAAGATCAGAGACTGATTAACGACAGGGACAAABAAGGCCCGCTTCCAGATCC	1363
Db	2222	ACCAAAACCAACGAGCACAACAAGAAAGGACAGAAABAAAGCCAGCTGGCCAGATCC	2281
OY	1364	GTTGTGGCCAAAACAGGCACTTCCATGCTATCTGACACGACAGGCGCAACGGGCTCTCA	1423
Db	2282	GAGACGCCAAAAGCGGAGTCCAAATGCTCATATGCAAGCAGAGCGGAATGGGCTACTGA	2341
OY	1424	ACGAGGCCCTGAGCTGACGGGCAACCCAGAAAGAGACACTTGGGCAAGACACCTTAC	1483
Db	2342	GCAACCACTGCACTGCTCCGAGAT---GAACGGCCTTCTATTAAGCAAACTGTGATCCA	2398
OY	1484	TCATTCAGAGCCAGCATCATCACTGTGCACTGCTGTGAAAAAACACTGGGTGTTCT	1543
Db	2399	GCTTTGAGACACAGCACCACTGCTTCACTGCTGGAAGAAACAC-----	2447
OY	1544	ATCTTGTGATGATCCCTGTTATCTGTACGAACCTCCACATCAAGAACACAGATTTA	1603
Db	2448	-----GAACATGAGTTTG	2461
OY	1604	TTGATGACAGATGTTTGAGCAGAACTGCATGAGAGTTCAATGCAAGAACTAACCTACA	1663
Db	2462	TCGATGACCAAGTCTTTGAAAGAACTGCATGGAAGTTGCCACCGTCATCGCCCATCAA	2521
OY	1664	CAAGAATCTCTCACTGTTCACGCCACCCAGGCTTACTTACCACTGTGCTTCCGTGTA	1722
Db	2522	GTCAACAGTCCCTCTCTCTCTCAACAAGAAGTACCAAGACCTTGTCTCAACGGAAC	2581
OY	1724	GTAAGAAGACACACACCTGCCAATTTCTAACCTGCAAGCTTCTGCGCTGGCAGCATGCG	1783
Db	2582	ACAAAABACCTTTCGCAATCTTAATGCCAATGTGTCCGGAAGCCATAGAGGCACTGTGC	2644
OY	1784	AAGAGCTCAGACGATTCACATCCAGGCGATGAGACGCTCCTTCAACAACAGTGTCT	1843
Db	2642	AAGAACTCAGTACATTCAGATCAATGTGTGAGAGAACTCCATCTATCCAAACAGCGAT	2701
OY	1844	CCAGGCTTAATTTGAAGCAGACGCACTGAGACCAAACTGCAAAAACATCCGAGATCA	1901
Db	2702	CCAGGTTAAATGCCAAAATGGAAGGTGTGTTAACTTAACTGTGAACAACCTTACGTGA	2761

QY	1904	CCAAGGCATCATATGAGATGCCCATCCGCTCCCGAGCGCTAAACCCGAGAGGGGGAAGTGGCG	1963
Db	2762	CCACAGCAATATATATAGCATCCCAACACCTCCAGTAACCAACCCGAGAGGCGACGACAGCG	2821
QY	1964	C	1964
Db	2822	C	2822
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LOCUS	AY406812		
DEFINITION	Homo sapiens KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY406812		
VERSION	AY406812.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
AUTHORS	Direct Submission		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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Query Match	42.6%; Score 904.6; DB 9; Length 1893;		
Best Local Similarity	67.6%; Pred. No. 3.5e-20;		
Matches 1286; Conservative 0; Mismatches 547; Indels 69; Gaps 4;			
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QY	133	CCGGTGGCACTGCCCATGCCCTGCGCC---GGCGACAGAACAACGGCAGAT	189
Db	61	CTGTGGCTTGGGGCTCATGCCCGCTCCCGAGGCGAGAGAGAAAGAACCCAAAT	120
QY	190	GAGCTGATTTGCTCAACGTAAGTGGGCGGAGGTTCCAGACTGGAGGACCACTGGAG	249
Db	121	GCTCTCATTTGCTGAAATGTATGTAGTGACACCGCTTCCAGAGTGGCAGAGACACCTGAA	180
QY	250	CGCTACCCGAGCACCTGCTGGGCGACGACGAGAGAAGATTCTTCTTCAACGAGACACC	309
Db	181	CGTTACCCAGACACTCTACTGCGGCGAGTTCTGAGAGGACTTTTCTACACCCAGAACT	240
QY	310	AAGAGATCTTCTTGACACCGGAGACCCCGAGGTTCCTGCTCGCTCACTTTTCAACCGC	369
Db	241	CAGCAGTATTTCTTTGACCGGTGACCCGACACATCTTCCGCGCACATCTCGAATTTCTTACCGC	300

Oy	370	ACGGGAAAGCTGACATACCCGGGCTACAGATGATCTCTGCTTACGACGACGAGCTGGCC	422
Db	301	ACTGGAAAGCTCATTATCTCTGCCACAGATGCACTCTGCTTACGATGATGAACCTGGCC	360
Oy	430	TTTACGGCATCTCTCCCGAGATCATCGGGGACTGTGCTACAGAGATGACAGACCGC	489
Db	361	TTCTTTGGCTTCATCCCGAATATCGCGAGCTGCTGTTATGAGGAGTACAAAGATGCG	420
Oy	490	AAGAGGGGAACGCCGACCGGCTCATGATCGACAAACGACTCGGAGAACCAACGAGAT--	547
Db	421	AGGCGAGGAACCGCCGACCGCTTGACAGACGACGGGATACGACACCGCTGGAGAGAC	480
Oy	548	-CCATGCCCTCGCTCAGCTTCCGACGACATATGAGCGGGCCCTTGAGAACCCCGACACC	606
Db	481	GCTTTGCCCATCATATCATGCAAGGAGAGGGGTCTGAGAGGGCCCTTGAGAACCCCGACACC	540
Oy	607	AGCACGCTGGCCCTGCTCTTCTTACTACGATGCTGCTTCTTATCGCTGTCTCGATC	666
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Oy	667	ACCAACGATGATGAGACGGATGCCGAGCGGACAGGTCCGGG--CAGCAAGGAGCTGGCCG	723
Db	601	GCGATGTGTGTGGAACAGTGCCTGGCGGATTAAGCCACAGGTCACTTTAAACACTGGCC	660
Oy	724	TGCGGGAGCGCTACTCTGATGGCTTCTTCTTGCTGACACGCGCTGCGTCAATGATCTTC	783
Db	661	TGTGGAGCGGTATGCTGTGGCTTCTTCTTGCTTGACACGGCGCTGGGTCAATGATCTTC	720
Oy	784	ACCGTGAATACCTCTCGGGCTCTTGCGGGTCCGACCGGTACCGCTTCAATCCGACGC	843
Db	721	ACAGTGAATATTTGCTTCCTCGCTGCTGCTGACGGCCCTAATGCTTACCGTCTTGTGTGAT	780
Oy	844	GTCATGACATCATCATGATGATGGTGGCCATCATGATGCCCTACATGATGCTGTGCATGACC	903
Db	781	GTCATGATATCATGATGATGGTGGCCATCTGCTTATTAATTTGGGCTGTGTATGACA	840
Oy	904	AACACGAGGACGTGTCCGGCGCTTGTGACGCTCGGGTCTTCGGGCTTTCAGATC	963
Db	841	GACATGAGGACGTGACGGGAGCTTTGTACACATCCAGATCTTCCGGGTCTTCAGATC	900
Oy	964	TTTCAAGTTTCCCGCACTCCCAAGGCGCTGGGATCTTGGGTACACACTGAAGGCTGT	1022
Db	901	TTTAAGTTTCCCGCACTCTCAAGGCGCTGGGATCTGGGGTACACACTGAAGGTTGT	960
Oy	1024	GCTTCGAACTGGGCTTCTTCTCTTCTCCCTCAGCATGGCCATCATCTTGGCACT	1083
Db	961	GCTTCGAAATGGGCTTCTGCTTCTTCTCTGCTCAGCATGGCTATCATCTTCCGTACA	1022
Oy	1084	GTGATGTTTATGCCGAGAGGGGCTCTCGGCACGAAAGTTCAACGATCCCTGCTCG	1143
Db	1021	GTTATGTTCTACGAGAGAGGGGCTTTCGGCTACCAAGTTACACGATCCCTGCAACC	1080
Oy	1144	TTTTGGTACCAATGTGACCATATGCAACATGAGATTCGAGATCATGGTGTCTAAGAGC	1203
Db	1081	TTTGTGTATCATATGTGATCATATGCAACACTAGAGATATGTGATATGGTGTCCAAAAGC	1144
Oy	1204	ATTGACGGGAAGATCTTCGGCTCATCTGCTCTTGAATGTGGCGTGTGTATTCCTGT	1263
Db	1141	ATTACGAGGAAGATTTTGGTTCTATCTATGTTGCTGAGTGGGGGTCTTGGTATCTCTCA	1200
Oy	1264	CCAGTCCCTGTGATTTGTTTCCACTTTTACCGGATTTTACACACAAATTCAGAGCTGAT	1322
Db	1201	CTGTGTCGGGATGTGATTCACAATTCAGTGCATCTACACAAATTCAGAGCAAC	1260
Oy	1324	AAACGCAAGGCAAAAGAAAGGCCCGCTTGCAGAGATCCGTGTGGCCAAAACAGCAGT	1383
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Oy	1384	TGGAATGATATCTGACACAGCAGGCGCAAGGGCTCTTCAACAGAGCGCTGAGCTGACG	1444
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[illegible]

RESULT 7				
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LOCUS	AY406814	1893 bp	DNA	linear GSS 15-DEC-2003
DEFINITION	Mus musculus KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,			
ACCESSION	AY406814			
VERSION	AY406814.1	GI:39762785		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	Clark,A.G., Glanauwaki,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 1893) Clark,A.G., Glanauwaki,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	location/Qualifiers			
SOURCE	1..1893 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"			

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 Matches 1276; Conservative 0; Mismatches 556; Indels 69; Gaps 4;

QY ATGCGCGCGGATGCGCGCTGCGCTGCTTGTCCCGCGGCTGCGCGCATCGGATGATG 132  
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 genomic survey sequence.  
 ACCESSION AY408063  
 VERSION AY408063.1 GI:39764034  
 KEYWORDS GSS.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1944)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1944)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 Best Local Similarity 72.9%; Pred. No. 6.3e-176;  
 Matches 1076; Conservative 0; Mismatches 375; Indels 24; Gaps 3;  
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 Db 1 ATGGCGCGAGCGCTGGCGACGTGGCTGCTTTGGCTGGCGAGCGAGTGGGTG 60  
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QY 604 ACCAGACGCTGGCGCTGCTTCTTCACTAGTGAATGGCTTCTTCAATGCTGTCCGTC 663  
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 Db 1321 GGTACACCAATGCTTCTGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371  
 QY 1438 CTGACGGGACCCCGAG 1497  
 Db 1372 AGCGGAGTGGCGAG 1431  
 QY 1498 CATATCACTGCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532  
 Db 1432 CATACCACTTGTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1466

RESULT 9  
 LOCUS AY408065 1956 bp DNA linear GSS 15-DEC-2003  
 DEFINITION Mus musculus KCNLI gene, virtual TRANSCRIPT, partial sequence.  
 ACCESSION AY408065  
 VERSION AY408065.1 GI:39764036  
 KEYWORDS GSS.





Db 1561 TCACAACAGAGATCACAGACCTCTGTTACAGACACAAAAAATTTCGCATC 1620  
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QY 1804 ATCCAGGCGAGTGAAGAGCCCTCTCAACCAAGTCTGCTCAAGCTTAAATTTGAAGCA 1863  
Db 1681 ATCAGATGTGTGAGAGAAACACCTGTGTCAACAGCGCATCCAGTTTAAATGCCAAATG 1740  
QY 1864 GACGAGGACGTAGACCAAACTGCAAAATCCCAATCAACAGCCATCATCAGCATC 1923  
Db 1741 GAAGATGTGTAACTAACTGTAACCACTTATGTGACNAGCAATTAATTAAGCATC 1800  
QY 1924 CCACTCTCCCAAGCGCTTAACCCGAGAGGGGAAAGTCGCGCA 1965  
Db 1801 CCAACACTCTCAGTAACACACAGAGAGAGATAGGCCA 1842

RESULT 11  
AY408064 1939 bp DNA linear GSS 15-Dec-2003  
LOCUS Pan troglodytes KEND1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY408064  
VERSION AY408064.1 GI:39764035  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 1939)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene cixos  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1939)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source location/Qualifiers  
1..1939  
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/mol\_type="genomic DNA"  
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Query Match 30.5%; Score 647.8; DB 9; Length 1939;  
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Matches 864; Conservative 0; Mismatches 587; Indels 24; Gaps 2;  
133 CGGTGGCCAACTGCCCCATGCGCTTGGCCCGGCGGCGAAGAAGAGGAGATGAG 192  
61 CCCTGGCCAGCAACCCCTGCCCCGCGCACCGGGGTGAAGCATCTCGAAGAGATGAG 120

193 CTGATTTCTCTAAGTGAAGTGGCGGAGGTTCCAGACTGAGAGACACGCTGAGCCG 252  
121 GTTCTGTGTGTAACGTCGAGCGGCGCTTTGAGTAAGAAATTCGTGAGCCG 180  
253 TACCGGAGACACCTGTGGGAGAGACGAGAAAGAGTTCTTCTTCAAGAGACACAG 312  
181 TACCGAGATACCTTGTGGGAGAGCTCGAGAAAGAAATTTCTTACGATCTGATCAGG 240  
QY 313 GAGTACTTCTGACCGGAGACCCGAGAGTGTCCGTGCGTCAACTTCAACGAGAG 372  
Db 241 GAGTACTTTTGTGATGCGACCCCTGACATGTTCCGATGTGTGAATCTTCAACGAG 300  
QY 373 GGGAGCTGACACTACCGCGGCTACAGATGATCTTGTCTTACAGACAGAGCTGGCTTC 432  
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QY 493 AGGAGAAACGCGAGCGCTCATGACGAC-----AACGACTCGAGAAC 537  
Db 421 NNN 480  
QY 538 AACGAGAGTCCATGCGCTCTGCTCAGCTTCCGACAGACATGTGCGGCGCTTCGAGAAC 597  
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QY 598 CCGCACACAGACAGCGTGGCCCTGTCTTCTAAGTACGATGCGCTTCTCATCGCTGTC 657  
Db 541 NNN 600  
QY 658 TCGGTATCATCAACAGCTGTGAGAGCGTGCCTGCGGACGAGTCCCGGAGACAGAGAG 717  
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QY 718 CTGCGCTGCGGAGAGCGCTACTGCGCTTCTTGTCTGAGACAGCGCGTGCATG 777  
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QY 778 ATCTTACCGTGAAGTACCTCTGCGGCTCTTGTGCGGCTCCAGCGGCTACGCGCTCATC 837  
Db 721 ATATTACAGGTAATATCTCTGCGGCTTGTGCGGCTCCAGCGGCTTGTGCGCTTCTG 780  
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QY 1018 AGCTGTGCTCGAACTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1077  
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QY 1078 GCCACTGTGATGTTTATGCCAGAAAGGCTCTCGGCGAGCAAGTTCAACAGATCCCT 1137  
Db 1021 GCCACTGTGATGTTTATGCTGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080  
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Db 1081 GCGGCTTCTGTGTATCACTGTGCAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1140  
QY 1198 AAGAGATGAGAGAGAAATCTTGTGCTCATGTGCTTGTGCTGAGGCTGTGCTAT 1257  
Db 1141 AGCAGCATTTGCTGAGAAATTTTGGGCTCATGTGCTCATGTGCTGCTGCTGCTAT 1200  
QY 1258 GCCCTGCAAGTCCCTGTGATGTTTCTCAACTTAACTTAACTTAACTTAACTTAACT 1317



Db 1201 GCCCTGCTGTCAGTATTTGTGCACTTTAGCCGATTTACACAGACAGCGG 1260  
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 Db 1261 GCTNAACAGCCCGGACAGACAGANAAGTGGCTTGGCAAGATCCGATGGCAAGAGT 1320  
 Qy 1378 GGCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437  
 Db 1321 GGTACCAACAAATGCTTCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371  
 Qy 1438 CTGACGGGACCCCAAG 1497  
 Db 1372 AGCCGAGTGGCGAG 1431  
 Qy 1498 CATCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1532  
 Db 1432 CATCACCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1466

RESULT 12  
 CNS0590A/c  
 LOCUS  
 DEFINITION  
 993 bp DNA linear GSS 01-SEP-2000  
 Tetradon nigroviridis genome survey sequence T3 end of clone  
 051G22 of library A from Tetradon nigroviridis, genomic survey  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 AL327691.1 GI:8221280  
 GSS: genome survey sequence.  
 Tetradon nigroviridis  
 Tetradon nigroviridis  
 Tetradon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorphi; Acanthopterygii; Perciformes; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE  
 AUTHORS  
 1  
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 Bernot, A., Fizames, C., Winkler, P., Brothier, P., Quetier, F.,  
 Saurin, W. and Weissenbach, J.  
 Estimate of human gene number provided by genome-wide analysis  
 using Tetradon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL  
 MEDLINE  
 PUBMED  
 20296633  
 10835645

REFERENCE  
 AUTHORS  
 2  
 Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,  
 Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
 Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the  
 freshwater pufferfish Tetradon nigroviridis

JOURNAL  
 MEDLINE  
 PUBMED  
 20359837  
 10899143

REFERENCE  
 AUTHORS  
 3  
 (bases 1 to 993)  
 Genoscope.  
 Direct Submission  
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr  
 This sequence is a single read and was generated as part of a large  
 scale clone-end sequencing project of the Tetradon nigroviridis  
 genome. For more information, please take a look at  
 http://www.genoscope.cns.fr/Tetradon.

FEATURES  
 source  
 1..993  
 /organism="Tetradon nigroviridis"  
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 /clone\_11b="A"  
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ORIGIN

Query Match 27.2%; Score 576.8; DB 9; Length 993;  
 Best Local Similarity 79.7%; Pred. No. 2.7e-124;  
 Matches 723; Conservative 0; Mismatches 178; Indels 6; Gaps 4;

Qy 279 GAGAGAGAGATGCTCTTCAACAGAGACACCAAGAGATCTTTCGACCGGAGACCCGA 338  
 Db 992 GNAAGAAANNTTTTTTTTNAAGAGAGAGGCAAGNGTACTTTTTTGAACCGGATCCCGA 933  
 Qy 339 GGTGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 398  
 Db 932 TGCCCTTCAAGAGATCTTCAACCTTNTACCGAGGNAAGCTCCANTACCTTCGACAGA 873  
 Qy 399 GTGATCTCTGCTCAACAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458  
 Db 872 GTGATCTCTGCTCAACAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813  
 Qy 459 GGAAGTCTGCTCAACAG 518  
 Db 812 CGAGTCTGCTCAACAG 753  
 Qy 519 CGACAG 578  
 Db 752 TGATCAG 696  
 Qy 579 GTGGCGGCTTTCAG 638  
 Db 695 GTGGCGGCTTTCAG 636  
 Qy 639 TGGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698  
 Db 635 AGGTTTCTTCAATCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 577  
 Qy 699 GATCCCGGAG 758  
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 Qy 759 GGAACAG 818  
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 Db 456 TAGCCGTTACAG 397  
 Qy 879 CTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938  
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 Db 98 GTAGATA 92

RESULT 13  
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 LOCUS  
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 MR4-NN0205-310101-201-e10 NN0205 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI033106 GI:14439732  
VERSION BI033106.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 567)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jorgensen, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-NN0205-310101-201-e10&t3=2001-01-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 567.  
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/dev\_stage="Adult"  
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/note="Organ: nervous normal; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
ORIGIN  
Query Match 26.1%; Score 552.8; DB 4; Length 567;  
Best Local Similarity 99.5%; Pred. No. 1.1e-118;  
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QY 1212 GAAGATTTGGGCTCCATCTGCTCTTGAGTGGCGTCTGTCATTGGCCGCAAGTCCC 1271  
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DB 447 GGCACAAAG 388  
QY 1392 ATATCTGCAAG 1451  
DB 387 ATATCTGCAAG 328  
QY 1452 AGAAG 1511  
DB 327 AGAAG 268

QY 1512 GCACTGCTGGAGAAAAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1571  
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DB 87 AGGCTCTACTACCAAG 28  
QY 1752 TAACCTGCAAG 1779  
DB 27 TAACCTGCAAG 1

RESULT 14  
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DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone 070F19 of library G from Tetradon nigroviridis, genomic survey sequence.  
ACCESSION AL267651 GI:7989467  
VERSION AL267651  
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SOURCE Tetradon nigroviridis  
ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradon.  
1

REFERENCE  
AUTHORS Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fischer, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
TITLE Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence  
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645

REFERENCE  
AUTHORS Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10892143

COMMENT  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon.  
FEATURES  
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1..1054  
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ORIGIN

Query Match 25.5%; Score 541.4; DB 9; Length 1054;  
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D 890 TGAATGCGGCTGCGGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 831
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D 830 TACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
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D 770 GAAAGTACCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 711
QY 307 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
D 710 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
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D 650 CGCAGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 591
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D 590 GCTTCTTACCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 531
QY 487 CGCAGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 546
D 530 CGCAGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 471
QY 547 TCCATGCGGCTGCTGCTTGTGCGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 603
D 470 TCCATGCGGCTGCTGCTTGTGCGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 411
QY 604 ACCAGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 663
D 410 ACCAGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 351
QY 664 ATCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
D 350 ATCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 291
QY 721 CCGTGGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 780
D 290 CCGTGGCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 231
QY 781 TTACCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 840
D 230 TTACCGGCGCGAGTTGCGGCTGCTGCTTGTGCGCGGCTGCGGCATCCGAG 171
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D 110 GACCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 51
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D 50 GATCTTCAAGTTTCCGCGCACTCCGAGGCG 19

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RESULT 15  
 AK033805  
 LOCUS AK033805 3302 bp mRNA linear HTC 03-APR-2004

## DEFINITION

Mus musculus adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230112B12 product:potassium voltage-gated channel, Shal-related family, member 1, full insert sequence.

## ACCESSION

AK033805

## VERSION

AK033805.1 GI:26329482

## KEYWORDS

HTC; CAP trapper.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Kono, H., Akiyama, U., Nishi, K., Kitahara, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,

Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kasahara, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Iwama, E., Ohara, E., Matsubara, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The PANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3302)

Adachi, J., Aizawa, K., Akiyama, T., Arikawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

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Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shihagawa, A., Shitaki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

## COMMENT

Prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>  
Location/Qualifiers

## FEATURES

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AUTHORS Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.
TITLE Human potassium channel polynucleotide and polypeptides and uses
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ACCESSION AF187964  
VERSION AF187964.1 GI:6007796  
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SOURCE  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.  
TITLE (bases 1 to 1984)  
JOURNAL Cloning and expression of the human Kv4.3 potassium channel  
U. Neurophysiol. 81 (4), 1974-1977 (1999)  
MEDLINE 99218223  
PUBMED 10200233  
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PUBMED 2 (bases 1 to 1984)  
AUTHORS Dilks,D., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.  
TITLE Direct Submission  
JOURNAL Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN  
8000, Room 1119A, Princeton, NJ 08543-8000, USA  
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1981 TAAA 1984

RESULT 4  
LOCUS AF120491 2722 bp mRNA linear PRI 17-APR-2000  
DEFINITION Homo sapiens Shal-related potassium channel Kv4.3 (KCND3) mRNA,  
long splice variant, complete cds.  
ACCESSION AF120491.1 GI:5059059  
VERSION AF120491.1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2722)  
AUTHORS Isbrandt,D., Leichter,T., Waldechut,R., Zhu,X., Luhnmann,U.,  
Michel,U., Sauter,K. and Pongs,O.  
TITLE Gene structures and expression profiles of three human KCND (Kv4)  
potassium channels mediating A-type currents (IT0) and I(SA)  
JOURNAL Genomics 64 (2), 144-154 (2000)  
MEDLINE 20195625  
PUBMED 10729221  
2 (bases 1 to 2722)  
AUTHORS Zgha,X.R., Waldechut,R., Isbrandt,D., Sauter,K. and Pongs,O.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-1999) ZMNH, Institut fuer Neurale

Signalverarbeitung, Martinistrasse 52, Hamburg 20246, Germany  
FEATURES  
Location/Qualifiers  
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ORIGIN  
Query Match 92.6%; Score 1912.2; DB 9; Length 2722;  
Best Local Similarity 94.8%; Pred. No. 1.2e-284;  
Matches 2011; Conservative 0; Mismatches 53; Indels 57; Gaps 1;  
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241 ACGCTGAGCGCTACCGGAGACACCTGCTGAGAGAGAGAGAGAGAGAGTCTTCTTCAAC 300  
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421 GAGCTGCGCTTCTACCGGATCTCCCGAGATCACTGCGGAGAGTCTGCTACAGAGATAC 480  
837 GAGCTGCGCTTCTACCGGATCTCCCGAGATCACTGCGGAGAGTCTGCTACAGAGATAC 896  
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Db	957	CAGAGATTCATGCCCTCGCTCAGCTTCGCGCAGACCATGTGCGGGCTTCGAGACCCC	1016
Qy	601	CACACGACGACGTGGCCCTGCTCTTCTACTAGCTGACGTGGCTTTCATCGCTGTCTCG	660
Db	1017	CACACGACGACGCTGGCCCTGCTCTTCTACTAGCTGACGTGGCTTTCATCGCTGTCTCG	1076
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Db	1077	GTCAATCAACCAAGTGTGTGAGACGCGTCCGTGCGGCAACGATCCCGGGCAGCAAGAACTG	1136
Qy	721	CCGATCGGGGAGCGCTACTCGGTGGCCCTTCTTGCCCTGAGCAGCGGGGTGCGTATATC	780
Db	1137	CCGTGCGGGAGCGCTACTCGGTGGCCCTTCTTGCCCTGAGCAGCGGGGTGCGTATATC	1196
Qy	781	TTCAACCGTGAAGTACTCTCTCGCGCTCTTGCGGCGCTCCAGCCGCTACCGCTTCATCCG	840
Db	1197	TTCAACCGGGGAGTACTCTCTCGGGCTTCTTGCGGGCTCCAGCCGCTACCGCTTCATCCG	1256
Qy	841	AGCGTCATGACATCATGACGTGTGTGGCCATCATGCCCTACTCATTCGTCTGTGATG	900
Db	1257	AGCGTCATGACATCATGACGTGTGTGGCCATCATGCCCTACTCATTCGTCTGTGATG	1316
Qy	901	ACCAACAACGAGGACGTGTCCGGGCGCTTGTCACGCTCCGGGGCTTCCGGTCTTCAG	960
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Db	1377	ATCTTCAGTTTCCCGCACCTCCAGGGCCCTGGGATCTTGGGCTACACACTGAAGC	1436
Qy	1021	TGTGCTTCGAACTGGGGCTTCTCTCTCTCTCTCCCTCACATGCGCATCATCTTTGCC	1080
Db	1437	TGTGCTTCGAACTGGGGCTTCTCTCTCTCTCTCCCTCACATGCGCATCATCTTTGCC	1496
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Db	1557	TGTTTTGGTACACCAATGTGCACCATGACACACACTGGGATACGAGACATGGTCCCTAAG	1616
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Qy	1501	CATCACTGCTGCACTGGCTGGAAAAAACACT-----	1533
Db	1917	CATCACTGCTGCACTGGCTGGAAAAAACACTGGGTTGTCTTATCTTGTGAATGATCCC	1976
Qy	1534	-----AACCAAGATTATTTGATGACAGATGTTT	1563
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Db	2037	GAGAGAAAGCTGCATGAGAGATTCAATGACAACTACCAATCCATCCACAAGAAAGTCCCTCACTG	2096
QY	1624	TCGAGCCACCCAGGCTCTCATCTACCACTGCTGCTCCGTGTAGTAAGAAAGACCAACAC	1683
Db	2097	TCGAGCAACCCAGGCTCTCATCTACCACTGCTGCTCCGTGTAGTAAGAAAGACCAACAC	2156
QY	1684	CTGGCCAAATTTACTACTGCGCAGCTACTGCGCTGGCGAGCANTGCAAGAGCTCAGCAGATC	1743
Db	2157	CTGGCCAAATTTACTACTGCGCAGCTACTGCGCTGGCGAGCANTGCAAGAGCTCAGCAGATC	2216
QY	1744	CACATCCAGGCGCATGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCACCTTAATTTGAAA	1803
Db	2217	CACATCCAGGCGCATGTGAGCAGCCCTCCCTCAACAACAGTCGCTCCACCTTAATTTGAAA	2276
Db	1804	GCAGACGACGGACTGAGACCAAACTGCAAAAATCCAGATCACACAGCCATCATGAC	1863
QY	2277	GCAGACGACGGACTGAGACCAAACTGCAAAAATCCAGATCACACAGCCATCATGAC	2336
Db	1864	ATCCCACTCCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGCCACCCCTGGCCAGCCCA	1923
QY	2337	ATCCCACTCCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGCCACCCCTGGCCAGCCCA	2396
Db	1924	GGCCCAACAGCAATCTCTTCATATACAGCAATGTGTCAAGGTCTGTCTGTGTAA	1983
QY	2397	GGCCCAACAGCAATCTCTTCATATACAGCAATGTGTCAAGGTCTGTCTGTGTAA	2456
Db	1984	AAATCCCGCGGCCATGCGCGCGCGGAGACATGCGTGGCCCAATTCGCTCATATAGTG	2043
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Db	2044	AGTCGTATTAAGCCGAATTC	2064
QY	2517	GGTGGTCACTGAGACCACTCC	2537
RESULT 5			
LOCUS	AF048712	1911 bp	mRNA
DEFINITION	Homo sapiens Kv4.3 potassium channel short splice variant (Kv4.3)		
ACCESSION	AF048712		
KEYWORDS	mRNA, complete cds.		
SOURCE	AF048712.1 GI:2935433		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1911)		
FEATURES	Kong,W. and Tomaseilli,G.F.		
source	Direct Submission		
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Query Match	92.4%;	Score 1906.2;	DB 9;	Length 1911;
Best Local Similarity	99.8%;	Pred. No. 1.1e-283;		
Matches 1908; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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OY	133	CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGGCCGACAAAGAACAGCGGCAAGATGAG	192
Db	61	CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGGCCGACAAAGAACAGCGGCAAGATGAG	120
OY	193	CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCACACTGGAGAGACCAAGCTTGGAGCCG	252
Db	121	CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCACACTGGAGAGACCAAGCTTGGAGCCG	180
OY	253	TACCCGCGACACCCCTGCTGGGCGACAGCGAGAGAGAGTTCTTCTTCAACGAGACACCGAAG	312
Db	181	TACCCGCGACACCCCTGCTGGGCGACAGCGAGAGAGAGTTCTTCTTCAACGAGACACCGAAG	240
OY	313	GAGTACTTCTTGACCGGGACCCCGAGGTTTCGCTGGCTGCTCAACTTCAACCGCACG	372
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OY	373	GGGAAGCTGCACCTAACCCGGGCTACGAGTGATCTGCGCTTACGACGACGAGCGTGGCCCTTC	432
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OY	673	GTGGTGGAGACGGTGCCTGGCGGCAACGGTCCCGGGGACGAAGAGGTGCCCGTCCGGGGAG	732
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OY	733	CGCTACTCGGTGGCCCTTCTTCTGCTCGCTGACACGGCGCTGGCTCATGATCTTCAACCGTGGAG	792
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Db	721	TACCTTCCTGGGCTCTTTCGGGCTCCCAAGCGCTTACCGCTTCAATCCGACGCTCATGAGC	780
OY	853	ATCATCGACGTGGTGGCCATCATGACCCTTACTCATCGGTTCTGGTCTCATGACCAACAGAG	912
Db	781	ATCATCGACGTGGTGGCCATCATGACCCTTACTCATCGGTTCTGGTCTCATGACCAACAGAG	840
OY	913	GACGTTGCCGGGCTTGGTCAACGCTCCGGGTTTTCGGGCTTTCAGAGATCTTCAAGTTT	972
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Db	961	CTGGGCTTTCTCTCTCTCTCCCTCACCATTGCATCATCTTTGSCACTGTGATGTTT	10202
OY	1093	TATGCCGAGMAGGGCTCTCGGCCAGACACTTCACAMGCAATCCCTGGCTCGTTTTGGTAC	115E3
Db	1021	TATGCCGAGMAGGGCTCTCGGCCAGAGTTTCAAGCAATCCCTGGCTCGTTTTGGTAC	1080
OY	1153	ACCAATTGTCACTAAGACCACTACCTGGAGTAAGSAGACATNGTGCTTAAGAACATTGCAAGG	12121
Db	1081	ACCAATTGTCACTAAGACCACTACCTGGGATAAGSAGACATNGTGCTTAAGACATTGCAAGG	1144
OY	1213	AAGATCTTCGGCTCATCTGCTCTCTTGAAGTGCGGCTCGGTGATTCCTCGCAAGTCCCT	12727
Db	1141	AAGATCTTCGGCTCATCTGCTCTCTTGAAGTGCGGCTCGGTGATTCCTCGCTCCAGTCCCT	12002
OY	1273	GTCATTTGTTTCCAATTTAAGCCGGAATTAACAACAGAAATCAGAAAGCTGATTAAGCGAAG	13323
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OY	1453	GAAGAAGACACANTGGGCAAGAACCACTCACTCAACGAGAGCCGACATCATCACTGCTGTG	15121
Db	1381	GAAGAAGACACANTGGGCAAGAACCACTCACTCAACGAGAGCCGACATCATCACTGCTGTG	1440
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Db	1501	TGCATGAGAGTTCAATGACGAAGTAATCCATCCACAAGAAAGTCCCTCACTGTCCAGCCAC	1560
OY	1633	CCAGGCTCACTACACCTGTGCTCCCGTGTATGTAAGAAACAACAACCTGSCCAAT	16922
Db	1561	CCAGGCTCACTACACCTGTGCTCCCGTGTATGTAAGAAACAACAACCTGSCCAAT	1620
OY	1693	TCTAACCTGACAGTACTGCTGCTGCGAGAGATGCAAGAGCTCAAGCAAGATCCATCTCAG	17522
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Db	1681	GGCAGTAGAGAGCCCTTCCCTTCAACAACAGTGTGCTCAGCCTTAATTGAAAGCAGAGAC	1740
OY	1813	GGAATGAGACCAAACTGCAAAAACATCCAGATCAACAAGCCATCATCAGATCCCACT	18722
Db	1741	GGAATGAGACCAAACTGCAAAAACATCCAGATCAACAAGCCATCATCAGATCCCACT	1800
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Db	1801	CCCCCAGCGTAAACCCCAAGGGGGGAAAGTGTGCGCAACCCCTGTCCAGCCCAAGGCCCAAC	1860
OY	1933	ACGAACATTCCTTCATATACCAAGAAATGTTGTCAAGGTCTCTGTCTTGTA	1983
Db	1861	ACGAACATTCCTTCATATACCAAGAAATGTTGTCAAGGTCTCTGTCTTGTA	1911

RESULT 6			
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LOCUS			
DEFINITION	A85164	2104 bp	DNA
	Sequence 1 from Patent WO9842833.		linear
			PAT 21-JAN-2000

ACCESSION AB5164  
VERSION AB5164.1 GI:6733867  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1 (bases 1 to 2104)  
Bil, A.M. and Calmel, T.P.  
TITLE  
KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL  
Patent: WO 9842833-A 1 01-OCT-1998;  
BIL ANTOINE MICHEL, ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)  
FEATURES  
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location/qualifiers  
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ORIGIN  
Query Match 92.3%; Score 1905; DB 6; Length 2104;  
Best Local Similarity 99.2%; Pred. No. 1,66-283;  
Matches 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 73 ATGGCGCGGAGTTGGGCGCTGGCTGCTTTGGCCGGGCTGGCGCATCGGGTGGATG 132  
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QY 133 CCGGTGGCCAACTGCCCCATGCCCCCTGGCCCCCGGCGCAAGAACAGCGGAGATGAG 192  
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QY 193 CTGATTGTCTTCAACGTGAGTGGCGGAGGTTCCAGACTGGAGAGCAAGCTGGAGCGC 252  
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DB 181 TACCCGAGCAACCCCTGCTGGGAGACAGGAGAGAGGTTCTTCAACGAGAGACCAAG 240  
QY 313 GAGTACTTCTTCAACCGGAGACCCGAGAGTGTTCGCTGCGTCACTTCACTTCAACGAGC 372  
DB 241 GAGTACTTCTTCAACCGGAGACCCGAGAGTGTTCGCTGCGTCACTTCACTTCAACGAGC 300  
QY 373 GGGAGCTGCACTACCGCGCTACGAGTGCATCTTGCCTTACGAGCAGAGCTGGCTTC 432  
DB 301 GGGAGCTGCACTACCGCGCTACGAGTGCATCTTGCCTTACGAGCAGAGCTGGCTTC 360  
QY 433 TAGGGCAATCCCTCGGAGATCATGGGGACCTGCTGCTACGAGAGAGTCAAGACCGGAG 492  
DB 361 TAGGGCAATCCCTCGGAGATCATGGGGACCTGCTGCTACGAGAGAGTCAAGACCGGAG 420  
QY 493 AGGAGAACCGCGAGCGGCTCATGAGACGACACTCGAGAACCAACAGAGTCCATG 552  
DB 421 AGGAGAACCGCGAGCGGCTCATGAGACGACACTCGAGAACCAACAGAGTCCATG 480  
QY 553 CCTGCTCAGCTTCCGCGAGACCATGTGGCGGCTTTCAGAAACCCGACACGAGCAG 612  
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QY 613 CTGGGCTGCTTCTTCACTAGTGAAGTGGCTTCTTCACTGCTGCTGGTCAATCAAC 672  
DB 541 CTGGGCTGCTTCTTCACTAGTGAAGTGGCTTCTTCACTGCTGCTGGTCAATCAAC 600  
QY 673 GTGTGAGAGAGGTGCGGTGGCGAGCGTCCGGGAGAGAGAGAGTGGCGTGGGAG 732  
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DB 1261 GCACAAAGAGGCGCGCTTGGCAGAGATCCGCTGAGGCAAAACAGAGATTTGAATGCA 1320  
QY 1393 TACCTGACAGCAAGCGCAACGCGCTCTTCAACGAGCGCTGGAGCTGAGCGGACCCA 1452  
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DB 1741 GGACTGAGACCAATTCAGAAACATTCAGATGATCAACAGCATCATTCAGATCCCACT 1800  
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DB 1801 CCCCAGCGCTAACCCCAAGAGGAGGAAAGTCCGCGACCCCTGCGAGGCCCAAC 1860

QY		1933	ACGAACATTTCTTCATTAACGAGCATGTGGTCAAGTGCTGTCTGTCTTGTAAATAATCCCGC	1992Z
Dd		1861	ACGAACATTCTTCATGCATGACCAGAATGTGTCAAAGTGCTCCGCTGTAAAAACAACCTGG	1920Z
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LOCUS	AR204884		2104 bp	DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 1 from patent US 6368823.			
ACCESSION	AR204884			
VERSION	AR204884.1		GI:21502324	
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified. 1 (bases 1 to 2104) Brill,A.,Michel,Alain., Calmels,T.Paul,Gerard., Favre,J.-F.,Simon,Pierre., Jayre,J.-L. and Rouanet,S. Kv potassium channel polypeptides and polynucleotides Patent: US 6368823-A 1 09-APR-2002; Location/Qualifiers 1..2104 /organism="unknown" /mol_type="unassigned DNA"			
TITLE	JOURNAL			
FEATURES	source			
ORIGIN				
Query Match	92.3%; Score 1905; DB 6; Length 2104;			
Best Local Similarity	99.2%; Pred.No.1,6e-283;			
Matches 1914; Conservative	0; Mismatches 15; Indels 0; Gaps 0;			
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Dd	181	TACCCGGACACCTCTGCTGGGCGACGCGAAGAGAGTTCTTCTTCAACGAGACACCAAG	240	
QY	313	GAGTACTTCTTCGACCGGGGACCCGAGGTTTCCGTCGCGGTCTCAATTCTACCGCAG	372	
Dd	241	GAGTACTTCTTCGACCGGGGACCCGAGGTTTCCGTCGCGGTCTCAATTCTACCGCAG	300	
QY	373	GGGAAGCTGACCTACCCCGCTCAAGAGTGCATCTGTGCTTACGACGAGAGCTGGCTTC	432	
Dd	301	GGGAAGCTGACCTACCCCGCTCAAGAGTGCATCTGTGCTTACGACGAGAGCTGGCTTC	360	
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QY	1273	GTGATTTGTTCCAACTTTAAGCCGATTTACACAGAAATCAAGAGCTGATTAACGCAAG	133
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Db	1561	CCAGGCTCATCAACCACTGTGCTTCCGTCGTAGTAAAGAGACCAACAACCTGTCCCAAT	162
QY	1693	TCTAACTGCGCAGCTACTGCTGCGGCAAGATGCAAGAGCTCAGCAAGATTCACATCCAG	175
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QY 1993 GGCATGCG 2001  
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DEFINITION complete cds.  
ACCESSION AF205856  
VERSION AF205856.1 GI:6644149  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1911)  
AUTHORS Calmejs, T.P.G., Falvire, J.-F., Javre, J.-L., Cheval, B., Rouanet, S.  
and Brill, A.  
TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,  
Expression, Electrophysiology, Pharmacology and Phosphorylation by  
Protein Kinase C  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1911)  
AUTHORS Calmejs, T.P.G., Falvire, J.-F., Javre, J.-L. and Brill, A.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline  
Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France  
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ORIGIN  
Query Match 92.2%; Score 1903; DB 9; Length 1911;

Best Local Similarity 99.7%; Pred. No. 3,3e-283;  
Matches 1906; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 73 ATGGGCGCGGAGGTTGGGCGTGGGCTGGGCTGCTTTGGCCCGGGCTGGCGGCAATCGGGTGAATG 132  
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QY 133 CCGGTGGCCAACTGCCCCATGCCCCCTTGCGCCCGGCGGCAAGAAACAAAGCGGAGATGAG 192  
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QY 193 CTGATGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACTCGAGAGCAACGCTGAGAGCCG 252  
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QY 253 TACCGGACACCCGTGGTGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312  
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Db	1081	ACCATTTGTACCATGACCACTGGGATACGGAGACATGTGTGCTTAAGACGATTTGCAGGG	1140
OY	1213	AAGATCTTCGGGCTCCATCTGCTCCTTGATGTGGCGCTCCGTGGCATTTGGCCCTGGACGTCCCT	1272
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OY	1273	GTGATTTGTTTCCACTTTAGCCGGATTTACCAACGATCCAGAGAGCTGATTAACGAGG	1332
Db	1201	GTGATTTGTTTCCACTTTAGCCGGATTTACCAACGATCCAGAGAGCTGATTAACGAGG	1260
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Db	1501	TGCATGAGAGATTCAATGACAGACATCCCATCCACAAGAAAGTCCCTCAGCTCCAGCCAC	1560
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Db	1561	CCAAGGCTCAATTACCACTGCTGCTCCCGTGTGATGAAGAAACACACACTTGCCCAAT	1620
OY	1693	TCTAATCTGCAGGTACTCGCTCGCTCGAGCATGTGCAAGAGCTCAGACGATCCACATCCAG	1752
Db	1621	TCTAATCTGCAGGTACTCGCTCGCTCGAGCATGTGCAAGAGCTCAGACGATCCACATCCAG	1680
OY	1753	GGCAGTGAAGCAAGCCCTCCCTCAACAACAAGTCGCTCCAGCTTAATTTGAAGCAGAGAC	1812
Db	1681	GGCAGTGAAGCAAGCCCTCCCTCAACAACAAGTCGCTCCAGCTTAATTTGAAGCAGAGAC	1740
OY	1813	GGACTGAGACCAAACTGCAAAAACATCCAGATTCACACAGGCATCATCAGATCCCACT	1872
Db	1741	GGACTGAGACCAAACTGCAAAAACATCCAGATTCACACAGGCATCATCAGATCCCACT	1800
OY	1873	CCCCCAGGCTAACCCCAAGAGGGGGAAAGTTGGCCACCCCTGTGCAGCCCAAGGCCCAAC	1932
Db	1801	CCCCCAGGCTAACCCCAAGAGGGGGAAAGTTGGCCACCCCTGTGCAGCCCAAGGCCCAAC	1860
OY	1933	ACGAAACATTCCTTCATATACCAAGAAATGTTGTCAAGGTCTCTGTCTTGTATA	1983
Db	1861	ACGAAACATTCCTTCATATACCAAGAAATGTTGTCAAGGTCTCTGTCTTGTATA	1911

RESULT 9	
LOCUS	AF187963
DEFINITION	Homo sapiens voltage gated potassium channel Kv4.3 long splice variant (Kv4.3) mRNA, complete cds.
ACCESSION	AF187963
VERSION	AF187963.1
KEYWORDS	GI:600794
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2041)
AUTHORS	Dilks,D., Lång,H.P., Cockett,M., Sokol,P. and Nunam,R.

FEATURES	source
REFERENCE	Cloning and expression of the human Kv4.3 potassium channel
AUTHORS	J. Neurophysiol. 81 (4), 1974-1977 (1999)
TITLE	99218223
JOURNAL	10200233
DOI	2 (bases 1 to 2041)
PubMed	Dilks, D.W., Ling, H.-P., Cockcroft, M., Sokol, P. and Numann, R.
Submitted	Direct Submission
Submitted	Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN
8000, Room 119A, Princeton, NJ 08543-8000, USA	
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73. .2040	
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GERSYAPFLDLTAQWITFTVEYLRLFAAPSRXYRTRSMYSIIDVAYIMPYIGLVY	
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QY	48	AAGACCGCAGAGAGAGAGAGAGCGCCGAGCGGCTCATATGACGACAAACGATCGGGAGAAAC	540
Db	481	AAAGATCCGAGAGAGAGAGAGAGCGCGAGCGGCTCATATGACGACAAACGATCGGGAGAAAC	540
QY	541	CAGAGATCATGCCCTCGCTCAGCTTCCGCCAGAACATATGAGCGGGCTTTCAGAAACCC	600
Db	541	CAGAGATCATGCCCTCGCTCAGCTTCCGCCAGAACATATGAGCGGGCTTTCAGAAACCC	600
QY	601	CACACGACGACGCTGGCCCTGCTCTTCTACATACGATGATGGCTTCTTATGCTGTCTCG	660
Db	601	CACACGACGACGCTGGCCCTGCTCTTCTTCTACATACGATGATGGCTTCTTATGCTGTCTCG	660
QY	661	GTCTATCAACAACTGTGTGAGACCGGTGCGTGCAGCAGTCCCGGAGCAGCAAGGACGTG	720
Db	661	GTCTATCAACAACTGTGTGAGACCGGTGCGTGCAGTCCCGGAGCAGCAAGGACGTG	720
QY	721	CCGTGCGGGAGCGCTACTCGGTGCGCTTCTTCTGTGCTGACACGGCGTGTCTATGATC	780
Db	721	CCGTGCGGGAGCGCTACTCGGTGCGCTTCTTCTGTGCTGACACGGCGTGTCTATGATC	780
QY	781	TTTCAACCGTAGATACCTCTGCGGGCTTTCGGGGCTCCAGCGGCTACCGGTTATCCGC	840
Db	781	TTTCAACCGTAGATACCTCTGCGGGCTTTCGGGGCTCCAGCGGCTTACCGGCTTATCCGC	840
QY	841	AGCGTATAGACATCATGACGTTGTGTGACATCATATGCCCTACTATCATGATGTGTGATG	900
Db	841	AGCGTATAGACATCATGACGTTGTGTGACATCATATGCCCTACTATCATGATGTGTGATG	900
QY	901	ACCAACCAACGAGAGACGTGTCCGGGCGCTTGTCAACGCTCCGGGTTTCCGGGTCTTACG	960
Db	901	ACCAACCAACGAGAGACGTGTCCGGGCGCTTGTGTCAACGCTCCGGGTTTCCGGGTCTTACG	960
QY	961	ATCTTCAAGTTTCCCGCACCTCCACAGGGCTGTGGGATCTGTGGCTACACTGAAAGGC	1020
Db	961	ATCTTCAAGTTTCCCGCACCTCCACAGGGCTGTGGGATCTGTGGGTTACACTGAAAGGC	1020
QY	1021	TGTGCTTCCGAACGTGGCTTCTTCTTCTTCTCTTCTCTACCAATGGCATATCATCTTTGCC	1080
Db	1021	TGTGCTTCCGAACGTGGCTTCTTCTTCTTCTCTTCTCTACCAATGGCATATCATCTTTGCC	1080
QY	1081	ACTGTGATGTTTTTATGACGAGAGAGGGCTCTCCGACAGCAAGTTTCAACAAGCATCTCTGCC	1140
Db	1081	ACTGTGATGTTTTTATGACGAGAGAGGGCTCTCTCCGACAGCAAGTTTCAACAAGCATCTCTGCC	1140
QY	1141	TCGTTTTTGGTACACCATTTGTACCATGACCAACTGGGATACGAGACATGGTGTCTAAG	1200
Db	1141	TCGTTTTTGGTACACCATTTGTACCATGACCAACTGGGATACGAGACATGGTGTCTAAG	1200
QY	1201	ACGATGTGAGAGGAAGATCTTTCGGCTCCATCTGTCTTGAATGGGGTCTGTGTCAATGGC	1260
Db	1201	ACGATGTGAGAGGAAGATCTTTCGGCTCCATCTGTCTTGAATGGGGTCTGTGTCAATGGC	1260
QY	1261	CTGCGACGTCCCTGTGATGTTTTCCAACTTTAGCGGGAATTTACACCAAGATCAAGAGACT	1320
Db	1261	CTGCGACGTCCCTGTGATGTTTTCCAACTTTAGCGGGAATTTACACCAAGATCAAGAGACT	1320
QY	1321	GATTAACCGCAGGGCACAAAAGAGGCCGCTTGTCCAGAGATCCGTGTGCCAAAGACGCG	1380
Db	1321	GATTAACCGCAGGGCACAAGAGAGGCCGCTTGTCCAGAGATCCGTGTGTGCCAAAGACGCG	1380
QY	1381	AGTTTCGATGTGATACCTGTGCAACGACAGCGGCAACGGGCTTCTTCAGCGGGCGCTTGAAGCTG	1440
Db	1381	AGTTTCGATGTGATACCTGTGCAACGACAGCGGCAACGGGCTTCTTCAGCGGGCGCTTGAAGCTG	1440
QY	1441	ACGGGCAACCCAGAGAGAGACCATGTGGCAAGACCACTCATCTATCGAAGCCAGCAT	1500
Db	1441	ACGGGCAACCCAGAGAGAGACCATGTGGCAAGACCACTCATCTATCGAAGCCAGCAT	1500
QY	1501	CATCACTGTCTGCACTGCTGTGAAAAAACCACT-----	1533
Db	1501	CATCACTGTCTGCACTGCTGTGAAAAAACCACTGTGTGTCTTATCTTGTGATGATGCC	1560

QY	1534	-----AACACAGATTATATGATGAGCAATGTT	1563
Db	1561	CTGTATCTGTAGCAACCTCCACCATCAAGAACACAGTTTATGATGACAGATGTT	1620
QY	1564	GAGCAGAACTGCATGAGAGATTCAATGCAGAACTACCATCCACAGAAAGTCCCTCACTG	1623
Db	1621	GAGCAGAACTGCATGAGAGATTCAATGCAGAACTACCATCCACAGAAAGTCCCTCACTG	1680
QY	1624	TTCAGGCACACGAGCCTCACTACCACTGCGTCCGCTGTAGTAAGAGACACACAC	1683
Db	1681	TTCAGGCACACGAGCCTCACTACCACTGCGTCCGCTGTAGTAAGAGACACACAC	1740
QY	1684	CTGCCCAATTTCTAACTTCGACAGCTACTCGCTCGCAGCATGCAAGAGCTTCAGACGATC	1743
Db	1741	CTGCCCAATTTCTAACTTCGACAGATACTCGCTCGCAGCATGCAAGAGCTTCAGACGATC	1800
QY	1744	CACATCCAGGCGATGAGAGCCCTCCCTCAACAACAGTGGCTCCACGCTTAAATTTGAAA	1803
Db	1801	CACATCCAGGCGATGAGAGCCCTCCCTCAACAACAGTGGCTCCACGCTTAAATTTGAAA	1860
QY	1804	GCAGACGACGAGTCTGAGACCAAACTGCAAAAACATCCAGATCACACAGCCATCATGAGC	1863
Db	1861	GCAGACGACGAGTCTGAGACCAAACTGCAAAAACATCCAGATCACACAGCCATCATGAGC	1920
QY	1864	ATCCCACTCCCCAGGCTTAAACCCCAAGGGGAAAAGTGGGCCACATCCCTCGCCAGCCCA	1923
Db	1921	ATCCCACTCCCCAGGCTTAAACCCCAAGGGGAAAAGTGGGCCACATCCCTCGCCAGCCCA	1980
QY	1924	GGCCCAACAGAAACATTTCTTCATTAACGACAAATGTTGCAAGTCTCTGTTTAA	1983
Db	1981	GGCCCAACAGAAACATTTCTTCATTAACGACAAATGTTGCAAGTCTCTGTTTAA	2040
QY	1984	A 1984	
Db	2041	A 2041	

RESULT 10				
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LOCUS	AB5168	2104 bp	DNA	linear
DEFINITION	Sequence 5 from Patent WO9842833.			PAT 21-JAN-2000
ACCESSION	AB5168			
VERSION	AB5168.1	GI:6733869		
KEYWORDS				
SOURCE	unidentified			
ORGANISM	unidentified			
	unclassified.			
REFERENCE	1 (bases 1 to 2104)			
AUTHORS	Brill, A.M. and Calmels, T.P.			
TITLE	KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES			
JOURNAL	Patent: WO 9842833-A-5 01-Oct-1998;			
	BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)			
FEATURES	Location/Qualifiers			

**ORIGIN**

Query Match	91.9%	Score 1897	DB 6	Length 2104
Best Local Similarity	99.0%	Pred. No. 2.7e-28		
Matches 1909, Conservative	0	Mismatches 20	Indels 0	Gaps 0

Qy 73 ATGCGCGCCGAGTGTGGGCGCTGGCTGCTCTTTTCCCGGAGCTGGGCGCATGGGTGATG 132  
 Db 1 ATGCGCGCGAGAGTGTGACGCTGGCTGCTCTTTTCCCGGAGCTGGGCGCATGGGTGATG 60  
 Qy 133 CCGGTGGCGCACTGCGCCCATGCGCTCTGAGCCCGGCGGACAAGAACGCGGACAGATGAG 192  
 Db 61 CCGGTGGCGCACTGCGCCCATGCGCTCTGAGCCCGGCGGACAAGAACGCGGACAGATGAG 120  
 Qy 193 CTGATTGCTCAACGTGAGTGGGCGGAGGTTCCAGACTTGGAGACCAAGCTGGAGCGC 252

Db	121	CTGATTGTCCTCAAGTGTAGTGGGGGAGGTTCCAGACTGTGAGGACCAAGCTGGAGGCG	180
OY	253	TACCCGGACACCTGTGCGGACGACACGGAGANGAGTTCTTTCACAGAGACACCAAG	312
Db	181	TACCCGGACACCTGTGCGGACGACACGGAGANGAGTTCTTTCACACGAGACACCAAG	240
OY	313	GAGTACTTCTTGACACGGGAGCCCGAGAGGTCCGCTGCTGATCTCAACTTTCACCGCACG	372
Db	241	GAGTACTTCTTGACACGGGAGCCCGAGAGGTTCGCTGCTGATCTCAACTTTCACCGCACG	300
OY	373	GGGAGACTGCACTACCCCGGCTACGAGTGCATCTGTGCTTACGACGACGAGCTGACCTTC	432
Db	301	GGGAGAGCTGCACTACACCGGCTACGAGTGCATCTGTGCTTACGACGACGAGCTGACCTTC	360
OY	433	TACGCGATCTTCCGGAGATCATCGGGGACTGTGCTGTACGAGAGTACAGGACCGCAAG	492
Db	361	TACGCGATCTTCCGGAGATCATCGGGGACTGTGCTGTACGAGAGTACAGGACCGCAAG	420
OY	493	AGGAGGAAGCGGACACGGGCTCATGAGACACACGACTCGGAGAACACACAGAGTTCATG	552
Db	421	AGGAGGAAGCGGACACGGGCTCATGAGACACACGACTCGGAGAACACACAGAGTTCATG	480
OY	553	CCCTGACTCAGGCTTCCGCGACAGACATGATGAGCGGGCTTCGAGAACCCCAACACGACGAG	612
Db	481	CCCTGACTCAGGCTTCCGCGACAGACATGATGAGCGGGCTTCGAGAACCCCAACACGACGAG	540
OY	613	CTGGCCCTGATCTTCTACTACGTGACTGAGCTTCTTCATCGCTGTCTGGTTCATCCAAAC	672
Db	541	CTGGCCCTGATCTTCTACTACGTGACTGAGCTTCTTCATCGCTGTCTGGTTCATCCAAAC	600
OY	673	GTGGTGGAGACGATGCGGTGCGGACAGGTCCTCCGGGACGAGAGGCTGCTGGCGGAGAG	732
Db	601	GTGGTGGAGACGATGCGGTGCGGACAGGTCCTCCGGGACGAGAGGCTGCTGGCGGAGAG	660
OY	733	CGCTACTGGATGGGCTTCTTCTGCGCTGAGACAGGGGTGGTCAATGATCTTTCACCGGTGAG	792
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OY	853	ATCATCGACGTGTGGCCATCATGCTCTTACATCGGTCTGTGATGACCAACAGAG	912
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OY	913	GACGTGTCCGGGCGCTTGTGTAAGCTCCGGGCTTCCCGCTTTCAGAGATCTTCAAGTTT	972
Db	841	GACGTGTCCGGGCGCTTGTGTAAGCTCCGGGCTTTCGCGCTTTCAGAGATCTTCAAGTTT	900
OY	973	TCCCGCACTCCCAAGGACTGTGGGATCTGAGGCTTACACTGAAGAGCTGTGCTCCGAA	1032
Db	901	TCCCGCACTCCCAAGGACTGTGGGATCTGAGGCTTACACTGAAGAGCTGTGCTCCGAA	960
OY	1033	CTGGGCTTCTTCTCTCTCTCCCTGACCAATGAGCATCATCTTTCGCACTGTGATGTTT	1092
Db	961	CTGGGCTTCTTCTCTCTCTCCCTGACCAATGAGCATCATCTTTCGCACTGTGATGTTT	1020
OY	1093	TATGCGGAGAGGGCTCTCTGGCCGACGAAGTTCAAGAAGATCCCTGCTCTGTTTGGTAC	1152
Db	1021	TATGCGGAGAGGGCTCTCTGGCCGACGAAGTTCAAGAAGATCCCTGCTCTGTTTGGTAC	1080
OY	1153	ACCATTTGACACATACCAACTGAGGATACGGAGATAGGTGCTTCAGACGATTCAGAGG	1212
Db	1081	ACCATTTGACACATACCAACTGAGGATACGGAGATAGGTGCTTCAGACGATTCAGAGG	1144
OY	1213	AAGATCTTCCGCTCATCTGTCTCTTGAATGAGCTGTGATTCATTTGCCCTGCAATGCCCT	1272
Db	1141	AAGATCTTCCGCTCATCTGTCTCTTGAATGAGCTGTGATTCATTTGCCCTGCAATGCCCT	1200
OY	1273	GTGATTTGTTTCCAACTTTAAGCCGGAATTACCAACGAATCAGAGAGCTGATTAAGCGCAG	1332
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Db	1261	GCACAAAAGAGGCCCGCTTGCCAGAGATCCGTGTGGCCAAACAGGAGTTCCAAATGCA	1320
QY	1393	TACCTGCACACCAAGCCGACGAGGCTCTTCAACGAGGCGCTGAGCTGACCGGACCCCA	1452
Db	1321	TACCTGCACACCAAGCCGACGAGGCTCTTCAACGAGGCGCTGAGCTGACCGGACCCCA	1380
QY	1453	GAAGAGAGGCATGAGGCGAABACCACTCTCATTCGAGAGCCAGCATCATCACTTCTGTG	1512
Db	1381	GAAGAGAGGCATGAGGCGAABACCACTCTCATTCGAGAGCCAGCATCATCACTTCTGTG	1440
QY	1513	CAGTGCCTGGAAAAAACCACTAACCGAGGTTTATGTAGCAGATGTTTGAGCAGAAC	1572
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QY	1813	GGACTGAGACCAAACTGCAAAAACATCCCAATCACACAGCCATCATATGAGATCCCACT	1872
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QY	1873	CCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGGCACCCCCTGGCAGGCCAGGCCCAAC	1932
Db	1801	CCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGGCACCCCCTGGCAGGCCAGGCCCAAC	1860
QY	1933	ACGAACATTCCTTCATTAACCGACGAATGTTGTCAAGTCTGTCTTGTAAAAAATCCCGC	1992
Db	1861	ACGAACATTCCTTCATTAACCGACGAATGTTGTCAAGTCTGTCTTGTAAAAAATCCCGC	1920
QY	1993	GGCATTGCGC 2001	
Db	1921	ACAGAGGCGC 1929	
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LOCUS	AR204886	2104 bp	DNA
DEFINITION	Sequence 5 from patent US 6368823.		
ACCESSION	AR204886		
VERSION	AR204886.1	GI:21502326	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2104)		
AUTHORS	Brill,A.,Michel,Alain., Calmels,T.,Paul, Gerard.,		
	Falvire,J.-F.,Simon,Pierre., Javre,J.-L., and Romanet,S.		
TITLE	Kv potassium channel polypeptides and polynucleotides		
JOURNAL	Patent: US 6368823-A 5-09-Apr-2002;		
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Best Local Similarity	99.0%;	Pred. No. 2,7e-282;	Length 2104;

ORIGIN	
Query Match	91.9%; Score 1897; DB 6; Length 2104
Best Local Similarity	99.0%; Pred. No. 2.7e-282;

Matches 1909; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 1 ATGGCGGCGGAGATTGGAGCTGGCTGGCTTTTGGCCGGGCTGGCCATCGGATGGATG 60
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Db 61 CCGGTGGCCAACTGGCCCATGCTCTGGCCCGGCGGCAAGAAAGAGGCGGATGAG 120
QY 193 CTGATTGCTCTCAACGAGTGGGCGGAGGTTCCAGCTGGAGACCAAGCTGGAGCGC 252
Db 121 CTGATTGCTCTCAACGAGTGGGCGGAGGTTCCAGCTGGAGACCAAGCTGGAGCGC 180
QY 253 TACCCGACACCTGCTGGGACAGACGAGAAAGAGTTCTTTCAACGAGACCAAG 312
Db 181 TACCCGACACCTGCTGGGACAGACGAGAAAGAGTTCTTTCAACGAGACCAAG 240
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Db 241 GAGTACTTCTTCAACGAGGACCCCGAGGTTCTGGCTGGCTCAACTTCAACGAG 300
QY 373 GGGAGGTGACATACCCGCGCTACGAGTGCATCTGGCTTACAGACGAGCTGGCTTC 432
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QY 433 TACGCGATCTCCCGAGATCATCGGAGGATCTGCTACGAGAGATCAAGACCGGAG 492
Db 361 TACGCGATCTCCCGAGATCATCGGAGGATCTGCTACGAGAGATCAAGACCGGAG 420
QY 493 AGGAGAGACCGCGAGCGGCTCATGAGACGACCACTCGAGAAACCAAGAGTCCAG 552
Db 421 AGGAGAGACCGCGAGCGGCTCATGAGACGACCACTCGAGAAACCAAGAGTCCAG 480
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Db 481 CCTCGCTGAGCTCCCGGACGACATGTGGCGGCTTCCAGAAACCCCGACACAGACG 540
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Db 661 CGCTACCTGGGCTTCTTCTGCTGGAGACAGCGCGTGCATGATCTTCAACCTGGAG 720
QY 793 TACCTCTGGGCTTCTGCGGCTCCGAGCGCTTCAACGCTTCACTGATGAGC 852
Db 721 TACCTCTGGGCTTCTGCGGCTCCGAGCGCTTCAACGCTTCACTGATGATGAGC 780
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Db 841 GAGCTGCTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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QY 1273 GTGATTGTTCCAACTTTAGCCGATTTTACACAGATCAGAGACTGATTAACGAG 1332
Db 1201 GTGATTGTTCCAACTTTAGCCGATTTTACACAGATCAGAGACTGATTAACGAG 1260
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Db 1501 TGCATGAGAGATTCAATGCAAACTTACCATCAACAAAGTCCCTCACTGTCAGCCAC 1560
QY 1633 CCAGGCTCACTACCACTGCTGCTCGTGGTGAAGAGCAACACCTGCCCAAT 1692
Db 1561 CCAGGCTCACTACCACTGCTGCTCGTGGTGAAGAGCAACACCTGCCCAAT 1620
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Db 1681 GGCAGTGAAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
QY 1813 GGACTGAGACCAAACTGCAAAACATCCAGATCACAGCCATCATCGATCCCACT 1872
Db 1741 GGACTGAGACCAAACTGCAAAACATCCAGATCACAGCCATCATCGATCCCACT 1800
QY 1873 CCCCAGCGCTAACCCAGAGGGGGAAGTGGGCAACCCCTGCGCAGCCAGGCCCAAC 1932
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ACCESSION AF048713  
VERSION AF048713.1 GI:2935435  
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ORGANISM Homo sapiens  
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REFERENCE  
1 (bases 1 to 1968)  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
AUTHORS  
Kong, W. and Tomasselli, G.F.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (17-FEB-1998) Medicine, Johns Hopkins University School  
of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA  
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## ORIGIN

Query Match 89.1%; Score 1839.2; DB 9; Length 1968;  
Best Local Similarity 97.0%; Pred. No. 2.1e-273;  
Matches 1908; Conservative 0; Mismatches 3; Indels 57; Gaps 1;

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## RESULT 13

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DEFINITION Sequence 3 from Patent W09842833.  
ACCESSION AB5166  
VERSION AB5166.1 GI:6733868

## KEYWORDS

unidentified  
unclassified.

REFERENCE 1 (bases 1 to 2072)  
AUTHORS Bril,A.M. and Calmels,T.P.  
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL Patent: WO 9842833-A 3 01-OCT-1998;  
BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)

## FEATURES

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## ORIGIN

Query Match 89.1%; Score 1838; DB 6; Length 2072;  
Best Local Similarity 96.9%; Pred. No. 3.2e-273;  
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;  
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DEFINITION AR204885  
ACCESSION AR204885.1 GI:21502325  
VERSION AR204885.1  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 2072)  
AUTHORS Brill,A.,Michel,Alain., Calmels,T.,Paul, Gerard.,  
TITLE Faltvre,J.-F.,Simon,Pierre., Javre,J.-L. and Rounet,S.  
JOURNAL Patent: US 6368823-A 3 09-APR-2002;  
FEATURES  
1. 2072  
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ORIGIN  
Query Match 89.1%; Score 1838; DB 6; Length 2072;  
Best Local Similarity 96.9%; Pred. No. 3,2e-273;  
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

Qy 73 ATGGGCGCGAGGAGTGGCGGCGCTGCTTTTGGCCGGGCTGGGCGCATGGGGTGAATG 132  
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LOCUS AX956786 Sequence 4 from Patent WO03097682.  
DEFINITION AX956786  
ACCESSION AX956786  
VERSION AX956786.1 GI:40785267  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Kaletta, T.J., Dewulf, N.E. and Plaetnick, G.K.  
TITLE Methods for identifying and developing compounds that interact with  
JOURNAL Voltage-gated potassium channels of the Kv4 family  
Patent: WO 03097682-A 4 27-NOV-2003,  
Devgen NV (BB)  
FEATURES  
source Location/Qualifiers  
1..1968  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

ORIGIN /db\_xref="taxon:9606"  
Query Match 89.0%; Score 1836; DB 6; Length 1968;  
Best Local Similarity 96.8%; Pred. No. 6.6e-273;  
Matches 1906; Conservative 0; Mismatches 5; Indels 57; Gaps 1;  
Qy 73 ATGCGCGCGGAGATTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132  
Db 1 ATGCGCGCGGAGATTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60  
Qy 133 CCGGTGGCCAACTGCCCCATGCCCCCTGCCCCCGGCGGCAAGAAACAAAGGCGGATGAG 192  
Db 61 CCGGTGGCCAACTGCCCCATGCCCCCTGCCCCCGGCGGCAAGAAACAAAGGCGGATGAG 120  
Qy 193 CTGATTGCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGAGGAGCAACGCTGAGCGC 252  
Db 121 CTGATTGCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGAGGAGCAACGCTGAGCGC 180  
Qy 253 TACCCGAGACCCCTGCTGGGCAAGCAAGAGAGATTCTTCAACAGAGCAACCAAG 312  
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Qy 313 GAGTACTTCTTGAACCGGAGACCCGAGGTTCCGCTGCTGCTCACTTCAACGAG 372  
Db 241 GAGTACTTCTTGAACCGGAGACCCGAGGTTCCGCTGCTGCTCACTTCAACGAG 300  
Qy 373 GGGAGCTGACATCAACCGGCTGAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432  
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Qy 433 TACGAGATCTCCCGAGATCATCGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492  
Db 361 TACGAGATCTCCCGAGATCATCGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Qy 493 AGGAGAAAGCGGAGCGGCTCATGAGACGACAGATCTGGAAGAAACCAAGAGTCCATG 552  
Db 421 AGGAGAAAGCGGAGCGGCTCATGAGACGACAGATCTGGAAGAAACCAAGAGTCCATG 480  
Qy 553 CCTGCTGAGCTTCCGAGACCATGAGGCGGCGCTGAGAGAACCCCAACACAGACG 612  
Db 481 CCTGCTGAGCTTCCGAGACCATGAGGCGGCGCTGAGAGAACCCCAACACAGACG 540  
Qy 613 CTGAGCCCTGCTTCTTCACTAGTGAATGCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTG 672  
Db 541 CTGAGCCCTGCTTCTTCACTAGTGAATGCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTG 600  
Qy 673 GTGTGAGACGAGTCCGCTGAGCAAGCTCCGCGGCAAGAGAGTCCGCTGCGGAG 732  
Db 601 GTGTGAGACGAGTCCGCTGAGCAAGCTCCGCGGCAAGAGAGTCCGCTGCGGAG 660  
Qy 733 CGCTACCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792  
Db 661 CGCTACCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Qy 793 TACCTCTGAGGCTCTTCCGAGCTCCAGCGGCTTCAATCCGAGCGTCAATGAGC 852  
Db 721 TACCTCTGAGGCTCTTCCGAGCTCCAGCGGCTTCAATCCGAGCGTCAATGAGC 780  
Qy 853 ATCATGAGTGTGAGCATCATGCTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912  
Db 781 ATCATGAGTGTGAGCATCATGCTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 913 GAGGTGCGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972  
Db 841 GAGGTGCGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Qy 973 TCCGCGCACTCCAGAGGCTGCGAGATCTGAGGCTAACAAGAGAGTGTGCTCGAA 1032  
Db 901 TCCGCGCACTCCAGAGGCTGCGAGATCTGAGGCTAACAAGAGAGTGTGCTCGAA 960  
Qy 1033 CTGAGGCTTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092



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CC human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been  
CC identified. One form is full-length (hKv4.3 long) while the second form  
CC has a deletion of 19 amino acids in the carboxy domain after the  
CC predicted sixth transmembrane domain (hKv4.3 short). Human heart  
CC primarily expresses hKv4.3 long, whereas human brain contains both forms.  
CC To obtain the present hKv4.3 short cDNA, PCR amplification was performed  
CC using primers that flanked the 57 bp insert in hKv4.3 long. The invention  
CC provides Kv4.3 polypeptides, polynucleotides, and methods for producing  
CC these polynucleotides. The Kv4.3 polypeptides and polynucleotides are  
CC useful in the diagnosis, treatment and screening of human diseases  
CC relating to an excess or deficiency of hKv4.3 activity, including  
CC Alzheimer's disease and heart disease  
CC  
XX

Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;

Query Match 100.0%; Score 2064; DB 6; Length 2064;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCTGAGTCACTGCGCGCGCGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
DB 61 GCTGAGTCACTGCGCGCGCGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 121 ATCGGGTGAATGCGGGTGCCTCACTGCGCGCGCGCGCGCGCTGCCCGCCCAAGA 180  
DB 121 ATCGGGTGAATGCGGGTGCCTCACTGCGCGCGCGCGCGCGCTGCCCGCCCAAGA 180  
QY 181 CGGCAAGATGAGTGTGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 CGGCAAGATGAGTGTGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 ACCTGGAAGGCTTACCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
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 RESULT 3  
 AAV61571 standard; cDNA; 2104 BP.  
 AAV61571;  
 11-JAN-1999 (first entry)  
 Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.  
 Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
 therapy; diagnosis; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 1..1908  
 /tag= a  
 W09842833-A2.  
 01-OCT-1998.  
 23-MAR-1998; 98WO-EP001901.  
 27-MAR-1997; 97GB-00006377.  
 09-DEC-1997; 97EP-00402971.  
 11-DEC-1997; 97EP-00403007.  
 (SMK) SMITHKLINE BEECHAM LAB PHARM.  
 Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;  
 WPI; 1998-542277/46.  
 P-P-SDB; AAW79589.  
 New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
 polynucleotide(s) useful in the treatment of disorders including cardiac  
 arrhythmias and Alzheimer's disease.  
 Claim 2; Page 24; 47pp; English.  
 This cDNA sequence codes for human Kv potassium channel hKv4.3 (see  
 AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3.  
 A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated  
 from human heart cDNA by PCR amplification (see AAV61574-77). Another  
 claimed polynucleotide (see AAV61572) encodes an isoform (see AAW9590)  
 of hKv4.3 having an additional 19 amino acids. The invention relates to  
 these hKv4.3 polynucleotides and polypeptides and to methods for  
 producing such polypeptides by recombinant techniques. Also claimed are  
 methods for utilizing the hKv4.3 polynucleotides for the treatment of  
 subjects in need of enhanced or reduced activity or expression of hKv4.3  
 polypeptide. These include the treatment of cardiac arrhythmias and  
 Alzheimer's disease. The invention can also be used to identify agonists  
 and antagonists of hKv4.3, and to detect disease associated with  
 inappropriate hKv4.3 expression or activity  
 Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other;  
 Query Match 92.3%; Score 1905; DB 2; Length 2104;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 73 ATGCGGCGGAGATGCGGCTGCTGCTTTGGCCGCGGCTCGGCGCATCGGATGATG 132  
 Db 1 ATGCGGCGGAGATGCGGCTGCTGCTTTGGCCGCGGCTCGGCGCATCGGATGATG 60  
 QY 133 CCGGTGGCCAACTGCCCCATGCCCTGGGCCCGGCGGACAAAGAACAGCGGAGATGAG 192



Db 61 CCGGAGGCAATGCGCCATGCGCTGGGCGCGGCGAGACAAAGAGGAGATGAG 120  
Qy 193 CTGATTGCTTCACAGTGAATGGGCGAGGTTCCAGACTGGAGCAACGCTGGAGCGC 252  
Db 121 CTGATTGCTTCACAGTGAATGGGCGAGGTTCCAGACTGGAGCAACGCTGGAGCGC 180  
Qy 253 TACCCGAGACCCGCTGCTGGGCGAGCGAGGAGGTTCTTCTTCAAGAGGACCGAG 312  
Db 181 TACCCGAGACCCGCTGCTGGGCGAGCGAGGAGGTTCTTCTTCAAGAGGACCGAG 240  
Qy 313 GAGTACTTCTTCCAGCCGAGGAGGTTGTTCCGCTGCTGCTCAACTTTCACCGCAG 372  
Db 241 GAGTACTTCTTCCAGCCGAGGAGGTTGTTCCGCTGCTGCTCAACTTTCACCGCAG 300  
Qy 373 GGGAGCTGCACTACCGCGCTACGAGTGCATCTTGCCTTACGAGCAGAGCTGGCTTC 432  
Db 301 GGGAGCTGCACTACCGCGCTACGAGTGCATCTTGCCTTACGAGCAGAGCTGGCTTC 360  
Qy 433 TACGGCATCTCCCGGAGATCATCGGGGACTGCTGCTACGAGAGTACAGACCGCAG 492  
Db 361 TACGGCATCTCCCGGAGATCATCGGGGACTGCTGCTACGAGAGTACAGACCGCAG 420  
Qy 493 AGGAGAAACGCGAGCGGCTATGAGACGACACGAGTGGAGAACGAGAGTCCATG 552  
Db 421 AGGAGAAACGCGAGCGGCTATGAGACGACACGAGTGGAGAACGAGAGTCCATG 480  
Qy 553 CCTGCTGAGCTTCCGCGAGACCATGTCGGGCGCTTCGAGAACCCCGACACGAGCAG 612  
Db 481 CCTGCTGAGCTTCCGCGAGACCATGTCGGGCGCTTCGAGAACCCCGACACGAGCAG 540  
Qy 613 CTGGCCCTGCTTCTTACTAGTGAATGAGCTTCTTCAATGCTGCTGCTCATACCGAC 672  
Db 541 CTGGCCCTGCTTCTTACTAGTGAATGAGCTTCTTCAATGCTGCTGCTCATACCGAC 600  
Qy 673 GTGGTGAAGACGATGCGCGGAGCAACGCTCCGCGGAGCAAGAGAGCTGCGGAGAG 732  
Db 601 GTGGTGAAGACGATGCGCGGAGCAACGCTCCGCGGAGCAAGAGAGCTGCGGAGAG 660  
Qy 733 CGTACTGATGAGCTTCTTCTGCTGAGCAACGCGGCTGATGATCTTCAACCGTGAAG 792  
Db 661 CGTACTGATGAGCTTCTTCTGCTGAGCAACGCGGCTGATGATCTTCAACCGTGAAG 720  
Qy 793 TACCTCTGCGGCTTCTTGGCGCTCCAGCGGCTACCGCTTATCCGAGGTCATGAGC 852  
Db 721 TACCTCTGCGGCTTCTTGGCGCTCCAGCGGCTACCGCTTATCCGAGGTCATGAGC 780  
Qy 853 ATCATGACGATGAGGAGCATGAGCCCTACTACATCGGCTGCTGATGAGCAACAGAG 912  
Db 781 ATCATGACGATGAGGAGCATGAGCCCTACTACATCGGCTGCTGATGAGCAACAGAG 840  
Qy 913 GACGATGCTGGGAGCTTGTGACAGCTCGGAGTCTTCCGCTTTCAGAGATCTTCAAGTTT 972  
Db 841 GACGATGCTGGGAGCTTGTGACAGCTCGGAGTCTTCCGCTTTCAGAGATCTTCAAGTTT 900  
Qy 973 TCCCGCACTCCAGAGGCTTGCAGATCTTGGGCTTACACACTGAGAGGCTGTGCGAA 1032  
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Qy 1033 CTGGGCTTCTTCTTCTTCTTCCCTACACATGAGCAATCTTGGCACTGATGTTT 1092  
Db 961 CTGGGCTTCTTCTTCTTCTTCCCTACACATGAGCAATCTTGGCACTGATGTTT 1020  
Qy 1093 TATGCGAGAGAGGCTCTCGGCGAGAGTTCACAGACATCCCTGCTGTTTGGTAC 1152  
Db 1021 TATGCGAGAGAGGCTCTCGGCGAGAGTTCACAGACATCCCTGCTGTTTGGTAC 1080  
Qy 1153 ACCATTGTCACATGACCACTGAGATACGAGACATGAGTCTTAAAGATTTGAGAGG 1212  
Db 1081 ACCATTGTCACATGACCACTGAGATACGAGACATGAGTCTTAAAGATTTGAGAGG 1140  
Qy 1213 AAGATCTTGGGCTCATGCTGCTTCTTGAAGGAGCTGATGATGAGCTGCGCAAGTCCCT 1272

Db 1141 AAGATCTTGGGCTCATGCTGCTTGTGAGTGGCGGCTGTGATGAGTCCCTGAGTCCCT 1200  
Qy 1273 GTGATTGTTTCCAACTTTAGCCGATTTTACCAACAGATTCAGAGCTGATTAACGAGG 1332  
Db 1201 GTGATTGTTTCCAACTTTAGCCGATTTTACCAACAGATTCAGAGCTGATTAACGAGG 1260  
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Db 1261 GCACAAAAGAGGCGCGCTTGCAGAGATCCGTGAGCAAAACGAGGATTTGAAATGCA 1320  
Qy 1393 TACCTGACAGCAAGCGCAAGGCTCCTCAACAGAGGCGCTGAGCTGAGCGGACCCCA 1452  
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Qy 1693 TCTAACCTGCAAGCTACCTGCGCTGCGAGCATGGAAGAGCTCAGACAGATCCATCCAG 1752  
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Qy 1753 GGCAGTGAAGACCCCTCCTCAACAGATGCTCCAGCTTAAATTGAAAGAGAGCAGC 1812  
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Qy 1993 GGCATGGC 2001  
Db 1921 ACAGAGGCG 1929

RESULT 4  
AAV61573  
ID AAV61573 standard; cDNA; 2104 BP.  
XX  
XX AAV61573;  
DE 11-JAN-1999 (first entry)  
XX  
XX Human Kv potassium channel hKv4.3 cDNA.  
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
KW therapy; diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 1..1911  
FT /\*tag= a

XX	PN	MO9842833-A2.
XX	PD	01-OCT-1998.
XX	PF	23-MAR-1998; 98WO-EP001901.
XX	PR	27-MAR-1997; 97GB-00006377.
XX	PR	09-DEC-1997; 97EP-00402971.
XX	PR	11-DEC-1997; 97EP-00403007.
XX	PA	(SMIK ) SMITHKLINE BEECHAM LAB PHARM.
XX	PI	Bril AMA, Calmeis TPQ, Faivre JSP, Javre J, Rouanet S;
XX	PI	WPI: 1998-542277/46.
XX	DR	P-PSDB; AAW79591.
XX	PT	New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
XX	PT	poly:nucleotide(s) useful in the treatment of disorders including cardiac
XX	PS	arrhythmias and Alzheimer's disease.
XX	PS	Claim 18; Page 27; 47pp; English.
CC	XX	This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC	CC	AAW79591). It was isolated using expressed sequence tag analysis. The
CC	CC	sequence has about 91% identity in 1914 nucleotide residues with rat
CC	CC	Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAW61571-72)
CC	CC	are also claimed. The invention relates to hKv4.3 polynucleotides and
CC	CC	polypeptides and to methods for producing such polypeptides by
CC	CC	recombinant techniques. Also claimed are methods for utilizing hKv4.3
CC	CC	polynucleotides for the treatment of subjects in need of enhanced or
CC	CC	reduced activity or expression of hKv4.3 polypeptide. These include the
CC	CC	treatment of cardiac arrhythmias and Alzheimer's disease. The invention
CC	CC	can also be used to identify agonists and antagonists of hKv4.3, and to
CC	CC	detect disease associated with inappropriate hKv4.3 expression or
CC	CC	activity
XX	XX	Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;
XX	XX	Query Match 91.9%; Score 1897; DB 2; Length 2104;
XX	XX	Best Local Similarity 99.0%; Pred. No. 0;
XX	XX	Matches 1909; Conservative 0; Mismatches 20; Indels 0; Gaps 0
QY	73	ATGCGCGCCGGAGTTGCGGCTGCTGCTCTTTTGCCCGGCTGCGGCAATCGGCTGGATG 132
DB	1	ATGGCGGAGGAGTTGCAAGCTCGCTGCTCTTTTGCCCGGCTGCGGCAATCGGCTGGATG 60
QY	133	CCGGTGGGCAATGCGCCCATGCGCCCTGGCGCCCGGCGCAAGAACAAGCGGAGATAG 192
DB	61	CCGGTGGGCAATGCGCCCATGCGCCCTGGCGCCCGGCGCAAGAACAAGCGGAGATAG 120
QY	193	CTGATTGTCTCTCAACGTGAGTGGGCGAGTTCCAGACCTGAGAGACCAAGCTGAGCGC 252
DB	121	CTGATTGTCTCTCAACGTGAGTGGGCGAGTTCCAGACCTGAGAGACCAAGCTGAGCGC 180
QY	253	TACCCGGACACCTCTGCTGGGCGACACGAGAAAGAGTTTCTTCTTCAAGAGACACCAAG 312
DB	181	TACCCGGACACCTCTGCTGGGCGACACGAGAAAGAGTTTCTTCTTCAAGAGACACCAAG 240
QY	313	GAGTACTTCTTTCGACCGGGACCCCGAGAGTTCGCGTGCGTCTCAACTTTTACGCGACG 372
DB	241	GAGTACTTCTTTCGACCGGGACCCCGAGAGTTCGCGTGCGTCTCAACTTTTACGCGACG 300
QY	373	GGGAAGCTGCACTTACCCGCGCTTACGAGTGCATCTTCTGCTTACGACGACGAGCTGGCTTC 432
DB	301	GGGAAGCTGCACTTACCCGCGCTTACGAGTGCATCTTCTGCTTACGACGACGAGCTGGCTTC 360
QY	433	TACGGCATCTTCCCGGAGATATATCGGGGACATGCTGTACGAGAGATACAAAGACCGCAAG 492
DB	361	TACGGCATCTTCCCGGAGATATATCGGGGACATGCTGTACGAGAGATACAAAGACCGCAAG 420
QY	493	AGGGAAGACCGCGAGCGGCTCTGACGACCAAGCTCGGAGAACCAACGAGATGCATG 552

Db	421	AGGAGAAAGCCCGAGGGCTCATAGAACAAAGACTCGAGAAACAAACGAGATCATG	480
Oy	553	CCCTCGCTCAGCTTCGCGCAGACCATGTGGCGGGCTTCGAGAAACCCCAACACGACG	612
Db	481	CCCTCGCTCAGCTTCGCGCAGACCATGTGGCGGGCTTCGAGAAACCCCAACACGACG	540
Oy	613	CTGGCCCTGTGCTCTCTACGTACGTGACTGGCTTCCTTCACTCGCTCTCTCGATCATCAAC	672
Db	541	CTGGCCCTGTGCTCTCTACGTACGTGACTGGCTTCCTTCACTCGCTCTCTCGATCATCAAC	600
Oy	673	GTGTGAGAGACGATGCCGTGCGGACGATGCCCGGACGAAAGACTGCCGTGCGGAG	732
Db	601	GTGTGAGAGACGATGCCGTGCGGACGATGCCCGGACGAAAGACTGCCGTGCGGAG	660
Oy	733	CGCTACCTCGATGGCTCTCTCTGCTGTGAGAACGCGCGGCGCTCATGATCTTCACTCGGAG	792
Db	661	CGCTACCTCGATGGCTCTCTCTGCTGTGAGAACGCGCGGCGCTCATGATCTTCACTCGGAG	720
Oy	793	TACCTCGTGGGCTCTTCGCGGCTCCGAGCGGCTACCGCTTCAATCCGACGCTATGAGC	852
Db	721	TACCTCGTGGGCTCTTCGCGGCTCCGAGCGGCTACCGCTTCAATCCGACGCTATGAGC	780
Oy	853	ATCATGCACGTGTGTGACATCATATGCTTACTAATCATCGGTCTGTGTATGACCAACAGAG	912
Db	781	ATCATGCACGTGTGTGACATCATATGCTTACTAATCATCGGTCTGTGTATGACCAACAGAG	840
Oy	913	GACATGTCCGGCGGCTTCGTACGCGTCCGGGCTTCGCGCTCTTCAGAGATCTTCAAGTTT	972
Db	841	GACATGTCCGGCGGCTTCGTACGCGTCCGGGCTTCGCGCTCTTCAGAGATCTTCAAGTTT	900
Oy	973	TCCCGCCACTCCAGGCGCTGCGGATCTGTGGCTACACACTGAAGAGCTGTGCTCCGAA	1032
Db	901	TCCCGCCACTCCAGGCGCTGCGGATCTGTGGCTACACACTGAAGAGCTGTGCTCCGAA	960
Oy	1033	CTGGGCTTTCTCTCTCTCCCTACACATGAGGCATCATATCTTTGGCACGTGATGTTT	1092
Db	961	CTGGGCTTTCTCTCTCTCCCTACACATGAGGCATCATATCTTTGGCACGTGATGTTT	1020
Oy	1093	TATGCGAGAAAGGCTCCTCGGCAGAGAGTTCAACAGCATCCCTGCTCGTTTGGTAC	1152
Db	1021	TATGCGAGAAAGGCTCCTCGGCAGAGAGTTCAACAGCATCCCTGCTCGTTTGGTAC	1080
Oy	1153	ACCATTTGTACCATGACCAACTGTGGATACGAGAGCATGTGTCTTAAGACATTTGCAGGG	1212
Db	1081	ACCATTTGTACCATGACCAACTGTGGATACGAGAGCATGTGTCTTAAGACATTTGCAGGG	1140
Oy	1213	AAGATCTTCGGCTCATCTGTGCTCTTGAAGTGGCGTCTGGGTCAATTTGCCAGTCCCT	1272
Db	1141	AAGATCTTCGGCTCATCTGTGCTCTTGAAGTGGCGTCTGGGTCAATTTGCCAGTCCCT	1200
Oy	1273	GTGATTTGTTCCAACTTTAAGCCGATTTTACCACAGATACAGAGCTGATTAAGCAGG	1332
Db	1201	GTGATTTGTTCCAACTTTAAGCCGATTTTACCACAGATACAGAGCTGATTAAGCAGG	1260
Oy	1333	GCACAAAAGAAAGGCCGCTTGGACAGATCCGTGTGGCCAAAACAGGACGTTGGAATGCA	1392
Db	1261	GCACAAAAGAAAGGCCGCTTGGACAGATCCGTGTGGCCAAAACAGGACGTTGGAATGCA	1320
Oy	1393	TACCTGCACAGCAAGCGCAACGGGCTCTCTCAACAGAGCGCTGAGCTGACCGGACCCCA	1452
Db	1321	TACCTGCACAGCAAGCGCAACGGGCTCTCTCAACAGAGCGCTGAGCTGACCGGACCCCA	1380
Oy	1453	GAAAGAGAGCACATGGGCAAGACCACTCTCACTCATGAGAGCCAGCATCATCACTGTG	1512
Db	1381	GAAAGAGAGCACATGGGCAAGACCACTCTCACTCATGAGAGCCAGCATCATCACTGTG	1440
Oy	1513	CACGTGCTGAAAAAACAATTAACAAGATTTATGATGACGAGATGTTTGAACAAGAC	1572
Db	1441	CACGTGCTGAAAAAACAATTAACAAGATTTATGATGACGAGATGTTTGAACAAGAC	1500
Oy	1573	TGCATGAGAGATTCAATGACAGAACTTACCATTCACAAAGAAAGTCCCTCACTGTCCAGCCAC	1632

Db 1501 TGATGAGAGGTTCAATGACGAACTACCACTCCAGAAAGTCCCTCACTGTCCAGCCAC 1560  
 Qy 1633 CCAGGCTCTCACTACCACTGCTGCTCCGCTGTAGTAAGAAAGACCAACACCTGCCCCAAT 1692  
 Db 1661 CCAGGCTCTCACTACCACTGCTGCTCCGCTGTAGTAAGAAAGACCAACACCTGCCCCAAT 1620  
 Qy 1693 TCTAACTGCGAGCTACTGCGCTGCGAGCATGCAAGAGCTGAGACGATCCACATCCAG 1752  
 Db 1621 TCTAACTGCGAGCTACTGCGCTGCGAGCATGCAAGAGCTGAGACGATCCACATCCAG 1680  
 Qy 1753 GCGAGTGAAGAGCCCTCCCTCAACAACAGTGTCTCAGGCTTAATTTGAAGACAGACGAC 1812  
 Db 1681 GCGAGTGAAGAGCCCTCCCTCAACAACAGTGTCTCAGGCTTAATTTGAAGACAGACGAC 1740  
 Qy 1813 GCGAGTGAAGAGCCCTCCCTCAACAACAGTGTCTCAGGCTTAATTTGAAGAGCTCCCACT 1872  
 Db 1741 GCGAGTGAAGAGCCCTCCCTCAACAACAGTGTCTCAGGCTTAATTTGAAGAGCTCCCACT 1800  
 Qy 1873 CCCCCAGGCTTAACCCGAGAGGAGGAAAGTGGGACCCCTGCGAGCCAGGCCCCCAAC 1932  
 Db 1801 CCCCCAGGCTTAACCCGAGAGGAGGAAAGTGGGACCCCTGCGAGCCAGGCCCCCAAC 1860  
 Qy 1933 ACGAATCTCTTCCATTAACAGCAATGTGTCAAGTCTCTGTCTTGAATAATCCGC 1992  
 Db 1861 ACGAATCTCTTCCATTAACAGCAATGTGTCAAGTCTCTGTCTTGAATAATCCGC 1920  
 Qy 1993 GGGCATGGC 2001  
 Db 1921 ACAGAGGGC 1929

## RESULT 5

AAV61572 standard; cDNA; 2072 BP.

AAV61572;

11-JAN-1999 (first entry)

Human Kv potassium channel hKv4.3 (longer isoform) cDNA.

Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia; therapy; diagnosis; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..1965

FT tag= a

FN W09842833-A2.

PD 01-OCT-1998.

PF 23-MAR-1998; 98MO-EP001901.

PR 27-MAR-1997; 97GB-00006377.

PR 09-DEC-1997; 97EP-00402971.

PR 11-DEC-1997; 97EP-00403007.

PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.

FI Bril AMA, Galmels TPG, Faivre JSP, Javre J, Rouanet S;

DR WPI; 1998-542277/46.

XX P-PSDB; AAM79590.

XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding

PT poly:nucleotide(s) useful in the treatment of disorders including cardiac

XX arrhythmias and Alzheimer's disease.

CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see  
 CC AAM79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.  
 CC A 1914 bp fragment corresponding to hKv4.3 (full-length cDNA was isolated  
 CC from human heart cDNA by PCR amplification (see AAV61574-77). Another  
 CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAM79589)  
 CC of hKv4.3 having 19 fewer amino acid residues. The invention relates to  
 CC these hKv4.3 polynucleotides and polypeptides and to methods for  
 CC producing such polypeptides by recombinant techniques. Also claimed are  
 CC methods for utilizing the hKv4.3 polynucleotides for the treatment of  
 CC subjects in need of enhanced or reduced activity or expression of hKv4.3  
 CC polypeptide. These include the treatment of cardiac arrhythmias and  
 CC Alzheimer's disease. The invention can also be used to identify agonists  
 CC and antagonists of hKv4.3, and to detect disease associated with  
 CC inappropriate hKv4.3 expression or activity  
 SQ Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;

Query Match 89.1%; Score 1838; DB 2; Length 2072;

Best Local Similarity 96.9%; Pred. No. 0; Mismatches 5; Indels 57; Gaps 1;

Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

Qy 73 ATGGGCGCGAGATTGCGGCTGCTGCTTTTGGCCGGGCTGCGGCATCGGGTGATG 132

Db 1 ATGGGCGCGAGATTGCGGCTGCTGCTTTTGGCCGGGCTGCGGCATCGGGTGATG 60

Qy 133 CCGGTGGCAACTGCGCCATGCTCCCTGCGCCCGGCGCAAGAACACAGCGAGATGAG 192

Db 61 CCGGTGGCAACTGCGCCATGCTCCCTGCGCCCGGCGCAAGAACACAGCGAGATGAG 120

Qy 193 CTGATTGCTCAAGTGAAGGAGGAGGTTCCAGACTGGAAGGACCAAGCTGAGAGGC 252

Db 121 CTGATTGCTCAAGTGAAGGAGGAGGTTCCAGACTGGAAGGACCAAGCTGAGAGGC 180

Qy 253 TACCGGAGACCTCTGCTGGGAGAGAGAGAGGAGTCTTCTTCAAGAGAGACCAAG 312

Db 181 TACCGGAGACCTCTGCTGGGAGAGAGAGAGGAGTCTTCTTCAAGAGAGACCAAG 240

Qy 313 GAGTACTTCTTGACCGGAGACCCGAGAGTGTCCGCTGCTGCTCACTTCTTCCGACG 372

Db 241 GAGTACTTCTTGACCGGAGACCCGAGAGTGTCCGCTGCTGCTCACTTCTTCCGACG 300

Qy 373 GGGAGCTGCACTCCCGGCTACAGAGTCACTCTGCTCAAGAGAGAGTGGCTTC 432

Db 301 GGGAGCTGCACTCCCGGCTACAGAGTCACTCTGCTCAAGAGAGTGGCTTC 360

Qy 433 TACGCAATCTCCGAGATCATCGGAGCTGCTGCTCAAGAGAGTCAAGAGCCGCAAG 492

Db 361 TACGCAATCTCCGAGATCATCGGAGCTGCTGCTCAAGAGAGTCAAGAGCCGCAAG 420

Qy 493 AGGAGAACCCGAGCGGCTATGAGAGCAAGCTGCGAGAACACAGAGATCCATG 552

Db 421 AGGAGAACCCGAGCGGCTATGAGAGCAAGCTGCGAGAACACAGAGATCCATG 480

Qy 553 CCTCGCTCAGCTCCGAGAGCATGAGGAGCTTTCGAGAACCCGACACGAGCAG 612

Db 481 CCTCGCTCAGCTCCGAGAGCATGAGGAGCTTTCGAGAACCCGACACGAGCAG 540

Qy 613 CTGCGCTGCTCTTCACTAGTACGCTTCTTCACTGCTGCTGCTGATCAACCAAC 672

Db 541 CTGCGCTGCTCTTCACTAGTACGCTTCTTCACTGCTGCTGCTGATCAACCAAC 600

Qy 673 GTGTGAGAGAGGTCGCGGAGAGAGTCCCGGAGAGAGAGAGTCCGTCGGGAG 732

Db 601 GTGTGAGAGAGGTCGCGGAGAGAGTCCCGGAGAGAGAGAGTCCGTCGGGAG 660

Qy 733 GGTACTGAGTGGCTCTTCTGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 792

Db 661 GGTACTGAGTGGCTCTTCTGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

Qy 793 TACCTCTGCGGCTCTTCTGCGGAGTCCAGCGGCTACCGCTTCATCCGAGGTCATGAGC 852

Db 721 TACCTCTGCGGCTCTTCTGCGGAGTCCAGCGGCTACCGCTTCATCCGAGGTCATGAGC 780

QY 853 ATCATGACGTGTGGCCATGATGCTTACATGCGTGTGATGACCAACAGAG 912  
 DB 781 ATCATGACGTGTGGCCATGATGCTTACATGCGTGTGATGACCAACAGAG 840  
 QY 913 GAGGTGTGGGCGGCTTGTGACGCTTCCGGGTCTTCCGGTCTTCAAGATTTT 972  
 DB 841 GAGGTGTGGGCGGCTTGTGACGCTTCCGGGTCTTCCGGTCTTCAAGATTTT 900  
 QY 973 TCCGCGCACTCCGAGGCGCTGCGGATCTGGGCTACACATGAAAGCTGTGCTCGAA 1032  
 DB 901 TCCGCGCACTCCGAGGCGCTGCGGATCTGCGGCTACACATGAAAGCTGTGCTCGAA 960  
 QY 1033 CTGGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092  
 DB 961 CTGGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020  
 QY 1093 TATGCCGAGAAAGGCTTCTTGGGCGAGATTCACAAAGATTCCTTGGTCTTGGTAC 1152  
 DB 1021 TATGCCGAGAAAGGCTTCTTGGGCGAGATTCACAAAGATTCCTTGGTCTTGGTAC 1080  
 QY 1153 ACCATTGTCAACATGACACACATGAGATACGAGACATGTGTGCTTAAAGATTCAGAG 1212  
 DB 1081 ACCATTGTCAACATGACACACATGAGATACGAGACATGTGTGCTTAAAGATTCAGAG 1140  
 QY 1213 AAGATCTTGGGCTTCAATGTGCTTCTTGAAGTGGCGCTGTGATCTTGGCTGCAATCCT 1272  
 DB 1141 AAGATCTTGGGCTTCAATGTGCTTCTTGAAGTGGCGCTGTGATCTTGGCTGCAATCCT 1200  
 QY 1273 GTGATGTTCACAACTTGTAGCGGATTTACACAGAAATGAGAGCTGATAAGCAGAG 1332  
 DB 1201 GTGATGTTCACAACTTGTAGCGGATTTACACAGAAATGAGAGCTGATAAGCAGAG 1260  
 QY 1333 GCACAAAGAGGCGCGCTTGGCAGGATCCGTGTGGCCAAACAGGCAATTGCAATGCA 1392  
 DB 1261 GCACAAAGAGGCGCGCTTGGCAGGATCCGTGTGGCCAAACAGGCAATTGCAATGCA 1320  
 QY 1393 TACCTGACACGACGAGCGCAAGCGGCTTCTTCAACGAGCGCTGAGCGGCAACCCA 1452  
 DB 1321 TACCTGACACGACGAGCGCAAGCGGCTTCTTCAACGAGCGCTGAGCGGCAACCCA 1380  
 QY 1453 GAGAGAGAGACATGGGCAAGACACCTGCTCATGAGAGCGAGCTATCACTGCTG 1512  
 DB 1381 GAGAGAGAGACATGGGCAAGACACCTGCTCATGAGAGCGAGCTATCACTGCTG 1440  
 QY 1513 CACTGCGTGAAGAAACCACT----- 1533  
 DB 1441 CACTGCGTGAAGAAACCACTGGGTTCTCTATCTTGTGATGATCCCTGTTATCTGTA 1500  
 QY 1534 -----AACCAAGATTATTGATGAGCAGATGTTTGAAGCAAACTGC 1575  
 DB 1501 CGAACTCCACATCAAGAAACCAAGATTATTGATGAGCAGATGTTTGAAGCAAACTGC 1560  
 QY 1576 ATGAGAGTTTCAATGCAAGATCACTCAACAAAGTCTTCACTGTCCAGCCACCA 1635  
 DB 1561 ATGAGAGTTTCAATGCAAGATCACTCAACAAAGTCTTCACTGTCCAGCCACCA 1620  
 QY 1636 GGGCTCACTACACCTGCTGCTCCCGTGTAGTAAGAAACAACACACTGCCCAATTC 1695  
 DB 1621 GGGCTCACTACACCTGCTGCTCCCGTGTAGTAAGAAACAACACACTGCCCAATTC 1680  
 QY 1696 AACCTGCACTACTGCTGCTGCGAGCATCAAGAGTCTGACAGATTCACATCCAGGC 1755  
 DB 1681 AACCTGCACTACTGCTGCTGCGAGCATCAAGAGTCTGACAGATTCACATCCAGGC 1740  
 QY 1756 AGTGAAGAGGCTTCTTCTTCAACAGTGTCTTCAAGCTTAAATTGAAAGAGAGAGGA 1815  
 DB 1741 AGTGAAGAGGCTTCTTCTTCAACAGTGTCTTCAAGCTTAAATTGAAAGAGAGAGGA 1800  
 QY 1816 CTGAGACCAAACTGCAAAATCCAGATCAACAGCCTATCATACATCCCACTGCC 1875  
 DB 1801 CTGAGACCAAACTGCAAAATCCAGATCAACAGCCTATCATACATCCCACTGCC 1860  
 QY 1876 CCAAGCGCTAACCCGAGAGGAGAAAGTGTGGCAACCCCTGCGACGCCAGGCCCAACAG 1935

DB 1861 CCAGCGCTTAACCCGAGAGGAGAAAGTCCGCCACCCCTGCGACGCCAGCCCAACAG 1920  
 QY 1936 AACATTCTTCCATACAGCAATGTTTCAAGGTCTGTGTGTA 1985  
 DB 1921 AACATTCTTCCATACAGCAATGTTTCAAGGTCTGTGTGTA 1970  
 RESULT 6  
 ADF91397  
 ID ADF91397 standard; cDNA; 1968 BP.  
 AC ADF91397;  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX  
 DE Wild-type hKv4.3 cDNA #SEQ ID 4.  
 XX  
 KW Antiarhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
 KW tranquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;  
 KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
 KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;  
 KW tachycardia; congestive heart failure; epilepsy; stroke;  
 KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
 KW Parkinson's disease; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1968  
 FT /-tag= a  
 FT /product= "hKv4.3"  
 PN MO2003097682-AL.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PF 14-MAY-2003; 2003MO-IB002453.  
 XX  
 PR 15-MAY-2002; 2002GB-00011123.  
 PR 15-MAY-2002; 2002US-0378076P.  
 PR 15-MAY-2002; 2002US-0378131P.  
 XX  
 PA (DEVG-) DEVGEN NV.  
 XX  
 PI Kaletta TV, Demulf NE, Plaetinck GRM;  
 XX  
 DR WPI; 2004-061981/06.  
 DR P-PDB; ADF91398.  
 XX  
 PT New nematode worm expressing a heterologous nucleotide sequence encoding  
 PT a functional voltage-gated potassium channel of the Kv4 family, useful  
 PT for determining compounds that interact with the voltage-gated potassium  
 PT channel.  
 XX  
 PS Example 1; SEQ ID NO 4; 82pp; English.  
 XX  
 CC The invention relates to a nematode worm that expresses a heterologous  
 CC nucleotide sequence encoding a functional voltage-gated potassium channel  
 CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,  
 CC part or fragment. The nematode worm is useful in determining whether a  
 CC compound interacts with the voltage-gated potassium channel of the Kv4  
 CC family or whether a compound is an agonist, antagonist, opener and/or  
 CC blocker of the voltage-gated potassium channel expressed by the nematode  
 CC worm. The methods are used for identifying and developing compounds that  
 CC interact with voltage-gated potassium channels of the Kv4 family. The  
 CC compounds may be used in the development and/or preparation of  
 CC compositions for pharmaceutical, agrochemical and/or veterinary use.  
 CC These may be used in preparing compositions for preventing or treating  
 CC diseases or conditions such as arrhythmia, tachycardia, congestive heart  
 CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,  
 CC Alzheimer's disease or Parkinson's disease. The current sequence  
 CC represents wild-type hKv4.3 cDNA.



DT 13-SEP-2001 (first entry)  
XX Human Kv4.2 cDNA.  
XX  
XX  
XX Human: Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;  
KM neurodegenerative disease; ischemia; stroke; Alzheimer's disease;  
KM Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;  
KW learning capacity; protein kinase activator; anti-arrhythmic; ss.  
OS  
XX Homo sapiens.  
XX  
XX  
XX Key location/Qualifiers  
FT CDS 433..2322  
FT /tag= a  
FT /product= "Kv4.2 alpha subunit"  
XX  
XX DE19963612-A1.  
XX  
XX 12-JUL-2001.  
XX  
XX 29-DEC-1999; 99DE-01063612.  
XX  
XX 29-DEC-1999; 99DE-01063612.  
XX  
XX (GENT-) FORSCHUNGSEBELLSCHAFT GENION MBH.  
XX  
XX WPI; 2001-426637/46.  
XX P-PSDB; AAB86319.  
XX  
XX  
XX New potassium channel subunit proteins, useful for identifying and  
PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological  
PT agents.  
XX  
XX  
XX Claim 11; Page 18-21; 50pp; German.  
XX  
XX  
XX This invention describes a novel potassium channel protein (I) that is  
CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium  
CC channels containing (I) are used to identify and test: (i) compounds for  
CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
CC activators of protein kinases. Host cells that express (I) can identify  
CC agents that do not interact significantly with channels and control I<sub>to</sub>  
CC (a quickly activated transient current), so lack the side effects of  
CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
CC for testing on organ cultures  
CC  
XX  
XX Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;  
SQ  
Query Match 48.5%; Score 1000.8; DB 4; Length 2351;  
Best Local Similarity 72.8%; Pred. No. 1.3e-188;  
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  
QY 66 AGTCAACATGCGCGCGAGTTGGCGCTGCGCTCTTTTGGCCGGGCTGCGCATCGG 125  
DB 423 AGTAAATCATGCGCGCGGCGGTGGCGAGCGTGGCTGCTTTTGGCAAGGCGCATCGG 482  
QY 126 GTGGATGCGGTGGCGCAACTGCCCATGCGCCCTGGCCCG---GGCGAACAAGACGC 182  
DB 483 GTGGATGCGGTGGCGCTCGGGGCGCTATGCGGCTCCCCGAGCGAGAGAGAAAGAC 542  
QY 183 GCAAGATGAGCTGATTTGCTCTCAACGTGAGTGGCGAGGTTCCAGACTGAGAGACAC 242  
DB 543 CCAAGATGCTCTATTGTGTGATGATGATGAGACCGGCTTCCAGAGTGGCAGAGACAC 602  
QY 243 GTGGAGCGCTACCGCGACACCTGCTGGCGACGACGAGAGAGAGTTCTTTCAACGA 302  
DB 603 CCGTGAACGTATCCACAGACTCTACTGCGGCACTTGAAGGAGACTTTTCTACACCC 662  
QY 303 GGAACCAAGAGACTTCTTTCGACCGGAGCCCGGAGGTGTCCGCTGCGCTCACTT 362  
DB 663 AGAAATCAGCAATATTCTTTGACCGTGAACCGAGACATCTTCCGACCAATCTGAATTT 722

QY 363 CTACCGCAGCGGAGAGCTGACTACCGCGCTACGAGTGCATCTCTGCTTACGACGACA 422  
DB 723 CTACCGCAGCTGGAGAGCTCACTATCTCGCCACGAGTCACTCTGCTTACGATMAAA 782  
QY 423 GCTGGCTCTTACCGGATCTCCCGAGATCATCGGGGACTGCTGTATAGAGAGTACA 482  
DB 783 ACTGGCTCTTCTTGGCTCATCCCGAATCATCGCGACTGTGTTATAGAGAGTACA 842  
QY 483 GGAACGCAAGAGAGAGAGAGCGGAGCGGCTCATGAGCAACGACTCGAGAGAACCA 542  
DB 843 GATGCGAGGCGAGAGAGAGAGCGGAGCGCTGACAGACGAGGAGATACCGACACCGCTG 902  
QY 543 GAG---TCATGCTCTGCTAGCTTCCGCAACATGAGCGGCTTGAAGACCC 599  
DB 903 GGAAGCGGCTTGGCCACCATGATGCAAGGAGAGAGGCTGTGAGAGGCTTTCAGAAACC 962  
QY 600 CCAACACAGACGCTGCGCTGCTTCTTACATGAGACTGCGCTTTCATGCTGCTTC 659  
DB 963 CCACACAGACGATGCGCTGCTTCTTACATGAGCGGCTTTCATGCTGCTTC 1022  
QY 660 GGTCTACACCAACGTGTGAGAGAGCGTGGCGGACGATCCCGG---CAGCAAGA 716  
DB 1023 TGTCAATCGGAATGTGTGAGAAACAGTGCCTGCGGATCAAGCCAGTCACTTAAAG 1082  
QY 717 GCTGCGGTGCGGAGCGCTACTCGGTGCTTCTTCTGCTGAGACAGCGCTGCTCAT 776  
DB 1083 ACTGCTGTGAGAGCGGTATGCTGTGCTCTTCTTCTGAGACAGCGCTGCTCAT 1142  
QY 777 GATCTTACCGTGAATACCTCTGCGGCTCTTCCGGGCTCCAGCGGCTTACCGCTCAT 836  
DB 1143 GATCTTACAGTGAATATTTGCTTGTGCTGCTGAGCGCTTACGCTTATGCTTGT 1202  
QY 837 CCGACGCTCATGAGCATCATGACGCTGTGCGCATATGCTTACTATCATCGCTGTGT 896  
DB 1203 GCGTATGCTATGATGATCATGACGCTGTGCGCATCTGCTTATCATGCTGTGT 1262  
QY 897 CATGACCAACAGAGAGCGTGTCCGCGCTTGTGACGCTCCGCGCTTCCGCTCTT 956  
DB 1263 GATGACCAACATGAGAGAGCGTGTCCGCGCATCTTGTCACTCCGAGTCTTCCGCTCTT 1322  
QY 957 CAGGATCTTCAAGTTTCCCGCATCTCCAGGCGCTCGGATCTCGGGCTTACACCTGAA 1016  
DB 1323 CAGGATCTTCAAGTTTCCCGCATCTCCAGGCGCTCGGATCTCGGGCTTACACCTGAA 1382  
QY 1017 GAGCTGTGCTCGGAATGCGGCTTCTTCTTCTCTCTCAACGAGGCTCATCATCTT 1076  
DB 1383 GAGTGTGCTCGGAATGCGGCTTCTTCTTCTCTCTCAACGAGGCTCATCATCTT 1442  
QY 1077 TGCACCTGATGTTTATGCGAGAGAGGCTCTCGCGACGAGTTCAACAGATCCC 1136  
DB 1443 CGCTACAGTATGTTTACGAGAGAGAGGCTCTCGGCTTACGAGATTCACGAGATCCC 1502  
QY 1137 TGCCTGTTTGTATACCACTTGTCAACATGACCACTGGATTAAGAGATGTGTC 1196  
DB 1503 TGCAGCTTGTATATACATGCTCAACATGACCACTAGGATGTATGTATGTGTC 1562  
QY 1197 TAAGAGATTTGAGGAGAGATTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1256  
DB 1563 AAAAATCATGAGAGAGATTTTGTGTTCTATCTGCTGATGAGGCTCTTGTGCTAT 1622  
QY 1257 TGCCTGCAAGTCTCTGATGTTTCAACTTATGCGGATTTTACCAAGATCAAG 1316  
DB 1623 TGTCTTACCTGTTCCGCTGATGTTATCAACTTCACTGCGATTCACCAAGATCAAG 1682  
QY 1317 AGCTGATTAACGAGAGGACAAAGAGAGGCGCTTGTGAGATCTGCTGTGCTCAAAAC 1376  
DB 1683 AGCAGCAACGAGAGGACAAAGAGAGGCTTACCTGCGCAGATCCGCGACCAAAAG 1742  
QY 1377 AGCAGTGAATGAGTACCTGACAGCAAGCGCAAGGCTCTCTCAACAGAGCGCTGGA 1436  
DB 1743 CGAAGCGCAATGCTTACATGAGAGCAACGAAATGTTTACTAGTATACGCTGCA 1802  
QY 1437 GCTGACGGGACCCAGAGAGAGGACATGAGGCAAGACCACTCATGAGAGCCA 1496





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QY 837 CCGGACGTCATGAGCATCATGCGTGTGGCCATCATGCGCTACTCATCGGTCTGGT 896
DB 1203 GCGTAGTCATGATGATCATGACGCTGGTGGCCATCTGCTCTTATTAATGGGCTGGT 1262
QY 897 CATGACCAACAGAGAGAGCTGTCGGGCGCTTCGTACGCTTCGGGCTCTTCCGCGCTTT 956
DB 1263 GATGACAGCAATAGAGAGAGCTGACGGAGGCTTTGTACATCTCGAGTCTTCGGGCTTT 1322
QY 957 CAGGATCTTCAAGTTTCCCGGCACTCCGAGGCTGCGGATCCTGGGCTACACACTGAA 1016
DB 1323 CAGGATCTTCAAGTTTCCCGGCACTCTCAGGCTGCGGATCCTGGGCTACACACTGAA 1382
QY 1017 GAGCTGTGCTCCGAATGCGGCTTCTCTCTTCTCCCTCAGGATGCGGATCATCTT 1076
DB 1383 GAGCTGTGCTCCGAATGCGGCTTCTCTCTTCTCTGCTCAGGATGCGGATCATCTT 1442
QY 1077 TGGCATCTGATGTTTATATGCGAGAGGCTCTCTGCGGATGCGGATGCGGATGCGG 1136
DB 1443 CCGTACAGTTATGTTTACGAGAGAGGCTCTCTGCGGATGCGGATGCGGATGCGG 1502
QY 1137 TGGCTGTTTGGTACACATGTCATGATGACCACTGGATGCGGATGCGGATGCGG 1196
DB 1503 TGGAGCTTCTGTTATACATGTCATGATGACCACTGGATGCGGATGCGGATGCGG 1562
QY 1197 TAAAGCATGACAGGAGAGATCTTGGCTCATCTGCTCTTGAATGCGGCTCTGCTCAT 1256
DB 1563 AAAAACAATAGAGAGAGAGATCTTGGCTCATCTGCTCTGCTGATGCGGCTCTGCTCAT 1622
QY 1257 TGGCCGCGGATGCTCTGATGTTTTCATGTTAGCGGATGTTTACACAGATGAG 1316
DB 1623 TGGCTTACCTGTTCCGTTGATGATTCATCTTACGATGATGATGATGATGATGATG 1682
QY 1317 AGCTGATTAACGAGGAGGACAAAAGAGGCGGCTTGGCAGATGCGGTGCGCAAAAC 1376
DB 1683 AGCAGACAAACGAGGAGGACAAAAGAGGCTTGGCAGATGCGGTGCGCAAAAC 1742
QY 1377 AGGAGTGTGAATGATGATCTGTCAGAGAGCGGAGCGGCTCTCTCAAGAGCGCTGGA 1436
DB 1743 CGGAGGCGCAATGCTTACATGAGAGCAAAAGGATGTTACTGATGATGAGCTGCA 1802
QY 1437 GCTGACGCGGACCCGAGAGAGAGCATGCGGAGAGCAACCTCATCTCATGAGGCCA 1496
DB 1803 GTCCTCAGAGAG--TGAGAGGCTTTTGTAGGAATCCGCGCTCCAGCTTTGAAACCA 1859
QY 1497 GCATCATCATCTGCTGTCATGCTGCAAAAACCACTAACAAGTTTATGATGAGCA 1556
DB 1860 GCACACACCTGCTGCTTACTGCTGCAAAAACCACTAACAAGTTTATGATGAGCA 1919
QY 1557 GATGTTGAGCAGAGATGATGAGAGATTCAATGACAGATCACTCAACAAGATGCC 1616
DB 1920 AGTCTTTGAAGAAAGCTGATGAGAGTTGCAAGTTTATGCTTCAAGTCAAGTCC 1979
QY 1617 CTCACTGTCCAGGACCCAGGCTCATCACTGCTGCTCTCTCTGTTAGTAAAGAC 1676
DB 1980 TTCACTGTCTTCAACAAGAGAGTCACTGCTGCTTCAAGAGAGACAAAAC 2039
QY 1677 CACACAGCTGCGCAATCTTAACCTGCGAGCTACGCTGCGAGCATGAGAGCTCAG 1736
DB 2040 TTTTTCGATCCCAATGCTCAATGATATCAAGAGAGCATCAAGATGATCAAGAACTCAG 2099
QY 1737 CAGGATCCATCCAGGAGGAGTGAAGAGCCCTCTCTCAACAAGTCTGCGCTTAA 1796
DB 2100 CAGGATCCATCCAGGAGGAGTGAAGAGCCCTCTCTCAACAAGTCTGCGCTTAA 2159
QY 1797 TTTGAAAGCAGAGAGAGCTGAGACCAAACTGCAAAATCCAGATCAACAAGCAT 1856
DB 2160 TGGCAAAATGAAAGAGTGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2219
QY 1857 CATCAGATGCGGCTGCGGAGGCTTAAACCCAGGAGGAGGAGGAGGAGGAGGAGGAG 1908
DB 2220 AATTAAGATCCCAACCTTCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2271

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RESULT 9
ADJ11252
ID ADJ11252 standard; DNA; 2351 BP.
XX
AC ADJ11252;
XX
DE 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SeqID 253.
XX
KW human; ds; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
XX cytostatic; gene.
XX
OS Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
XX
PF 14-FEB-2003; 2003US-00369186.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2004-178717/17.
XX
DR P-PSDB; ADJ11258.
XX
PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
XX
PS Example 12; SEQ ID NO 253; 222bp; English.
XX
CC This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide is a human ovarian tumour antigen DNA
CC sequence given in an exemplification of the invention.
XX
SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
Query Match 48.5%; Score 1000.8; DB 12; Length 2351;
Best Local Similarity 72.8%; Pred. No. 1.3e-188;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;
QY 66 AGTCACCATGCGGCGGAGTTCGCGCTGCTGCTTTTGGCGGCTGCGGCTGCGG 125
DB 423 AGTATCATGATGCGCGCGGCTGCGAGCTGCTGCTTTTGAAGGCGCAAGCTATCGG 482
QY 126 GTGAGATGCGGATGCGGCACTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 182
DB 483 GTGATGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542

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QY 183 GCAGATGAGCTGATTTGCTTCATCGTAGTGCGGAGGTTCCAGACCTGGAGGACAC 242  
 Db 543 CCAAGATCTCTCATTTGCTGTAATGTAGTGACACCGCTTCCAGACGTGGCAGAGACAC 602.  
 QY 243 GCTGAGGCTTACCCGGAACCTCTGCGGACGACGAGAAAGAGATTCTTTCACAGA 302  
 Db 603 CTTGGAAGCTTACCAGACACTCTACTGGGAGTTCTGAGAGGAGACTTTTCTACACACC 662  
 QY 303 GGAACCAAGAGATCTTCTGACCGGAGACCCCAAGTGTTCGGCTGCTCAACTT 362  
 Db 663 AGAAATCTAGAGATTTCTTTGACCGTGAACCAACATCTTCCCACTCTCAATTT 722  
 QY 363 CTACCGGACGGGAGAGCTGACCTACCCGGGCTACGAGTGAATCTTGCTTACGAGAGA 422  
 Db 723 CTACCGGACCTGGAGAGCTCACTATCTTCGCAAGATGACATCTTGCTTACGAGAGAGA 782  
 QY 423 GCTGGCTTCTTACGAGCATCTCCCGGAGATGATCGGGGACTGCTCTACGAGAGTACA 482  
 Db 783 ACTGGCTTCTTTGGCTCATCCGGGAATCATCGGCACTGCTTTAATGAGAGTACA 842  
 QY 483 GGACCGGAGAGGAGAAACCGGAGCGGCTCATGAGCAACAACGACTGGAGAACCA 542  
 Db 843 GGATCGGAGGAGAGAAACCGGAGCGGCTCATGAGCAACAACGACTGGAGAACCA 542  
 QY 543 GGAG---TGCATGCCCTGCTCAGCTTCCGCAAGCAATGCGCGGCTTCCGAGAACCC 599  
 Db 903 GGAAGCGCTTGGCCACCATGATCTGCAAGGAGAGGCTCTGAGAGGCTTCCGAGAACCC 962  
 QY 600 CCACACGACGACGCTGCGCTGCTCTTCTTACTACCTGAGCTGAGCTTCTTATCGCTGCTC 659  
 Db 963 CCACACGACGACGATGCGCTGCTGCTTCTTACTATGTCACGGGCTTCTTATCGCTGCTC 1022  
 QY 660 GGTATCAACCAAGTGTGAGACGCGTCCGCGGACGCTCCCGG---CAGCAAGAA 716  
 Db 1023 TGTATCGCGATGTGTGAGAAACAGTCCGCTGCGATCAAGCCAGGCTTCACTTAAAGA 1082  
 QY 717 GTCGCGGAGGAGGAGGCTACTCGTGGGCTTCTTCTGCGCTGAGCAGGGGTGGTAT 776  
 Db 1083 ACTGCTGCTGAGAGGCGGTATGCTGTGCTTCTTCTGCTGAGCAGGCGCTGCTGAT 1142  
 QY 777 GATCTTCAACCGTGAAGTACTCTGCGGCTCTTCCGCGCTCCACGCGCTTACCGCTTAT 836  
 Db 1143 GATCTTCAACGTTAGATTTGCTTCCGCTGCGCTGAGACGCGCTTATCCGCTTAT 1202  
 QY 837 CCGAGCGCTATGAGCATCATGACGTGTGGCCATCATGCCCTTACTATCATGCTGTGT 896  
 Db 1203 GCGTAGTGTATGATGATCATGACGTGTGGCCATCATGCCCTTACTATCATGCTGTGT 1262  
 QY 897 CATGACCAACAGAGACGCTGTCCGCGCTTGTACAGCTCCGAGTCTTCCGCTT 956  
 Db 1263 GATGACAGACATGAGAGCGTCAAGGAGCGCTTGTGTACACTCCGAGTCTTCCGCTT 1322  
 QY 957 CAGGATCTTCAAGTTTTTCCGCACTCCGAGGCGCTGGAGATCCGAGGCTTACACATGAA 1016  
 Db 1323 CAGGATCTTCAAGTTTTTCCGCACTCCGAGGCGCTGGAGATCCGAGGCTTACACATGAA 1382  
 QY 1017 GAGCTGTGCTTCCGAACTGGGCTTCTTCTTCTCCCTACCAATGAGCATCATCTT 1076  
 Db 1383 GAGTTGTGCTTCCGAACTGGGCTTCTTCTTCTCCCTACCAATGAGCATCATCTT 1442  
 QY 1077 TGCACATGATGTTTTTATGCGGAGAGGCTCTCCGCGCAAGTTCAACAGATCCC 1136  
 Db 1443 CGCTACAGTTATGTTTATGCGAGAGAGGCTTCTCCGCTGACAGTTCAACAGATCCC 1502  
 QY 1137 TGCTCGTTTGTATACCATGTTCAACCATGACCACTGGGATACGAGACATGATGCC 1196  
 Db 1503 TGCAAGCTTCTGTATACCATGTTCAACCATGAGGATGATGATGATGATGCC 1562  
 QY 1197 TAAAGCATGACGAGGAGATCTTGGCTCATGCTGCTCTTGAAGTGGCTGTGCTAT 1256  
 Db 1563 AAAAACAATAGCAGGAGATTTTGTGTTTATCTGTTGCTGAGTGGGCTGTGCTAT 1622  
 QY 1257 TGCCCTGCAAGTCCCTGTGATTTTCCAACTTAAAGCGGATTTACCAACCAAGATCAAG 1316

Db 1623 TGCTTACTCTTCTTCCGAGATTTGATATCAACTTGAAGTGCATCTTACCAAGATCAAG 1682  
 QY 1317 AGCTGATTAACGACGAGGACAAAGAGAGCCGCTTCCAGAGATCGTGTGCCAAAC 1376  
 Db 1683 AGCAGACAAAGAGAGGACAAAGAGAGATGATGATGCTGAGATCCGCGGAGCCAAAG 1742  
 QY 1377 AGGAGTTGGAATGATCTCTGACAGAGAGGAGAGGAGGCTTCAAGAGGAGCTGA 1436  
 Db 1743 CGAAGCGCAATGTTATCATGACAGAGCAACGAGATGTTTACTAGTATCACTGCA 1802  
 QY 1437 GCTGACGAGGACCCCAAGAGAGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1496  
 Db 1803 GTTCTCAGAGAG---TGAGAGGCTTTTGTATGAGAAATCCGGCTCAGCTTTGAACCA 1859  
 QY 1497 GCATCATCACTGCTGACCTGCTGAGAAACCACTTACCAAGATTTATGATAGCA 1556  
 Db 1860 GCACCAACCTGCTTCACTGCTGAGAAACCAAGATCAAGATGATGATGATGATGATGAT 1919  
 QY 1557 GATGTTTGAAGAGATGATGAGAGTTCATGAGATGATGATGATGATGATGATGATGAT 1616  
 Db 1920 AGTCTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1979  
 QY 1617 CTCATGTCAGGACACCGAGGCTCATACCAAGGCTGCTCCGCTGATGAGAGAG 1676  
 Db 1980 TTCACTGCTTTCACACAGAGATGACAGAGCTGCTGCTTTCACAGAGACACAAACAA 2039  
 QY 1677 CACACACCTGCCCAATTTTAACTGCGAGTACTGCGCTGCGAGCATGACAGAGCTGAG 1736  
 Db 2040 TTTTGCATGCTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099  
 QY 1737 CACGATCCATTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1796  
 Db 2100 CACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2159  
 QY 1797 TTTGAAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1856  
 Db 2160 TGCCAAATGAGAGAGTGTGTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 2219  
 QY 1857 CATGACATCCCACTCCCGAGGCTTAAACCCAGAGAGGAGGAGGAGGAGGAGGAGGAG 1908  
 Db 2220 AATAAGATTCACCACTCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271

RESULT 10  
 ADM43513  
 ID ADM43513 standard; DNA; 2351 BP.  
 XX  
 AC ADM43513;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human ovarian cancer cDNA homologous DNA #7.  
 XX  
 KW ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.  
 OS Homo sapiens.  
 PN US2003129192-A1.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PE 02-AUG-2002; 2002US-00212677.  
 XX  
 PR 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00970966.  
 XX  
 PA (CORI-) CORIXA CORP.



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RESULT 11
ADM10923
ID ADM10923 standard; cDNA; 5333 BP.
XX
XX
AC ADM10923;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human O647SgenomicContig3 homologue cDNA #5.
XX
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytosolic; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
XX US2003206918-A1.
XX
XX 06-NOV-2003.
XX
XX 05-FEB-2003; 2003US-00361811.
XX
XX 10-SEP-1999; 99US-00394374.
XX 01-MAY-2000; 2000US-00561778.
XX 15-AUG-2000; 2000US-00640173.
XX 07-SEP-2000; 2000US-00656668.
XX 14-NOV-2000; 2000US-00713550.
XX 03-APR-2001; 2001US-00825294.
XX 02-OCT-2001; 2001US-00970966.
XX 02-AUG-2002; 2002US-00212677.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
XX
XX MPI; 2003-901037/82.
XX
XX P-PSDB; ADM10929.
XX
XX New polynucleotides encoding tumor proteins, treating or inhibiting the
XX development of cancer, particularly ovarian cancer, and for stimulating
XX and/or expanding T cells specific for a tumor protein.
XX
XX Example 12; SEQ ID NO 254; 221bp; English.
XX
XX This invention describes a novel ovarian tumour protein which can be used
XX to detecting the presence of an ovarian cancer in a patient by
XX stimulating and/or expanding T cells specific for the tumor protein. The
XX products of the invention can also be used in a method to inhibit the
XX development of a cancer in a patient comprising (a) incubating CD4+
XX and/or CD8+ T cells isolated from a patient with at least one ovarian
XX tumour protein, such that T cell proliferate and (b) administering to the
XX patient the proliferated T cells. The cytosolic polynucleotides or
XX polypeptides described in the invention are useful for treating or
XX inhibiting the development of cancer, particularly ovarian cancer and for
XX stimulating and/or expanding T cells specific for a tumour protein or for
XX gene therapy.
XX
XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
XX
XX Query Match 48.5%; Score 1000.8; DB 11; Length 5333;
XX Best Local Similarity 72.8%; Pred. No. 15e-188;
XX Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;
QY 66 AGTACCATGAGCGCGAGGTTGCGGCTGCTGCTTTTGCCCGGCTGCGGCATCGG 125
DB AGTATCATGCGCGCGGGGTGCGAGCGTGTGCTTTTGGCAAGGGCAGCGGCTATGG 1018
QY 126 GTGATGCGCGGTGCGCACTGCGCCATGCTCCCTGCGCCC--GCGCAGACAAGAAAGCG 182
DB GTGATGCTGCTGCGGCTTATGCGGCTCCCGGAGCGAGAGGAAAGAGAC 1078
QY 183 GCAGATGAGCTGATGCTCTCAACGTAGTGGGCGAGGTTCCAGACCTGGAGACAC 242
DB
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DB 1079 CCAAGATGCTCTCATTTGTTGATGATGATGAGGACCCGCTTCCAGAGCTGGCAGAGCAC 1138
QY 243 GCTGAGGCTTACCCGAGACCTTCTGTGGCAGACCGAGAGAGATTCTTTCAAGCA 302
DB 1139 CTTGGAAGCTTACCCAGACACTCTACTGTGGGAGTTCTGAGAGGAGACTTTTCTTACACCC 1198
QY 303 GGACACCAAGAGATCTTCTTCCAGCGGAGACCCGAGGGTTCCGCTGGCTCAACT 362
DB AGAAATCAAGATATTTCTTTGACCGTACCAACATCTTCCGACATCTTGATATT 1258
QY 363 CTACCGCAAGGAGAGCTGACCTACCCGCTACAGTGCATCTGTGCTTACAGACGA 422
DB CTACCGCACTGGAGAGCTTCACTATCTTCGACAGATGCTCTGTGCTTACAGAGAG 1318
QY 423 GCTGCTCTTCTACGCGCATCTTCCGAGATCATCTGCGGAGCTGCTGCTACAGAGATCAA 482
DB ACTGCTCTTCTTGGCTCATCTCCGAAATCATCGGCACTGCTGTATGAGAGATCAA 1378
QY 483 GGACCGCAAGGAGAGAGACCGGAGCGGCTCATGAGACGACGCTGGAGAACACCA 542
DB GATGCGAGGAGAGAAACGCGAGCGCTTGAGAGACGCGATACCGACACCGCTGG 1438
QY 543 GGAG---TCCATGCTCTGCTCAGCTTCCGCAAGCATGTGGCGGCTTGGAGAACCC 599
DB GAGAGAGCCCTTGGCCACATGACTGCAAGGAGGCTTGGAGGCTTTCAGAGAACCC 1498
QY 600 CCACACGACACGCTGCGCTTGTCTTCTACTACGTGACTGAGCTTCTTCTGCTGCTC 659
DB CCACACGACACGAGTGGCTTGTCTTCTACTATGTCACGAGGCTTTCATGCGCTGC 1558
QY 660 GGTATTCACCAACGTGTGAGAGACGCTGCGGACGAGTCCCGG---CAGCAAGA 716
DB TGTATTCGCAATGTGTGAGAAACAGTCCGTGCGATCAAGCCAGGTCACTTAAAGA 1618
QY 717 GCTGCGGTGCGGAGCGCTACTCGGTGCGCTTCTTGTGCTGCAAGCGCGTGCAT 776
DB ACTGCTCTGTGAGAGCGGTATGCTGTGCTTCTTCTGCTTGGACAGGCTGCTCAT 1678
QY 777 GATCTTCAACGATGAGTACTCTGCGGCTCTTCCGCGCTCCACGCGCTACCGCTTAT 836
DB GATCTTCAACGATGAGTATTTGCTTCCGCTGCGACGCGCTAGTCTTACCGTTTGT 1738
QY 837 CCGAGCGCTCATGAGCATCATGAGTGTGCGCATATGCGCTCATCTACGTCTGCT 896
DB GGTATGCTCATGATATCATCATGAGTGTGCGCATCTGCTTATTCATTTAGGCTGCT 1798
QY 897 CATGACCAACAGACAGAGAGTGTGCGGCGCTTGTGCAAGCTTCCGCGCTT 956
DB GATGACCAACATATGAGAGCTCAGCGAGGCTTGTGCACTCCAGAGCTTCCGCGCTT 1858
QY 957 CAGATCTTCAAGTTTCCCGCACTCCAGAGGCTGCGATCTGCGCTACACTGA 1016
DB CAGATCTTCAAGTTTCCCGCACTCCAGAGGCTGCGATCTGCGCTACACTGA 1918
QY 1017 GAGCTGTGCTTCCAGTCTGCGCTTCTTCTTCTTCCCTCAACATGCGCATCATCTT 1076
DB GAGTGTGCTTCCAGATTTGCGCTTCTTCTTCTTCCCTCAACATGCGCATCATCTT 1978
QY 1077 TGCCACTGTGATGTTTATATGCGAGAGAGGCTCTCGGCGCAGAGTTCAAGATCC 1136
DB CGCTTCACTTATGTTCTTACGAGAGAGGCTCTTCCGCTTACAGAGTTCAAGATCC 2038
QY 1137 TGCCCTGTTTGTATACCATTTGTCACCATGACACCACTGGGATACGAGACATGTGCC 1196
DB TGCAAGCTTGTGATATGATCATGATCATCAACACTAGGATATGTGATGATGTGCC 2098
QY 1197 TAAAGCATTTACAGAGAGATCTTCCGCTCATCTGCTCTTGAAGTGCCTGCTGTAT 1256
DB AAAAACAATACAGAGAGATTTTGTGATCTATCTGTTGATGTGAGTGGGCTTGTGAT 2158
QY 1257 TGCCCTGCAAGTCCCTGATGTTTTCACATTTAGCGGATTTTACACAGAAATCAGAG 1316
DB TGCTTCACTGTTCCGATGATTTATCACTTCACTGATGATCTTACACAGAAATCAGAG 2218
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Oy	1317	GGCTGATTAAGCGCAGGGGACAAAGAAAGAGAGCCGCTTCGACAGGATTCGCTGAGGCAAAAC	1376
Db	2219	AGCAGACAAACGAAAGGCGACAAAGAAAGAAAGCTAGACTGCGCAGGATCCGGGACGCCAAAG	2278
Oy	1377	AGGCAATTGCAATGCATTAACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGA	1436
Db	2279	CGGAAGCGCAATGCTTATCATGCGAGCAACGGAATGTTTATCTCAGTAATCAAGCTGCA	2338
Oy	1437	GCTGACGGGACCCCGAAGAGAGACATGGGCAAGCAACCTTCATCATCGAGAGCA	1496
Db	2339	GTCTCTCAAGGA---TGAGAGGGCTTTTGTATGACAAATCCGAGCTCCAGCTTTTGAACCCA	2395
Oy	1497	GCATCATCAACCTGCTGCACCTGCGCTGGAAAAAACACTAACACGAGTTATTTGATGAGCA	1556
Db	2386	GCACCAACCACTGCTCTTCACTGCTGAGAAAAAACAAGATACAGAGTTTGTGACGAACA	2455
Oy	1557	GATGTTTGAGCAGAACTGATGAGAGTTTCATGACGAATCAACCATCCACAAGAAAGTCC	1616
Db	2456	AGTCTTTGAAGAAAGCTGATGGAAGTTGCAACAGTTATATGTCCTTCAATCACAAGTCC	2515
Oy	1617	CTCACTGTCCAGCCACCAAGGCTCTACTACAACCTGCTGCTCCGTCGTAGTAAGAGAC	1676
Db	2516	TTCACTGCTTTCACAACAAGAGATGCCAGAGACCTGCTGTTCACGACCACAAAAAAAC	2575
Oy	1677	CACACACCGGCCAATTTCTAAACCTGCGCAGCTACTCGCTGGCGACATGCAGAAAGCTCAG	1736
Db	2576	TTTTTGCAATCCCAAAATGCCAAATGTAATCAAGAAAGCCATCAAGGTAGTAACAAGAACTCAG	2635
Oy	1737	CACGATCCACATCCAGGGCAGTGAAGCAAGCCCTCCCTCCAACAACAGTCGCTCCAGCTTAA	1796
Db	2636	CACGATTCAGATCAGATGTGTGGAGAGAAACAACCTCTGTCTTAAACAGCGCATCAAGTTTAA	2695
Oy	1797	TTTGAAGCAGACGACGAGCTGAGACCAAACTGCAAAACATCCACAGATACCAAGCCAT	1856
Db	2696	TGCCAAATGGAAGAGTGTGTTAAACTAAACTGTGAACAACCTTATGTGACTACAGCAAT	2755
Oy	1857	CATCAGCATCCCACTCCGCCACGCGCTTAAACCCAGAGGGGAAAGTCCGCCA	1908
Db	2756	AATAAGCATCCCAACCACTTCCAGTAAACAACCAACAAAGAGACGATAGGCCA	2807

Query Match	Best Local Similarity	Matches 1348;	Conservative	0;	Mismatches 492;	Indels 12;	Gaps 4;
66	AGTACCACTGCGCGCCGAGATGGCGGCTGGCTGCTTTGGCCCGGGCTGCGGCATTCG	48.5%;	Score 1000.8;	DB 11;	Length 5333;		
959	AGTATATCATGCGCGCGGGGGTGGAGAGCGGTGCTCCCTTTGGCAAGGCGAGGCTATACGG	72.8%;	Pred. No. 1.5e-188;				
126	GTGATGCGCGGTGGGCAACTGCGCCCATGCGCCCTGCGCCCGCCCGCCCGCAAGAACGCG						
1019	GTGATGCTGTGCTTGGCTTCGGGGCCCTATGCGCGCTCCCGCCGAGGAGAGAGAAAGAGAC						
183	GCAGATGAGCTGATTTGTCTTCAACGTGAGTGGCGGAGGTTTCCAGACTTGGAGAGACAC						
1079	CCAGATGCTCTCATTTGTGCTGAAATGTGAGTGGAGACCCGCTTCCAGAGTGGAGAGAC						
243	GCTGGAGCGCTAACCCGAGACCTCTGCTGGGCGACAGCGAGAGAGATTTCTTTCAACGA						
1139	CCTGGAAGTTATCCAGACACTCTACGTGGGAGTTCGTGAGGGGACCTTTTCTACACCC						
303	GGACACCAAGAGATTACTTCTTGACCGGGGACCCCGAGGCTGTCGCTGCGCTCAACTT						
1199	AGAACTCAGCAGTATTTCTTTGACCGGACCCAGACCAATCTTCCGACACATCTGAAATTT						
363	CTACCGCAGGGGAGAGTCACTACCCGCGCTACGAGTGCATCTCTGCTTACGACGACGA						
1259	CTACCGCACTGGGAGAGCTCCACTATCTCCGCAAGAGTGCATCTCTGCTTACGATGAGA						
423	GCTGGCTTTTACCGGATCTCTCCGAGATCATCGGGAGCTGCTGCTACGAGAGTACAA						
1319	ACTGGCTTTCTTTGGCTCTATCCGGAATCATCGGCGACTGCTGTTATGAGAGTACAA						
443	GGACCGCAAGAGAGAAAGCGCCGAGCGGCTCATGAGACGACAAAGACTCGGAGAACACCA						
1379	GGATGCGAGGGGAGAGAAAGCGCGGCTTCAAGACGACCGGATACCGACACCGCTGG						
543	GGAG---TCCATGCGCTGCTCAGCTTCCGCGACAGCATGTGGGGGCTTCGAGAACCC						
1439	GGAGAGCGCTTGGCCCACTGACTGACGAGGAGGAGGCTTGGAGGGCTTCGAGAACCC						
600	CCACACCAAGCAGCTGAGCCCTGATCTTCTTACATGATGATGAGCTTCTTCACTGCTGCTC						
1499	CCACACCAAGCAGATGCGCCCTGGATTTCTACTATGTACAGGGGATTTTCAATGGCGCTTC						
660	GGTCATCAACCAAGTGTGAGACGATGCTCCGTCGCGACGGTCCCGGG---CAGCAGGA						

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Db      1559 TGTCAATCGGAATGTGTGGAAAAGTGTGCGGATGCAAGCCAGTCAACATTTAAAGA 1618
Qy      717 GCTGCCGTGGGGAGGCGCTACTCGGTGGCTTTCTTCTGCTGGAGACGGCGGTGCTCAT 776
Db      1619 ACTGCCCTGTGAGAGCGGTGATGTGTGTGCTCTTCTCTCTTGGACACGGCGCTGCTCAT 1678
Qy      777 GATCTTCAACCGTGGAGTACTCTCTGGGTGCTTTCGGGGCTCCAGCGCGTACCGGCTCAT 836
Db      1679 GATCTTCAACAGTTGAGTATTTGCTTGTGCTGGCTGAGCGCTTATGCTTACCGTGTGT 1738
Qy      837 CCGAGCGCTCATAGCATCATGACGTGTGGCCATCATGCTTACCTTACATCGGTGTGT 896
Db      1739 GGTGTGTGTATGATGATATCATGAGTGTGTGCGCATCTGCTTATTAATTTAGGTGTGT 1798
Qy      897 CATGACCAACAAAGAGAGAGTGTCCGGCGCTTTCGTACGCTCCGGGTCTTCCGGCTTT 956
Db      1799 GATGACAGACATAGAGAGAGTGTCCGGCGCTTTCGTACGCTCCGGGTCTTCCGGGTCTT 1858
Qy      957 CAGGATCTTCAAGTTTCCCGCACTCCGAGGGCGTGGGATCTGGGGCTAGACACTGA 1016
Db      1859 CAGGATCTTCAAGTTTCCCGCACTCCGAGGGCGTGGGATCTGGGGCTAGACACTGA 1918
Qy      1017 GAGCTGTGCTCCGAACTGGGCTTCTTCTCTCTCTCTCCCTCACCATGGCCATCATCTT 1076
Db      1919 GAGTGTGTGCTCAGAAATGGGCTTCTGTCTTCTTCTGCTCAGCATGGCTATCATCATCTT 1978
Qy      1077 TGCCACTGTGATGTTTATGCGAGAGAGGCTCTCGGCGAGCAAGTTCAACAGCATCC 1136
Db      1979 CGCTACAGTTATGTTCTACGAGAGAGAGGCTCTCGGCTAGCAAGTTCAACAGCATCC 2038
Qy      1137 TGCCCTGTGTTGTATACCATATGTACCACTGACCACTGACGATACGAGAGATGTTGTC 1196
Db      2039 TGCAAGCTTCTGTATACCATATGTACCACTGACCACTGACGATACGAGATGTTGTC 2098
Qy      1197 TAAAGCATTTGAGGAGAAAGATCTTGGGCTCTGCTCTGAGTGGGCTGCTGCTCAT 1256
Db      2099 AAAAACAATAGAGAGGAAAGATTTTGTGTCTATGCTGTGAGTGGGCTCTGCTCAT 2158
Qy      1257 TGCCCTGCCAGTCCCTGTGATGTTTCCAACTTTAAGCGGATTTACACACAGAAATCAG 1316
Db      2159 TGCTCTACCTGTTCCGGTATATTGTATCCAACTTCAAGTGCATCTACACAGAAATCAAG 2218
Qy      1317 AGCTATTAACCGCAGGAGCAAAAAGAGCCCGCTTGTGCAAGATCCGTGTGCGCCAAAAC 1376
Db      2219 AGCAACAACAAACGAGAGGCAAAAAGAAAGCTAGAGCTGCGGAGAGCCCAAG 2278
Qy      1377 AGGCAATTCGAATGATACCTGACAGAGAGGCAACGGGCTCTCAAGAGAGCGCTGGA 1436
Db      2279 CGGAAGCGCAATGCTTACATCAGAGCAACGGAATGTTTACTAGTATCAAGCTGCA 2338
Qy      1437 GCTGACGGGCAACCCAGAGAGAGCACTGGGCAAGCAACACTGCACTCATGAGAGCCA 1496
Db      2339 GTCTCAGAGGA--TGAGCAGGCTTTTGTAGCAAAATCCGGCTCAGCTTTGAAACCA 2395
Qy      1497 GCATATATACCTGTGCACTGCTGGAAGAAAAACACTAAACAGATTATGTAGAGGA 1556
Db      2396 GCACACCAACCTGCTTCACTGCTGGAAGAAAAACAGATCAAGATTGTGTGAGAGAA 2455
Qy      1557 GATGTTTGAAGCACTGATGATGAGAGTTCATATGAGAACTAACCTATCAAGAAAGTCC 1616
Db      2456 AGTCTTTGAAGAAAGTGTGATGAGAGTTCATCTGTATTCGTTCTTCAAGTCAAGTCC 2515
Qy      1617 CTGACTGTCCAGCCCAAGGCGCTCACTACACCTGTGCTCCGTGTGTAAGAGAGC 1676
Db      2516 TTCACTGTCTTCAACAAGAGAGTCAACGACGCTGTCTTCAACGACGACCAAAAAAC 2575
Qy      1677 CACACACCTGCGCAATTTCTAACCTGCGAGTACTGGCCGCGCAGATCCAGAGACTGAG 1736
Db      2576 TTTTGGCAATCCCAAAATGCAATGTATCAGAGAGCACTAAGGTATGATTAAGAAATCCG 2635
Qy      1737 CACGATTCACATTCAGGAGAGTGTGAGAGAGCTTCCCTCAACACAGTGTCTCAGGCTTAA 1796
Db      2636 CACGATTCAGATTCAGATGTGTGTGAGAGAGACCTCTGTCTAAGCCGATTCAGTTTAA 2695

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Qy      1797 TTTGAAGCAGACGACGACTGAGACCAAACTGCAAAAATCCGATCAACAGCCAT 1856
Db      2696 TCCCAAAATGGAAGGTGTGTTAACTAACTGTGAACAACCTTATGTGACTACAGCAAT 2755
Qy      1857 CATGACATTCCTCCCTCCCGCAGCGCTAAACCCAGAGGGGAGAAAGTCCGCCA 1908
Db      2756 AATAAGATTCCAACCTCCAGTACCAACACCAAGAGAGAGATAGGCCCA 2807

RESULT 13
ADJ11253
ID ADJ11253 standard; DNA; 5333 BP.
XX
XX ADJ11253;
XX
XX 15-APR-2004 (first entry)
XX
XX DE Human ovarian tumour antigen DNA SeqID 254.
XX
XX KW human; ds; ovarian cancer; immunogenic; antibody;
XX KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
XX KW cytostatic; gene.
XX
XX OS Homo sapiens.
XX
XX PN US2003232056-A1.
XX
XX PD 18-DEC-2003.
XX
XX PF 14-FEB-2003; 2003US-00369186.
XX
XX PR 10-SEP-1999; 99US-00394374.
XX PR 01-MAY-2000; 2000US-00561778.
XX PR 15-AUG-2000; 2000US-00640173.
XX PR 07-SEP-2000; 2000US-00565668.
XX PR 14-NOV-2000; 2000US-00713550.
XX PR 03-APR-2001; 2001US-00825294.
XX PR 02-OCT-2001; 2001US-00970966.
XX PR 02-AUG-2002; 2002US-00212677.
XX PR 05-FEB-2003; 2003US-00361811.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Fanger GR, Fling SP.
XX
XX DR WPI; 2004-178717/17.
XX
XX PT P-PSDB; ADJ11259.
XX
XX PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
XX PT polypeptide, useful as probes of primers for detecting presence of cancer
XX PT in a patient.
XX
XX PS Example 12: SEQ ID NO 254; 2222p; English.
XX
XX CC This invention relates to novel isolated polynucleotides and methods for
XX CC the therapy and diagnosis of cancer, particularly ovarian cancer.
XX CC Specifically, it refers to these polynucleotides and the encoded
XX CC polypeptides thereof, as well as immunogenic peptides, antibodies,
XX CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
XX CC that are targeted to those cells expressing the proteins of interest. The
XX CC present invention describes methods that are useful for stimulating and/or
XX CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
XX CC therapy). Furthermore, compositions can be used for the diagnosis,
XX CC treatment and/or prevention of ovarian cancer by stimulating an immune
XX CC response in a patient. Accordingly, these compositions exhibit cytostatic
XX CC activity. This polynucleotide is a human ovarian tumour antigen DNA
XX CC sequence given in an exemplification of the invention.
XX
XX SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
XX
XX Query Match 48.5%; Score 1000.8; DB 12; Length 5333;
XX Best Local Similarity 72.8%; Pred. No. 1.5e-188;

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Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

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QY 66 AGTACCATGCGCGCGAGTTGGCGCTGCTGCTTTTGGCCGCGCTGCGCATCGG 125
Db 959 AGTAATCATGCGCGCGAGTTGGCGCTGCTGCTTTTGGCAAGGCGCATCGG 1018
QY 126 GTGATGCGCGTGGCCAACTGCCCCCATGCCCC--GGCGACAAGAACGCG 182
Db 1019 GTGATGCGCTGTGGCTCGGCGCTGATGCGGCTCCCCGAGGAGGAGAAAGGAC 1078
QY 183 GCAGATGATGCTGATTTGCTTCAACGTGAGGGCGGAGGTTCCAGACTGAGGACAC 242
Db 1079 CCAAGATGCTCTCATTTGTGCTGAATGAGTGGACCCCGCTTCCAGACGTGGACGAC 1138
QY 243 GCTGAGCGCTACCGGACACCTGCTGGGACGACGAGAGAGAGTTCTTCTTCAACGA 302
Db 1139 CTGGAACGTTACCCAGACACTACTAGGGAGTTTGAGAGGAGCTTTTCTTACACCC 1198
QY 303 GGACACCAAGAGATCTTTTCCACCGGAGCCCGAGGTGTTCCGCTGCTCAACTT 362
Db 1199 AGAACTCAGACAGTATTTCTTTGACCGTGAACCGACATCTTCCGCACTCTGAATTT 1258
QY 363 CTACCGGACGCGGAGGTGACACTACCGCGCTAGAGTGCATCTTGGCTTACGACGCA 422
Db 1259 CTACCGGACCTGGAGAGCTTCCACTTCTTCCGACAGAGTGCATCTTGTCTTACGAGAA 1318
QY 423 GCTGACCTTCTACCGCATCTTCCCGAGATCATCGGAGACTGCTGCTACGAGAGTACA 482
Db 1319 ACTGGCTTCTTTGGCTCATCCCGGAATCATGGGAGCTGCTGTTATGAGGAGTACAA 1378
QY 483 GGACCGCAAGAGAGAAACCGCGAGCGCTCATGAGACAGACACTCGGAGAACACCA 542
Db 1379 GGAATCGAGAGAGAAACCGCGAGCGCTGACAGAGACGAGCGATCCGACACCGCTGG 1438
QY 543 GGAG---TCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
Db 1439 GGAGAGCGCTTGGCCCACTGATCTGCAAGGAGAGAGGCTTGGAGGCGCTTCCAGAACCC 1498
QY 600 CCAACACGAGACGCTGCGCTGCTGCTTCTTACTAGTGAATGCTGCTTCTTCACTGCTGCTC 659
Db 1499 CCACACGAGACGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 1558
QY 660 GGTGATCAACCACTGCTGAGACGCTGCGCTGCGGACGCTGCTGCTGCTGCTGCTGCTG 716
Db 1559 TGTGATGCGAGATGCTGAGAAACGCTGCGGATCAAGCCCAAGTACATTAAGA 1618
QY 717 GCTGCGGAGGAGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
Db 1619 ACTGCGCTTGGAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1678
QY 777 GATCTTCAACGATGAGTACTCTGCGGCTTTCGCGGCTCCAGCGCTTACGCTTCAT 836
Db 1679 GATCTTCAACGATGAGTACTCTGCGGCTTTCGCGGCTTTCGCGGCTTTCGCTTTCAT 1738
QY 837 CCGGAGCGTATGAGCATCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
Db 1739 GCGTATGCTATGATGATCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1798
QY 897 CATGACCAACAGAGAGAGCTGCTGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCG 956
Db 1799 GATGACCAACAGAGAGAGCTGCGGAGCTTTCGCACTCCGAGATCTTCGCGGCTTTCG 1858
QY 957 CAGGATCTTCAAGTTTTCGCGCACTCCAGAGGCTGCGGATCTTGGGCTTACACATGAA 1016
Db 1859 CAGGATCTTCAAGTTTTCGCGCACTCCAGAGGCTGCGGATCTTGGGCTTACACATGAA 1918
QY 1017 GAGCTGCTGCTGCGAATCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1076
Db 1919 GAGTGTGCTGCTGCGAATCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1978
QY 1077 TGGCAGCTGATGTTTATGCGGAGAGGCTCTCCGCGCAGACAGTCCACAGCATCCC 1136
Db 1979 CGCTACAGTATGTTTCTTACGAGAGAGGCTTTCGCGCTAGCAAGTTTCAACAGCATCCC 2038

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QY 1137 TGCCTGTTTGTGATCACCATTTGTCAACATGACCACTGAGGATACGAGACATGTGTCC 1196
Db 2039 TGCAGCTTCTGTGATATACCATGCTCACCATGACCACTAGGGTATGTGACATGTGTCC 2098
QY 1197 TAAGATGATTTGACGAGGAATCTTGGCTTCATCTGCTCTTGAAGTGGTCTGTGCTAT 1256
Db 2099 AAAAACCATGACGAGGAATTTTGTGTTCTATGCTGTGCTGAGTGGGCTCTTGTGCTAT 2158
QY 1257 TGCCTGCGAGTCCCTGTGATTTTCCAACTTTAGCCGGAATTTTACACAGATCAGAG 1316
Db 2159 TGTCTTACTGTTCCGCTGATTTGTATCCACTTTCAGTCCGATCTTACCAACAGATTAAG 2218
QY 1317 AGCTGATTAACGAGGAGCAAAAAGAGGCCCGCTTGCAGAGATCGTGTGCCAAAAC 1376
Db 2219 AGCAGACAAACGAAAGGAGCAAAAAGAACTAGACTGCGCAGAGATCCGGGACAGCCAAAG 2278
QY 1377 AGGCACTTGGATGCTATCTGACAGCAAGGCGCAACGAGCTCTTCAAGAGGCGCTGCA 1436
Db 2279 CGGAACGCAAAATGCTTACATGACAGCAACGGAATGGTTTACTGATATCAGCTGCA 2338
QY 1437 GCTGACGCGGACCCCGAAGAGAGACATGGGCAAGACCACTCACTCATCGAGAGCA 1496
Db 2339 GTCTCTAGAGAG---TGACAGGCTTTTGTAGCAAAATCCGCTCCAGCTTTGAAACCA 2395
QY 1497 GCATCATCACTGCTGCACTGCTGCTGCAAAAACCACTTAACTAGATTTATGATGAGA 1556
Db 2396 GCACACACACCTGCTTCACTGCTGCTGCAAAAACCAAGATTCAGAGTTTGTGAGACGACA 2455
QY 1557 GATGTTTGAAGACAACTGATGAGAGTTCAATGACGAACCTACCATCCACAAAGAGTCC 1616
Db 2456 AGCTTTTGAAGAAAGTGTGATGAGAGTTGCACTGTATATGCTTCAAGTACAGTCC 2515
QY 1617 CTCTAGTGCAGGACCCAGGCTCTCACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676
Db 2516 TTACTGTCTTTCACAAAGAGTCAACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2575
QY 1677 CACACACTGCGCAATTTCTTAACTGCGACCTACTGCTGCTGCGAGATGCAAGAGTCCAG 1736
Db 2576 TTTTGCATCCCAATATGCAATGATATCAGAGACCTCAAGGATGATATCAAGAACTCAG 2635
QY 1737 CAGATTCACATCAGAGGAGTGAAGACGCCCTTCCACAAACAGTGCCTCCAGCTTAA 1796
Db 2636 CAGGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2695
QY 1797 TTTGAAGAGAGACGAGAGCTGAGACCAAACTGCAAACTCCAGATCAACAGAGTCCAG 1856
Db 2696 TGCAGAAATGGAAGAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2755
QY 1857 CATCAGCATCCCACTCCCGCAGCGCTTAAACCCGAGAGGAGGAAAGTCCGCGCA 1908
Db 2756 AATATGATCCCAACACTCCAGTAAACCAACAGAGAGAGAGATGAGGCA 2807

RESULT 14
ADJ11251
ID ADJ11251 standard; DNA; 5333 BP.
XX
XX ADJ11251;
AC
XX 15-APR-2004 (first entry)
DE
XX Human ovarian tumour antigen DNA SeqID 252.
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; Apc; immune system cell; T cell; tumourigenic;
XX cytosolic; gene.
XX
XX Homo sapiens.
PN US2003232056-A1.
XX
XX 18-DEC-2003.
PD

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XX 14-FEB-2003; 2003US-00369186.  
XX 10-SEP-1999; 99US-00394374.  
XX 01-MAY-2000; 2000US-00561778.  
XX 15-AUG-2000; 2000US-00640173.  
XX 07-SEP-2000; 2000US-00656668.  
XX 14-NOV-2000; 2000US-00713550.  
XX 03-APR-2001; 2001US-00825294.  
XX 02-OCT-2001; 2001US-00970966.  
XX 02-AUG-2002; 2002US-00212677.  
XX 05-FEB-2003; 2003US-00361811.  
XX (CORI-) CORIXA CORP.  
XX Fanger GR, Fling SP,  
XX WPI; 2004-178717/17.  
XX P-PSDB; ADJ11257.  
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor  
XX polypeptide, useful as probes of primers for detecting presence of cancer  
XX in a patient.  
XX Example 12; SEQ ID NO 252; 222bp; English.  
XX This invention relates to novel isolated polynucleotides and methods for  
XX the therapy and diagnosis of cancer, particularly ovarian cancer.  
XX Specifically, it refers to these polynucleotides and the encoded  
XX polypeptides thereof, as well as immunogenic peptides, antibodies,  
XX antigen presenting cells (APCs) and immune system cells (e.g. T cells)  
XX that are targeted to those cells expressing the proteins of interest. The  
XX present invention describes methods that are useful for stimulating and/  
XX or expanding T cells specific for a tumorigenic protein (i.e. T cell  
XX therapy). Furthermore, compositions can be used for the diagnosis,  
XX treatment and/or prevention of ovarian cancer by stimulating an immune  
XX response in a patient. Accordingly, these compositions exhibit cytostatic  
XX activity. This polynucleotide is a human ovarian tumour antigen DNA  
XX sequence given in an exemplification of the invention.  
XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
Query March 48.5%; Score 1000.8; DB 12; Length 5333;  
Best Local Similarity 72.8%; Pred. No. 1.5e-186;  
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  
QY 66 AGTCACTGAGCGGCGAGTTGCGGCTGCTTTTGGCCGGGCTGCGGCATCGG 125  
DB 959 AGTATCTATGCGCGCGGGGTGGCAGCTGCTGCTTTTGGCAAGGGCAGCGGCTATCGG 1018  
QY 126 GTGATGCGGTGGCCAACTGCGCCATGCCCTGCGCC--GCGCGACAAAGAACAGCG 182  
DB 1019 GTGATGCTGTGGGCTCGGGGCTATATGCGGCTCCCCGAGGCGAGAGAAAGAGAC 1078  
QY 183 GCAGATAGCTGATGTTGCTTCAAGTGAAGTGGGCGAGGTTCCGAGCTGGAGACAC 242  
DB 1079 CCAAGATCTCTCATTTGCTGAATGTAGTGGCACCGGCTTCCAGAGTGGCAGAGAC 1138  
QY 243 GCTGAGGCTACCGGACACCGCTGCGGAGCAGCGAGAAAGAGTTCTTCTTCAACA 302  
DB 1139 CTTGGAAGCTTACCAGACCTTACTGAGGAGTTCTGAGAGGACCTTTTCTACACCC 1198  
QY 303 GAGACCAAGAGATCTTCTTGAACCGGAGCCCGAGGTGTTCCGCTGCTCAACTT 362  
DB 1199 AGAAACTAGAGAGTCTTCTTGAACCGGAGCCCAACATCTTCCGCAATCTGAATTT 1258  
QY 363 CTACCGCAGCGGAGAGCTACCGGCTACCGGCTACGAGTGAAGTCTGCTTACGAGAGA 422  
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QY 423 GCTGCGCTTCTTACGAGCATCTCCCGAGAGATCATCGGAGACTGCTGCTACGAGAGTACA 482  
DB 1319 ACTGCGCTTCTTGTGCGCTCATCTCCGGAATATATGGGCGACTGCTTATGAGAGATACA 1378

QY 483 GACCCGAGAGAGAGAGAGAGCGGCGCTCATGAGACAAAGCATCTGGAGAACACCA 542  
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DB 1499 CCACACGACAGAGATGCGCTGCTGCTTCTTACTAGTGAAGTGGCTTCTTCACTGCTGCTC 1558  
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DB 1619 ACTGCGCTGTGAGAGCGGTATGCTGTGCTTCTTCTGCTTGGACACAGGCTGCTCAT 1678  
QY 777 GATCTCAACGAGAGTACCTCTGCGGCTTCTGCGGCTCCAGCGGCTTACCGCTTAT 836  
DB 1679 GATCTTCAAGTGTGATTTGCTTCCGCTGAGCGGCTAGTGGTACCGCTTTGT 1738  
QY 837 CCGACGCTATGAGCATCATGACGTGTGGCCATATGCGCTTACTATCATCGTGTGT 896  
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QY 897 CATGACCAACAGAGAGAGAGTGTCCGGGCTTGTGTCACGCTCGGCTTCCGCTT 956  
DB 1799 GATGACAGCAATAGAGAGAGTGTGAGAGGCTTGTGTCACGCTTCCGCTT 1858  
QY 957 CAGATCTTCAAGTTTCCGCACTCCAGAGGCTGGAGTCTGGGCTTACACACTGAA 1016  
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QY 1017 GAGCTGTGCTTCCGCACTCCGCTTCTTCTTCTTCCCTGACCATGAGCATATCTT 1076  
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QY 1197 TAAAGCATTCAGAGAGAGATCTTGGCTCATCTGCTCTTGAAGTGGCGTCTGTAT 1256  
DB 2099 AAAAACAATACAGAGAGAGATTTTGTGTTCTTATCTGCTGAGTGGGCTTGTGAT 2158  
QY 1257 TGCCCTGCAAGTCCCTGATGTTTTCATTTTCAATTTAGCCGATTTTACCAACCAAGAT 1316  
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QY 1317 AGCTGATTAACGAGAGGACAAAGAGGCGGCTTGGCCAGATTCGTTGTGCAAAAC 1376  
DB 2219 AGCAGACAAAGAGAGGAGCAAAAGAAAGCTAAGATGCGCAGATTCGCGGACCAAAAG 2278  
QY 1377 AGGAGTTTGAATGATCTCTGCAAGAGAGCGCAAGGCTCTTCAAGAGGCGCTGGA 1436  
DB 2279 CGAAGGCGCAATCTTATCATGAGAGAGAAACGAAATGTTTACTAGTATTCAGCTGCA 2338  
QY 1437 GCTGACGGGACCCCGAAGAGAGACATGGGCAAGCACTTCACTCATCGAGGCA 1496  
DB 2339 GTCTCAAGAGA--TGAAGGCTTTTGTATGCAATTCGGCTTCAGCTTTGAACCA 2395  
QY 1497 GCATCATCACTGTGTCATGCTCTGAGAAACCACTTACACAGAGTTTATGTATGACA 1556  
DB 2396 GCACACACCACTGTCTTCACTGCTGAGAAACCAACGAAATCAGAGTTTGTGAGCAACA 2455



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Db 1979 CGCTACAGTATGTTCTACGAGAGAGAGGGGCTTCGGGCTAGCAAGTTCAACGACATCCC 2038
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Db 2039 TGCAGCCCTTCTGTATACCATGTCACATGACACACTAGGGTATGGTACATGTGCC 2098
Qy 1197 TAAGCATGTGAGGGAAGATCTTGGGCTCCATGCTCCTTGAGTGGGCTGTGCAT 1256
Db 2099 AAAAACTAGAGGGAAGATTTTGGTTCTATCTGTTCTGAGTGGGGCTTGTGCTAT 2158
Qy 1257 TGCCCTGCGAGTCCCTGTGATTTGTTCCAACTTTAGCCGATTTACCAACCAATCAGAG 1316
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Qy 1317 AGCTGATTAACGAGGGGCAAAAGAGGCCCGCTTCCAGGATCCGTGTGCCAAAC 1376
Db 2219 AGCAGACAAAGAGGGGCAAAAGAAAGCTAGACTGGCCAGGATCCGGGCGACCAAG 2278
Qy 1377 AGGAGTTGGAATGATACCTGACAGAGAGGGCAAGGGCTCCCTCAACGAGGGCTGGA 1436
Db 2279 CGAAGCGCAATAGCTTACATGACAGAGCAAAAGGATGGTTTACTAGTATCAGCTCA 2338
Qy 1437 GCTGACGGGCAACCCAGAGAGAGACATGGGCAAGACCACTCACTCATGAGAGCCA 1496
Db 2339 GTCCCTCAGAGGA---TGAGCAGGCTTTTGTATAGCAATCCGGCTCCAGCTTGAACCA 2395
Qy 1497 GCATCATCACTGTGCTGCACTGCTGGAACCACTAACCAAGATTTATTTGATGACA 1556
Db 2396 GCACACACCACTGCTTCACTGCTGGAACCACTAACCAAGATTTGATGAGACA 2455
Qy 1557 GATGTTTGAAGAGAACTGCAATGAGAGATTCAATGCAAACTAACCAAGATTC 1616
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Qy 1617 CTCACCTGTCAGGCCCAACGAGGCTCACTACCACTGCTGCTCCGTCGATGAAGAGAC 1676
Db 2516 TTCACTGTCTTCAACAAGAGATCAACGACACTGCTGTTCAGACACACAAAAAAC 2575
Qy 1677 CACACACCTGCGCAATTTTAACCTGACGCTAAGCTGCGCAGCATGCAAGACTCAG 1736
Db 2576 TTTTCGATCCCAATGCAATGATATGATGAGAAAGCCATCAGGTATATACAAAGACTCAG 2635
Qy 1737 CACGATCCACATCCAGGCACTGAGACAGCCCTCCCTCAACCAAGTCCGCTCAGCCTTA 1796
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Qy 1797 TTTGAAGCAGACGAGCGACTGAGACCAAACTGCAAAACATCCGATCACACAGCCAT 1856
Db 2696 TGCCAAAATGGAAGAGTGTGTTAACTTAACGTGACACACCTTATGTACTACAGCAAT 2755
Qy 1857 CATCAGCATCCCACTCCCGCAGCGCTAACCCAGAGGGGGAAGTCGAGCA 1908
Db 2756 AATAAGCATCCCACTCCAGTAAACCAACCAAGAGAGAGATAGGCCA 2807
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 13:43:09 ; Search time 345.233 Seconds  
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9782.597 Million cell updates/sec

Title: US-10-062-879-3

Perfect score: 2064

Sequence: 1 gatttgctgaactaactcca.....gtcgatataaagccgaattc 2064

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1997	96.8	2121	US-09-178-109-1	Sequence 1, Appli
3	1905	92.3	2104	US-09-142-791A-1	Sequence 1, Appli
4	1897	91.9	2104	US-09-142-791A-5	Sequence 5, Appli
5	1838	89.1	2072	US-09-142-791A-3	Sequence 3, Appli
6	1000.8	48.5	5333	US-09-949-016-957	Sequence 957, App
7	843.2	40.9	3424	US-09-336-643A-9	Sequence 9, Appli
8	326.4	15.8	3260	US-09-949-016-2456	Sequence 2456, Ap
9	240	11.6	3004	US-09-949-016-2293	Sequence 2293, Ap
10	240	11.6	7055	US-09-949-016-12066	Sequence 12066, A
11	240	11.6	7056	US-09-949-016-14035	Sequence 14035, A
12	236.8	11.5	3004	US-09-949-016-324	Sequence 324, App
13	216	10.5	1802	US-09-949-016-1604	Sequence 1604, App
14	216	10.5	2483	US-08-464-340A-3	Sequence 3, Appli
15	216	10.5	2483	PCT-US94-08449A-3	Sequence 3, Appli
16	216	10.5	5802	US-09-949-016-13346	Sequence 13346, A
17	213	10.3	1341	US-10-162-012-7	Sequence 7, Appli
18	206	10.0	1994	US-08-527-152-1	Sequence 1, Appli
19	202.2	9.8	2118	US-09-016-434-1304	Sequence 1304, Ap
20	196	9.5	1599	US-08-288-405A-9	Sequence 9, Appli
21	185.4	9.0	1542	US-09-949-016-4417	Sequence 4417, Ap
22	183.8	8.9	2127	US-08-464-340A-1	Sequence 1, Appli
23	183.8	8.9	2127	PCT-US94-08449A-1	Sequence 1, Appli
24	162.6	7.9	2022	US-09-719-919A-18	Sequence 18, Appli
25	159.8	7.7	4234	US-09-949-016-335	Sequence 335, App
26	159.8	7.7	4237	US-09-949-016-2146	Sequence 2146, Ap
27	159.8	7.7	8237	US-09-949-016-12067	Sequence 12067, A

28	159.8	7.7	8237	US-09-949-016-13888	Sequence 13888, A
29	159	7.7	2084	US-09-949-016-1989	Sequence 3989, Ap
30	159	7.7	2266	US-09-181-339-11	Sequence 11, Appli
31	159	7.7	2293	US-09-336-643A-5	Sequence 5, Appli
32	159	7.7	19161	US-09-949-016-15731	Sequence 15731, A
33	154.2	7.5	3102	US-09-336-643A-17	Sequence 17, Appli
34	150.4	7.3	2494	US-09-181-339-6	Sequence 6, Appli
35	146.8	7.1	1805	US-07-955-916-6	Sequence 1, Appli
36	146	7.1	1638	US-09-833-466-2	Sequence 2, Appli
37	146	7.1	2103	US-09-833-466-1	Sequence 1, Appli
38	145.6	7.1	248	US-09-016-434-790	Sequence 790, App
39	145.4	7.0	197	US-09-016-434-1040	Sequence 1040, Ap
40	143.4	6.9	10304	US-09-949-016-16159	Sequence 16159, A
41	141.8	6.9	1518	US-09-719-919A-2	Sequence 2, Appli
42	141.2	6.8	17879	US-09-949-016-12992	Sequence 12992, A
43	140	6.8	3186	US-09-949-016-1250	Sequence 1250, Ap
44	139.6	6.8	601	US-09-949-016-55210	Sequence 55210, A
45	136.6	6.6	3080	US-09-336-643A-7	Sequence 7, Appli

#### ALIGNMENTS

RESULT 1  
US-09-178-109-3  
Sequence 3, Application US/09178109  
Patent No. 6395477  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang Ling, Hui-ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
FILE REFERENCE: amp-98089  
CURRENT APPLICATION NUMBER: US/09/178.109  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 2064  
TYPE: DNA  
ORGANISM: human  
US-09-178-109-3

Query Match 100.0%; Score 2064; DB 3; Length 2064;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GATTTCGTAACCTAATCCAAAGCTGTGTGCTTACGCTCCGCGGCTGCGCCCAAGA	60
DB	1	GATTTCGTAACCTAATCCAAAGCTGTGTGCTTACGCTCCGCGGCTGCGCCCAAGA	60
QY	61	GCTGAGTCAACCAAGGCGCGGAGTTCGCGCTGCTTTCGCGCGGCTGCGGCC	120
DB	61	GCTGAGTCAACCAAGGCGCGGAGTTCGCGCTGCTTTCGCGCGGCTGCGGCC	120
QY	121	ATTCGGTGAATGCGCGTGTGCAATGCGCCATGCGCCCTGCGCCCGCGCAAG	180
DB	121	ATTCGGTGAATGCGCGTGTGCAATGCGCCATGCGCCCTGCGCCCGCGCAAG	180
QY	181	CGGAGATGAGTGTGCTTCAACGTCGAGTGGCGAGATTCAGACTGAGAGACC	240
DB	181	CGGAGATGAGTGTGCTTCAACGTCGAGTGGCGAGATTCAGACTGAGAGACC	240
QY	241	ACGCTGAGGCGCTACCGCGACCCCTGCTGGCGAGCAACGAGAGAGTTCTTCAAC	300
DB	241	ACGCTGAGGCGCTACCGCGACCCCTGCTGGCGAGCAACGAGAGAGTTCTTCAAC	300
QY	301	GAGGACACCAAGAGTACTTCTTGAACCGGACCCCGAGGTGTTCCGCTGCTCAAC	360
DB	301	GAGGACACCAAGAGTACTTCTTGAACCGGACCCCGAGGTGTTCCGCTGCTCAAC	360

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QY 361 TTCTACCGACGGGGAAGCTGCACTACCGCGCTACGAGTGCATCTCTGCTTACGAGAC 420
Db 361 TTCTACCGACGGGGAAGCTGCACTACCGCGCTACGAGTGCATCTCTGCTTACGAGAC 420
QY 421 GACCTGGCTTTCTACGGCATCTCTCCGAGATCATCGGGAGCTGTCTCTACGAGAGTAC 480
Db 421 GACCTGGCTTTCTACGGCATCTCTCCGAGATCATCGGGAGCTGTCTCTACGAGAGTAC 480
QY 481 AAGGACCGCAAGAGGAGAAAGCGCGAGCTCATGAGACGACACTCGAGAAACAAAC 540
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QY 601 CACACCCAGCACGCTGGCTGTGTCTTACTAGTGCATGCTGCTTCTTATGCTGTCTG 660
Db 601 CACACCCAGCACGCTGGCTGTGTCTTACTAGTGCATGCTGCTTCTTATGCTGTCTG 660
QY 661 GTCATCCACAACTGGTGGAGACGCTGCGCGAGCAAGTCCCGGAGCAAGAGACTG 720
Db 661 GTCATCCACAACTGGTGGAGACGCTGCGCGAGCAAGTCCCGGAGCAAGAGACTG 720
QY 721 CCGTGGCGGAGGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGCTGCTATGATC 780
Db 721 CCGTGGCGGAGGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGCTGCTATGATC 780
QY 781 TTACCGTGGAGTACCTCTGCGCTTGTGCGCGCTCCGAGCGCTACCGCTTATCCGC 840
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QY 841 AGCGTCATGAGCATCATCGAGCTGTGAGCATCATGCTTACTACTAGCTGTGATG 900
Db 841 AGCGTCATGAGCATCATCGAGCTGTGAGCATCATGCTTACTACTAGCTGTGATG 900
QY 901 ACCAACAAGAGAGCTGTGCGCGCTTGTGCAAGCTTGTGCGGTCTTCCGCTTCAAG 960
Db 901 ACCAACAAGAGAGCTGTGCGCGCTTGTGCAAGCTTGTGCGGTCTTCCGCTTCAAG 960
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QY 1021 TGTGCTCCGAACTGGCTTCTTCTCTCTCCCTCACTGAGCATCATCTTGGC 1080
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QY 1081 ACTGTGATGTTTTATGCGAGAAAGGCTCTCGGCGAGCAAGTTCAAGAGCATCTCTGCC 1140
Db 1081 ACTGTGATGTTTTATGCGAGAAAGGCTCTCGGCGAGCAAGTTCAAGAGCATCTCTGCC 1140
QY 1141 TCGTTTTGTGATACATTTGTCACCATGACCACTGGGATACGGAACATGTGCTTAAAG 1200
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QY 1201 ACGATTGCAAGGAAATCTTCCGCTCATGCTCTTGAATGCGCTGCTGATTTGGC 1260
Db 1201 ACGATTGCAAGGAAATCTTCCGCTCATGCTCTTGAATGCGCTGCTGATTTGGC 1260
QY 1261 CTGCGAGTCCCTGTGATGTTTTCACATTTAGCCGAGATTTACACAGAAATCAGAGACT 1320
Db 1261 CTGCGAGTCCCTGTGATGTTTTCACATTTAGCCGAGATTTACACAGAAATCAGAGACT 1320
QY 1321 GATTAAGCGAGGAGCAAAAAGAGCCGCTTGGCAGATTCCTGTGGCCAAAACAGGC 1380
Db 1321 GATTAAGCGAGGAGCAAAAAGAGCCGCTTGGCAGATTCCTGTGGCCAAAACAGGC 1380
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QY 1441 ACGGGAACCCCAAGAGAGCAATGAGCAAGCACTCATCATGAGAGCAGCAT 1500

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Db 1441 ACGGGAACCCCAAGAGAGCAATGAGCAAGCAAGCACTCATCAAGAGCCGAGAT 1500
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Db 1501 CATCACTGTGCTCACTGCTGAGAAAAAACCACTAACCAAGATTTATTGATGAGCAGATG 1560
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Db 1621 CTGTCCAGCAACCCAGGCTCACTACCACTGTGCTCTCGTGTGATGAAAGACACA 1680
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Db 1681 CACCTGGCCCAATTCTAACCTGCGAGTACTCGCTGCGAGAGATGCAAGAGCTCAGCAG 1740
QY 1741 ATCCATATCCAGGAGAGTGAAGAGCCCTCTCAACCAAGTCTGCTCAGCCTTAATTTG 1800
Db 1741 ATCCATATCCAGGAGAGTGAAGAGCCCTCTCTCAACCAAGTCTGCTCAGCCTTAATTTG 1800
QY 1801 AAGCAGAGAGAGAGTGAAGAGCCCAATGCAAAATCTCCAGATCACACAGCATCATC 1860
Db 1801 AAGCAGAGAGAGAGTGAAGAGCCCAATGCAAAATCTCCAGATCACACAGCATCATC 1860
QY 1861 AGCATCCCACTCCCGAGGCTAACCCCAAGAGGAGAAAGTGGACCCCTGCGAGC 1920
Db 1861 AGCATCCCACTCCCGAGGCTAACCCCAAGAGGAGAAAGTGGACCCCTGCGAGC 1920
QY 1921 CCAGGCCCAACAGAACTTCTTCATTAACAGCAATGTGTCAAGGTCTTGTCTTG 1980
Db 1921 CCAGGCCCAACAGAACTTCTTCATTAACAGCAATGTGTCAAGGTCTTGTCTTG 1980
QY 1981 TAAAAATCCCGGCGCATGAGCGGCGGAGCATGCGAGTCTGCGGCCCAATTCGCTTATA 2040
Db 1981 TAAAAATCCCGGCGCATGAGCGGCGGAGCATGCGAGTCTGCGGCCCAATTCGCTTATA 2040
QY 2041 GTGAGTGTGATTTAAAGCCGAATTC 2064
Db 2041 GTGAGTGTGATTTAAAGCCGAATTC 2064

RESULT 2
US-09-178-109-1
; Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cocker, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hwai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
; US-09-178-109-1

Query Match 96.8%; Score 1997; DB 3; Length 2121;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 57; Gaps 1;
QY 1 GATTTGCTGAACCTAATCCAGTGTGTGCTTGTGCTGCGCGCTGCGGCGCCCAAGA 60
Db 1 GATTTGCTGAACCTAATCCAGTGTGTGCTTGTGCTGCGCGCGCTGCGGCGCCCAAGA 60

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OY	61	GTGTGAAGTACCAATGAGCGGCGGAAAGTGGAGGAGCTTGGTCCGCGGCTCGGCG	120
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OY	121	ATTCGGGTGGATGTCGGGTGGCCAACTGCGCCCATGCGCTTGGCCCGGCGCAAGAA	180
Db	121	ATTCGGGTGGATGTCGGGTGGCCAACTGCGCCCATGCGCTTGGCCCGGCGCAAGAA	180
OY	181	CGGCAAGATGAGCTGATATTTGTTCTTCAAAGTGAATGGGCGGAGGTTCCAGACTG	240
Db	181	CGGCAAGATGAGCTGATATTTGTTCTTCAAAGTGAATGGGCGGAGGTTCCAGACTG	240
OY	241	ACGCTGAGAGCGCTACCCGGACACACTGTGCTGGGACAGACGAGAAAGAGTTCTT	300
Db	241	ACGCTGAGAGCGCTACCCGGACACACTGTGCTGGGACAGACGAGAAAGAGTTCTT	300
OY	301	GAGGACACCAAGAGAGTACTTCTTTCGACCGGGAACCCCGAGGTGTCGCTGCTCAAC	360
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OY	361	TTCTACCGGACGGGGAGCTGACCTAACCCGCGCTACGATGATCTGCGCTTACAGACAC	420
Db	361	TTCTACCGGACGGGGAGCTGACCTAACCCGCGCTACGATGATCTGCGCTTACAGACAC	420
OY	421	GAGCTGAGCTTCTTACGGGATCCTCCCGGAGATCATTCGGGGACTGCTGCTACGAGAGTAC	480
Db	421	GAGCTGAGCTTCTTACGGGATCCTCCCGGAGATCATTCGGGGACTGCTGCTACGAGAGTAC	480
OY	481	AAAGACCGGCAAGAGGAGAGACGCGGAGCGGCTCATATGACACACACGACTCGGAGAACAC	540
Db	481	AAAGACCGGCAAGAGGAGAGACGCGGAGCGGCTCATATGACACACGACTCGGAGAACAC	540
OY	541	CAGAGAGTCATAGCCCTCGCTAGCTTCCGCGCAGACCATGTGGCGGAGCTTTCGAGAACCC	600
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OY	601	CACACGAGACGCTGAGCCCTGTGCTTCTTACTACGATGAGCTGAGCTTCTTCACTGCTCG	660
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OY	661	GTCTATCACCAACGTGTGTGAGACGAGTGGCCGTGCGGACGAGTCCGGGACGAGAGAGCTG	720
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OY	721	CGGTGCGGGAGCGCTACTCGGTGAGCTTCTTCTGCTGTGACACGAGCGGTGCTCATATGATC	780
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OY	841	AGCGTCATGAGATATGACGCTGTGGTGGCCATCAAGCCCTTACATGATGCTTGGTCAATG	900
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OY	901	ACCAACACGAGAGAGTGTGCGGCGCTTTCGTCACGCTTCGGGTCTTTCGCGCTCTTCAAG	960
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Db	961	ATCTTCAAGTTTTCCCGCATCTCCCAAGGAGCTGTGGGATCTGTGGGCTTCAACACTGAAGAGC	1020
OY	1021	TGTGCTCCGAACGTGGGCTTCTTCTTCTTCTTCCCTCAACATGGGCATCATCTTTGGC	1080
Db	1021	TGTGCTCCGAACGTGGGCTTCTTCTTCTTCTTCCCTCAACATGGGCATCATCTTTGGC	1080
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Db	1081	ACTGTGATGTTTTATGCGGAGAGGAGCTCTTGGCGACAGTTTCAACAGCATCCTCGCC	1140

QY	1141	TCGTTTGGTACACCATTTGTACATATGACACACATGGGATATGGAGATATGGTCCTAAG	1200
Db	1141	TCGTTTGGTACACCATTTGTACATATGACACACATGGGATATGGAGATATGGTCCTAAG	1200
QY	1201	ACGATTTGACAGGAAAGATCTTCGGCTCCATCTGCTCTTGAATGGCGTCTTGATTCGCC	1260
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QY	1261	CTGCCAGTCCCTGTGATTTGTTTCCAACTTTTAGCCGGATTATCCACAGAAATCAAGAGCT	1320
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QY	1321	GATTAACGACAGGGACAAAAGAGAGCCCGCTTGCCAGATCCGCTGTGGCCAAAACAGCG	1380
Db	1321	GATTAACGACAGGGACAAAAGAGAGCCCGCTTGCCAGATCCGCTGTGGCCAAAACAGCG	1380
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QY	1441	ACGGGACACCCAGAAAGAGAGACATATGGGCAAGACCTTCATCTCATATCGAGAGCCAGAT	1500
Db	1441	ACGGGACACCCAGAAAGAGAGACATATGGGCAAGACCTTCATCTCATATCGAGAGCCAGAT	1500
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Db	1501	CATCACCTGCTGCACCTGCTGGAAAAAACCTGGGTTCCTATCTTTGTGGATGATGCC	1560
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Db	1621	GAGCGAAATCTGCATGAGAGAGAGTTCAATGCAAACTAACCCATTCACAAAGAAAGTCCCTCACTG	1680
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QY	1684	CTGCCCAATTTCTAACCTGCGACGTACTCGCTGCGCAGATGCAAGAGCTCAGCAGATC	1743
Db	1741	CTGCCCAATTTCTAACCTGCGACGTACTCGCTGCGCAGATGCAAGAGCTCAGCAGATC	1800
QY	1744	CACATTCAGGCGCATGAGCAGCCCTCCCTCACAACAAGTGGCTTCACACTTAATTTGAAA	1803
Db	1801	CACATTCAGGCGCATGAGCAGCCCTCCCTCACAACAAGTGGCTTCACACTTAATTTGAAA	1860
QY	1804	GCAACAGCAGGACTGAGAACCAAACTGCGAAAAATCCAGATACCAAGCCATCATGAGC	1863
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QY	1864	ATCCCACTCCCCAGGCGCTAACCCCGAGGGGAAAGTGGGCCACCCCTCTGCCAGCCCA	1923
Db	1921	ATCCCACTCCCCAGGCGCTAACCCCGAGGGGAAAGTGGGCCACCCCTCTGCCAGCCCA	1980
QY	1924	GGCCCCAACAGAACATTTCTTCATATACAGCAAGCATTTGTCAAGGCTCTGTCTTTTAA	1983
Db	1981	GGCCCCAACAGAACATTTCTTCATATACAGCAAGCATTTGTCAAGGCTCTGTCTTTTAA	2040
QY	1984	AAATTCGCGGCGCATATGCGCGCGCGGAGCATATGCACTGCGGAGCCCAATTCGCCCTAATAGTG	2043
Db	2041	AAATTCGCGGCGCATATGCGCGCGCGGAGCATATGCACTGCGGAGCCCAATTCGCCCTAATAGTG	2100
QY	2044	AGTCGATATTAAGCCGAATTC	2064
Db	2101	AGTCGATATTAAGCCGAATTC	2121

RESULT 3  
US-09-142-791A-1  
; Sequence 1, Application US/09142791A  
; Patent No. 6368823



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/ GENERAL INFORMATION:
/ APPLICANT: Antoine Michel Alain Bril
/ APPLICANT: Thierry Paul Gerard Calmels
/ APPLICANT: Jean-Francois Simon Pierre Faivre
/ APPLICANT: Jean-Luc Javre
/ APPLICANT: Sabine Rouanet
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GH-30012
/ CURRENT APPLICATION NUMBER: US/09/142,791A
/ PRIOR FILING DATE: 1999-02-02
/ PRIOR APPLICATION NUMBER: PCT/EP98/01901
/ PRIOR FILING DATE: 1998-03-23
/ PRIOR APPLICATION NUMBER: UK 9706377.0
/ PRIOR FILING DATE: 1997-03-27
/ PRIOR APPLICATION NUMBER: EP 97402971.2
/ PRIOR FILING DATE: 1997-12-09
/ PRIOR APPLICATION NUMBER: EP 97403007.4
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 2104
/ TYPE: DNA
/ ORGANISM: HOMO SAPIENS
/ US-09-142-791A-1

Query Match      92.3%; Score 1905; DB 3; Length 2104;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 73 ATGGCGGCGGAGTGTGGGCTGTGGCTGCTTTTGGCCGGGCTGGGCGATCGGAGTGAATG 132
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DB 61 CCGGTGGCCCACTGCCCCCATGCCCCCTTGGCCCCCGGCGCAAGAAAGGCGGAGATGAG 120
QY 193 CTGATTTCTCTCAACGTGAGTGGGCGGAGGTTCCAGACTGAGAGCAACGCTGAGAGCG 252
DB 121 CTGATTTCTCTCAACGTGAGTGGGCGGAGGTTCCAGACTGAGAGCAACGCTGAGAGCG 180
QY 253 TACCCGAGCAACCTGCTGGGCGAGACGAGAAAGAGTCTTTTCAACGAGACACCAAG 312
DB 181 TACCCGAGCAACCTGCTGGGCGAGACGAGAAAGAGTCTTTTCAACGAGACACCAAG 240
QY 313 GAGTACTTCTTTCACCGGAGACCCCGAGAGTGTCCGCTGCGTGTCAACTTTCACCGGACG 372
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DB 301 GGGAGCTGACTACCCGCGCTACGAGTGCATCTGCTCTACGACGAGAGCTGGCCCTTC 360
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DB 361 TACGGACTCTCCGAGATCATCGGAGACTGCTCTACGAGAGTCAAGAGACCGGACG 420
QY 493 AGGAGAAACCCGAGCGGCTCATGAGACAAAGACTCGGAGAAACACAGAGTCCATG 552
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QY 553 CCGCTGCTGAGCTTCCGCGAGACCATGTGGGCGGCTTTCGAGAACCCCGACACAGGACG 612
DB 481 CCGCTGCTGAGCTTCCGCGAGACCATGTGGGCGGCTTTCGAGAACCCCGACACAGGACG 540
QY 613 CTGGCCCTGATCTTCTAATGATGATGCTTCTTCTTCAATGCTGTCTCGATATCAACAC 672
DB 541 CTGGCCCTGATCTTCTAATGATGATGCTTCTTCTTCAATGCTGTCTCGATATCAACAC 600
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DB 1141 AAGATCTTGGGCTCATGCTCTCTTGAAGTGGGATCTGTATTCCTGACGAGCCCT 1200
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DB 1201 GTGATTTGTTTCCAACTTTTACCGGATTTTACCAACAGATACAGAGACTGATAACGAG 1260
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QY 1393 TACTGTACAGCAAGGCGCAACGCGGCTCTCAACGAGGCGTGGAGCTGACGCGGACCCCA 1452
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Db	481	CCCTCGCTCAGCT	TCCGCGACAGCATGTGGCGGGGCTTC	GAGAAACCCCAACCGACGACG	540
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Qy	673	GTGGTGAAGACG	GTGTCGTCGGTCAACGAT	CCCCGGGACAGAGAGCTGCCGTGCGGGAG	732
Db	601	GTGGTGAAGACG	GTGTCGTCGGTCAACGAT	CCCCGGGACAGAGAGCTGCCGTGCGGGAG	660
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Qy	853	ATCATTCGACGT	GTGTGGCCATCATGACCTTA	CTAATTCGCTGTGTGATGACCAACA	CGAG 912
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Db	841	GACGTGTCCGGG	CGGCTTCTGTACAGCTCCGGGCTT	TCCGGCTTCAAGATCTTCAAGTTT	900
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Db	901	TCCGCGCACTCC	ACAGGGGCTCTGCGATCTCTGGGCTAC	ACACTGAGAGCGTGTGCTCCGAA	960
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Db	1021	TATGCCCCAGAA	GGGGCTCTCTGGGCGACGACAT	TCCCTGCTCTGTTTGTGAC	1080
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DB 1861 ACCGAATCTCTCTCAATACCAAGATGTTGTCAAGTCTCTCTTGTAAAAATCCCGC 1920  
QY 1993 GGCATGGC 2001  
DB 1921 ACAGAGGCG 1929

## RESULT 5

US-09-142-791A-3  
; Sequence 3' Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Bril  
; APPLICANT: Thierry Paul Gerard Calmeis  
; APPLICANT: Jean-Francois Simon Pierre Falvire  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanez  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142, 791A  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2072  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; US-09-142-791A-3

Query Match 89.1%; Score 1838; DB 3; Length 2072;  
Best Local Similarity 96.9%; Pred. No. 0;  
Matches 1908; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

QY 73 ATGGCGGCGGAGTTGGCGGCTGCTGCTTTTGGCCGGGCTGGGCGCATCGGGTGATG 132

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DB 61 CCGGTGGCCCACTGGCCCAATGACCCCTGAGCCCGGCGCAACAAGAGGAGATGAG 120  
QY 193 CTGATTGCTCAACGTAGTGGGCGAGTTCAGACTGTGAGAGCAACGCTGAGCCG 252  
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QY 253 TACCCGAGACCTCTGTGGGCGAGCAGAGAGAGATTCTTTCAACGAGAGACCAAG 312  
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QY 1153 ACCATTGTCAACATGACACTGGGATACGAGACATGGTGTGATGAGATTTGAGAGG 1212





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 QY 1664 GTAGTGAAG 1720  
 Db 1860 GAG 1919  
 QY 1721 GCATCAAG 1780  
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 Db 1974 GCGCTTCCAGGCTTCAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2033  
 QY 1841 AGATCAACAG 1900  
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 QY 1901 GTCGAG 1926  
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 US-09-949-016-2456  
 ; Sequence 2456, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: C1001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241, 755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237, 768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231, 498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FASTSEQ For Windows Version 4.0  
 ; SEQ ID NO 2456  
 ; LENGTH: 3260  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-2456  
 Query Match 15.8%; Score 326.4; DB 4; Length 3260;  
 Best Local Similarity 66.2%; Pred. No. 2.4e-62;  
 Matches 487; Conservative 0; Mismatches 246; Indels 3; Gaps 1;  
 QY 1173 ACTGGATACAG 1232  
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 QY 1233 CTCCTGATGAG 1292  
 Db 62 TTCGATGATGAG 121  
 QY 1293 CCGGATTTACAG 1352  
 Db 122 TCGATTTACAG 181  
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 QY 1533 TAAACAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1592  
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QY 1713 CTGCGGACGATGCAAGAGCTCAGCAGATCCACATCCAGGGCAGTGAAGACCCCTCT 1772  
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Db 539 TCAGAGTAGTATCAAAAGCTCAGCAGATTCAGATGATGTGTGAGAGAAACCTCT 538  
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Db 599 GTCTAACAGCCGATCCAGTTTAATGCAAAATGAGAGAGTGTTAACCTTAACCTGTA 658  
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QY 1833 AACATCCAGATCAACACAGCCATCATCAGATCCCACTCCCGCCTTAACCCGAGA 1892  
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Db 719 AGGAGACGATAGGCCA 734  
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RESULT 9  
US-09-949-016-2293  
; Sequence 2293, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2293  
; LENGTH: 3004  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2293

Query Match 11.6%; Score 240; DB 4; Length 3004;  
Best Local Similarity 53.4%; Pred. No. 2.5e-43;  
Matches 712; Conservative 0; Mismatches 575; Indels 47; Gaps 8;

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| | | | |  
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| | | | |  
Db 667 ATCTCATTTGTATCTTCTGCTGAGAGCGCTGCGGAGTTCGCGAGCAAGAGACTAC 726  
| | | | |  
QY 667 ACCAATGTGTGAGACGCTGCGGCAAGTCCCGGCAAGAGAGAGTCCGCTG 726  
| | | | |  
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QY 727 GGGGAG-----GCTACTCGGTGCGCTTCTTCTGCGGAGACAGCGGCTGCTGATATC 780  
| | | | |  
Db 787 GCGAGAGCTTCACAGCTTTCGATCCCTTCTGTGTGAGAGCGTGTGATCATCTGG 846  
| | | | |  
QY 781 TTACCGTGTGATGACTCTGCGGCTTTCGCGGCTCCAGCGGCTTACCGCTTATCCG 840  
| | | | |  
Db 847 TTCTCTTGAACGTGTGTGCGGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTG 906  
| | | | |  
QY 841 AGGTATGAGATCATTCAGAGTGTGCGGCTTATGCTTCAATCATGCTGTGATG 900  
| | | | |  
Db 907 AACATATGAACTGTATGACATGTGGCATATCTTATTTATTCATCTGCGGTACC 966  
| | | | |  
QY 901 ACCAA-----CAACGAGAGCGTTCGCGGCTTCTGCTTCTGCTTCTGCTTCTG 945  
| | | | |  
Db 967 GAGCTGCGGAGACGAGGCAATGAGACAGAGGCAATGTCTTGTGCAATCTGAGGGTTC 1026  
| | | | |  
QY 946 TTCCGC-----GTCTTCAAGATCTTCAAGTTTCCGCGCATCCAGGGGCTGCGG 996  
| | | | |  
Db 1027 ATCCGCTGGTAAAGGCTTTCGCGCATCTTCAAGCTTTCGCGCATCCAAAGGGGCTGCA 1086  
| | | | |  
QY 997 ATCTGCGCTACACATGAAAGCTGTGCTCCGAACTGGGCTTCTTCTTCTTCTCCTC 1056  
| | | | |  
Db 1087 ATCTTGGGCAACGCTGAAGGCTCATGCGGAGCTGGGATTTGCTCATCTTCTTCTC 1146  
| | | | |  
QY 1057 ACCATGGCCATCATCTTCTTGGCACTGTGATGTTTATGCGGAGAAAGGCTTCTGCGC 1116  
| | | | |  
Db 1147 TTTATTTGGGTATCTTCTTCTTCTGAGCGGCTTCTTCTGAGGAGCAAGACCCCACT 1206  
| | | | |  
QY 1117 AGCAATTTCAAGACATCCCTGCTGCTTGTGTGATACCATTTGTCAACATGACACACT 1176  
| | | | |  
Db 1207 TCAGTTTGAAGAGCATCCCGGATGCTTCTGTGTGAGAGTGTGATCAATGACAAAGTG 1266  
| | | | |  
QY 1177 GATATGAGAACATGTGTGCTAAGAGATTTGACAGGAAAGATCTTCCGCTTCATCTGCTC 1236  
| | | | |  
Db 1267 GGTATGAGGAGTATGACCAAGTGAACATTAAGGAGGAAATGTGTGAGTCTCTTGTGCC 1326  
| | | | |  
QY 1237 TTGAGTGGGCTGCTGCTATGCTGCTGCGCATGCTCTGTGATTTTTCACATTTAGCCGG 1296  
| | | | |  
Db 1327 ATCCGCGGTGTCTTGAACATTCGATTCGAGTTCCGCTGATTTCTTCAACTTCAATTAC 1386  
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QY 1297 ATTATCACCAAGAA 1310  
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Db 1387 TTCTACCAACGAGGA 1400  
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RESULT 10  
US-09-949-016-12066







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Db 366 TACTTCTTGACGCGAACCAGCCGACGCTTGAAGCATCTCTACTATAGTCCGGG 425
Qy 376 AAGC---TGACATACCCGCGCTACAGAGTCACTCTGCTTACAGACGAGCTGCGCTTC 432
Db 426 GCGCCATCCGCGCGCGCGCTCAACGTCGCCATCGACATTTCTCCGAGAGATCCGCTTC 485
Qy 433 TACGGCATCTCCGCGAGATCATCGGGGCTGCTGTACAGAGATGACAGACCGGAG 492
Db 466 TACGAGCTGGCGAGAGAGGCGCATGAGAGTTCCGAGAGACGAGGCTCTTCCGCGGG 545
Qy 493 AAGGAAACGCGGAGCGCTCAATGACGACGACGACGACGACGACGACGACGACGACG 552
Db 546 GAGGAGCGGCGCTTCCCGCGCGCGCTTCCAGCGCGAGT---TGCGTCTTCCAG 602
Qy 553 CCCTGCTCAGCTTCCGCGACGACATGTCGCGCGCTTCCAGACCGCGACGACGACG 612
Db 603 TACCCGAGAGCTCCGCGCGCGCGCGCGCATGCGCATGTCGTCGTCGTCATCCTC 662
Qy 613 CTGCGCTGCTCTTACTACTGCTGCTT-----CTTATGCTGCTCTGCTGCTATC 666
Db 663 ATCTCATTTGATCTTCTGCTGAGACGCTGCGGAGTTCCGAGACGAGAGATAC 722
Qy 667 ACCAAGTGTGAGACGCTGCGCGCGACGCTCCGCGGAGAGAGCTGCGCTGAC 726
Db 723 CCGCGCTGAGCTGCGAGACATCTTCAAGACGCGCGAGACGACGCTGCGGCTCCGC 782
Qy 727 GGGGAG-----CGTACTCGGTGCGCTTCTTCTGCTGAGACGCGCGCTGCTCATATC 780
Db 783 GCAGAGAGCTCCAGCTTCCGATCCCTTCTTCTGTCGTCGTCGTCGTCGTCGTCG 842
Qy 781 TTTCACGTCGATCTCTCTGCGCTTCTTCTGCGCTTCCAGCGCTTCCAGCTTCCG 840
Db 843 TTCTCTTCTGACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 902
Qy 841 AGCGTCATGAGCATGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 900
Db 903 AACATCATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 962
Qy 901 ACCAA-----CAAGAGAGCGTCGTCGCGCGCTTCTGTCGTCGTCGTCGTCG 945
Db 963 GAGTCGCGGAGACGAGGCGACATGAGACGAGGCGCATGTCCTGCGCATCTGAGGGTC 1022
Qy 946 TTCCGC-----GTCTTCAAGATCTTCAAGTTTCCCGCATCTCCAGGCGCTGCG 996
Db 1023 ATCCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1082
Qy 997 ATCTGCGCTCACTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1056
Db 1083 ATCTGCGCGCAACGCTGAGAGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1142
Qy 1057 ACATGCGCATCATCTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1116
Db 1143 TTTATTTGGGTCATCTTCTTCCAGCGCGCTTCTTCCAGGAGGAGACGACCCACT 1202
Qy 1117 AGCAATTCACAGCATCTTCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1176
Db 1203 TCAGGTTTCAGAGCATCCGCGATCTTCTGTCGTCGTCGTCGTCGTCGTCGTCG 1262
Qy 1177 GGAATCGGAGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1236
Db 1283 GATTAAGCGGATGACACCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1322
Qy 1237 TTGAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1296
Db 1323 ATCCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1382
Qy 1297 ATTTCACGCGAGAA 1310
Db 1383 TTCTAACACCGGGA 1396

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RESULT 13

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US-09-949-016-1604
; Sequence 1604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1604
; LENGTH: 1802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1604

Query Match      10.5%; Score 216; DB 4; Length 1802;
Best Local Similarity 53.7%; Pred. No. 4.2e-38;
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;

Qy 294 CTTCAACGAGGACCAAGAGTACTTCTTGAACCGGAGCCCGAGTGTTCGCTGAGT 353
Db 207 CTACGACCCCGGCAAGCGCGAGTCTTCTTGAAGGAGCCCGAGCGCTTCAAGTGT 266
Qy 354 GCTCACTTCAACGAGGAGGAGTCTGACTACCCGCTCAACGAGTCACTTCTGCTA 413
Db 267 CATGAGGTGTAATTTCCGGGAGTCCATGAGAGAGGCAATCCCATCTGCTT 326
Qy 414 CGAGAGAGTGGCTTCTTCAAGGATCTCCGAGATCTTCCGAGATCTTCCGAGTCTGCTA 470
Db 327 CAAGAGAGATGAGCTTCTGAGAGTGAACCTCAAGTCTTCAAGCAGCTTTCAGAG 386
Qy 471 -----CGAGAGTCAAGACCCGCAAGAGGAGAACCCGAGCGGCTCATGAGCA 521
Db 387 CCACCTGAGCGAGAGCGCGAGAGTGAAGAGATCGCGCGCGCGCTGAGCTCATCT 446
Qy 522 CAACGATCGGAGAACCAAGAGTCCATCTCTGCTCACTTCTGCGAGACATGTCG 581
Db 447 GAGCAGACTGCGCTGAGACGCGCGCGAGGCGCTGCGCGCTGCGCGAGAGTGTG 506
Qy 582 GCGGCGCTTCAAGAACCCCGACACAGACGCTGCGCTGCTTCTTCAAGTGTG 641
Db 507 GAGGTTCTTGAAGAGCCCGAGTGTGTCGTCGCGCGCGGAGTGTGCGGCTCTCTT 566
Qy 642 CTTCTTATGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 701
Db 567 CTGCTATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 626
Qy 702 CCGCGGAGCAAGAGTCTGCGTCGCGGAGCGCTACTCGTGTGCTTCTTCTGCTGGA 761
Db 627 GCTGAGAGCGGAGG-GCAACCGGCTGAGCAACCGAGCTGAG-----AAGTGA 677
Qy 762 CAGCGCTGCTCATGATCTTCAACCGTGAAGTACTCTGCGGCTTCTTCCGCGCTCAG 821
Db 678 GACGCGCTGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 737
Qy 822 CCGGACGCTTCAATCCGAGCGTCATGAGCATGAGCATGAGTGTGAGCATGAGCTTCA 881
Db 738 CAAGTCGATCTTCCGCGCTGCTTCAAGATGAGATGAGTGTGAGCTGAGCTTCCCTT 797
Qy 882 CTACATCGTGTGTCATGACCAACAGAG-----ACGTGTC 920
Db 798 CTACGTGAGCTTCAAGCTTCAAGCAGCTGAGGCGCGCATGATGAGCTGACCAAGTGA 857
Qy 921 CGGCGCTTCTGTCAGCTCCGCGTCTTCCGCTTCAAGATCTTCAAGTTTCCCGCA 980

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Db 858 GCAGCGCGTCAAGCGCTGCGGATCAAGCGCATGCGCGCATCTTCAAGCTGGCCGCCA 917  
Qy 981 CTCGCCAGGGCTGCGGATCTCGGCTACACATGGAAGAGTGGCCCGAATGGGCTT 1040  
Db 918 CTCCTCGGGCTGAGAGCCCTCACTATGCTTCAAGCGGAGCTTCAAGAACTGGGGCT 977  
Qy 1041 TCTTCTCTCTCTCTCAACATGAGCATCATCTTTCGACATGATGATTTTATGCGGA 1100  
Db 978 GCGGCTCATGTAAGTGGGATGAGGATCTTCTGCTTCTGCGGCTGAGCAACATGGA 1037  
Qy 1101 GAAGGCTCTCTCGGCGCAAGTTACAGAGATCCCTGCTGTTTGGTACCACTTGT 1160  
Db 1038 GCAGAGCATTCAGAGACCTGTTTAAAGACATCCCAAGTCTTCTGATGGCCATCAT 1097  
Qy 1161 CACCATACACACTGGGATACGAGACATGATGCTTACAGATTCGAGGAAGATCTT 1220  
Db 1098 CACCATGACACCTCGGCTACGCGGACATCTTACCCCAAGACAGCTGGCAAGCTCAA 1157  
Qy 1221 CGGCTCATCTGCTCTTGAAGTGGCGTCTGATTCATTCGCGCATTCCTGATTTGT 1280  
Db 1158 CGGCGCATGATGCTTCTTGTGTGTGTGTCATCGCATGCGCTGCGCATCAACCCATCAT 1217  
Qy 1281 TTCCACTTTAGCCGATTTTACCAACAGAAATC 1312  
Db 1218 CAACAACTTTGTGAGTACTACAAACAGACAGC 1249

RESULT 14  
US-08-464-340A-3  
; Sequence 3, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,340A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449  
; FILING DATE: 28 JUL 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: cDNA  
; US-08-464-340A-3

Query Match 10.5%, Score 216, DB 1, Length 2483;

Best Local Similarity 53.7%; Pred. No. 4,7e-38;  
Matches 565; Conservative 0; Mismatches 445; Indels 42; Gaps 4;  
Qy 294 CTTCAACGAGGACACCAAGAGTACTTCTTCACCGGGAGCCCGAGGTGTCGCGCT 353  
Db 891 CTACGACCCCGGAGAGCGGAGATTCTTACTTGAACAGGACCGGAGCCTTCAAGTGT 950  
Qy 354 GCTCACTTCTACCGGAGGGGAGAGTGCATACCGCGCTACAGATGCATCTGCTCA 413  
Db 951 CATGAGGTGTAATTTTGGGGAGGTCCACATGAAGAGGGGATGTGCCCCATCTGCTT 1010  
Qy 414 CGACGAGAGTGGCTTCTTACGCGATCTCCCGAGATCATCGGGACTGCTGCTA--- 470  
Db 1011 CAAGAACGAGATGGAATTTGAGAGGTGACCTCAAGTCTCGAGACTGTTGCAAGAG 1070  
Qy 471 -----CGAGGATTAAGAGACCGCAAGAGGGAGAAAGCGGAGCGCTCATGAGCA 521  
Db 1071 CCACTGAGGAGAAACGAGAGAGCTGAGAGAGATGCGCGCGCGCTGACATCTCT 1130  
Qy 522 CAACGACTCGGAGAAACCAACAGAGTCCATGCTCTGCTCAGCTTCGCGCAGACATGTG 581  
Db 1131 GAGACACTGGGCGTGGAGAGCGGCGGAGGCGGCTGGCGCGCTGCGCAAGAGCGTCTG 1190  
Qy 582 GCGGCGCTTGAGAACCCCAACACAGACGCTGCGCTGCTTCTTACTAGTGAAGT 641  
Db 1191 GAAGTTCGAGAGAAACCGAGTCTGTCGCGCGCGGAGTGGCCGAGCTCTCTT 1250  
Qy 642 CTTCTTCATCGCTGCTCGGTGATCAACAGGTGAGAGAGCGGTGCGGAGCGGCT 701  
Db 1251 CTGCTCATCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310  
Qy 702 CCGGCGAGAGAGAGAGCTGCGGAGAGCGCTACTCGGTGCGCTTCTTCTGCTGGA 761  
Db 1311 GCTGAGAGCGGAGAG-GCAACCGGCTGAGAGACCGGAGCTGAG-----AACGTGA 1361  
Qy 762 CAGGCGTGGTATATCTTACCGTGAAGTACTCTGCGGCTTCTGCGGCTCCGAG 821  
Db 1362 GAGGCGGTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421  
Qy 822 CCGCTACCGCTGATCCGAGCGGTGATGAGATCATGAGAGTGGGAGCATATGCGCTA 881  
Db 1422 CAAGCTGACTTGGCTGCTGCTGCTTCAATGAAATTTGAGAGCTGCTGCTGCTT 1481  
Qy 882 CTACATCGTGTGATGATCAACCAACAGAG-----ACGTGTC 920  
Db 1482 CTACATGAGCTACGCTTACGCACTGGGTGCGGAGATGATGAGCTGACCAAGTGA 1541  
Qy 921 CGGCGCTTGTGATCGCTCGGCTCTTCCGCTCTTCAAGATCTTCAAGTTTCCGCGCA 980  
Db 1542 GCAGCGCTGAGAGCGCTGCGGATGATGCGCATCGGCGCATCTTCAAGCTGCGCGCA 1601  
Qy 981 CTCGCCAGGGCTGGGATCTGGGCTACACATGAGAGATGCTCGGAATGGGCTT 1040  
Db 1602 CTCCTCGGGCTGCAACCTTCACTTATGCTTCAAGCGAGTTTAAAGAACTGGGGCT 1661  
Qy 1041 TCTTCTCTCTCTCTCAACATGAGCATCATCTTTCGACATGATGATTTTATGCGGA 1100  
Db 1662 GCTGCTCATGTAAGTGGGATGAGTGTCTTCTGCTTCTGCGCTGGGCTACCAATGGA 1721  
Qy 1101 GAAGGCTCTCGGCGAGCAAGTTCAACAGATCCCTGCTGTTTGGTACCACTTGT 1160  
Db 1722 GCAGAGCATTCAGAGACCTGTTTAAAGAACTCCCAAGTCTTCTGATGGGCTCAT 1781  
Qy 1161 CACCATGACACACTGGGATACGAGACATGATGCTTACAGATTCGAGGAAGATCTT 1220  
Db 1782 CACCATGACACCTGGGCTACGCGGACATCTAACCCCAAGACAGCTGAGCAAGCTCAA 1841  
Qy 1221 CGGCTCATCTGCTCTTGAAGTGGCGTCTGATTCATTCGCTGCGCTGCTGATTTGT 1280  
Db 1842 CGGCGCATGATCTTGTGTGTGTGTGTCATGCGCTGCGCATCAACCCATCAT 1901  
Qy 1281 TTCCACTTTAGCCGATTTTACCAACAGAAATC 1312



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Result No.	Score	Query Match	Length	DB	ID	Description
1	2064	100.0	2064	13	US-10-062-879-3	Sequence 3, Appl1
2	1997	96.8	2121	13	US-10-062-879-1	Sequence 1, Appl1
3	1000.8	48.5	2351	15	US-10-212-677-453	Sequence 253, Appl1
4	1000.8	48.5	2351	17	US-10-361-811-553	Sequence 253, Appl1
5	1000.8	48.5	2351	17	US-10-361-186-553	Sequence 253, Appl1
6	1000.8	48.5	5333	15	US-10-212-677-252	Sequence 252, Appl1
7	1000.8	48.5	5333	15	US-10-212-677-254	Sequence 254, Appl1
8	1000.8	48.5	5333	17	US-10-361-811-553	Sequence 252, Appl1
9	1000.8	48.5	5333	17	US-10-361-811-554	Sequence 254, Appl1
10	1000.8	48.5	5333	17	US-10-361-186-552	Sequence 252, Appl1
11	1000.8	48.5	5333	17	US-10-361-186-554	Sequence 254, Appl1

12	843.2	10.9	3424	14	US-10-121-746-9	Sequence 9, Appl
13	823	39.9	2578	17	US-10-296-115-373	Sequence 373, Appl
14	823	32.9	5404	15	US-10-312-677-255	Sequence 255, Appl
15	679	32.9	5404	17	US-10-361-811-255	Sequence 255, Appl
16	679	32.9	5404	17	US-10-369-186-255	Sequence 255, Appl
17	634.2	30.7	1121	16	US-10-029-386-24777	Sequence 24777, Appl
18	354.4	17.2	1597	15	US-10-212-677-256	Sequence 256, Appl
19	354.4	17.2	1597	17	US-10-361-811-256	Sequence 256, Appl
20	354.4	17.2	1597	17	US-10-369-186-256	Sequence 256, Appl
21	338	16.4	612	9	US-09-864-761-66304	Sequence 26304, A
22	324.6	15.7	3254	15	US-10-212-677-251	Sequence 251, Appl
23	324.6	15.7	3254	17	US-10-361-811-251	Sequence 251, Appl
24	324.6	15.7	3254	17	US-10-369-186-251	Sequence 251, Appl
25	266	12.9	2882	18	US-10-377-139-19	Sequence 19, Appl
26	240	11.6	3004	18	US-10-322-281-95	Sequence 95, Appl
27	240	11.6	3303	19	US-10-772-636-9	Sequence 9, Appl
28	240	11.6	2305	18	US-10-322-281-94	Sequence 94, Appl
29	230	11.1	1408	16	US-10-029-386-20260	Sequence 20260, Appl
30	221.2	10.7	2565	17	US-10-435-935-10	Sequence 10, Appl
31	221.2	10.7	3756	18	US-10-377-139-18	Sequence 18, Appl
32	216	10.5	2483	13	US-10-143-103-3	Sequence 3, Appl
33	216	10.5	2483	14	US-10-325-891-3	Sequence 3, Appl
34	215.6	10.4	1747	9	US-09-804-014-7	Sequence 7, Appl
35	215.6	10.4	1371	9	US-09-974-712-1	Sequence 1, Appl
36	214.6	10.4	1792	9	US-09-974-712-3	Sequence 3, Appl
37	213	10.3	1341	10	US-09-875-321-7	Sequence 7, Appl
38	213	10.3	1341	14	US-10-162-012-7	Sequence 7, Appl
39	213	10.3	1341	17	US-10-162-102-7	Sequence 7, Appl
40	213	10.3	1341	19	US-10-316-061-7	Sequence 7, Appl
41	213	10.3	6823	9	US-09-989-920-16	Sequence 16, Appl
42	211.4	10.2	4372	9	US-09-993-811-1	Sequence 1, Appl
43	211.4	10.2	4372	15	US-10-254-010-3	Sequence 3, Appl
44	207.6	10.1	1587	18	US-10-322-281-92	Sequence 92, Appl
45	207.6	10.1	21587	18	US-10-322-281-91	Sequence 91, Appl

## ALIGNMENTS

RESULT 1  
US-10-062-879-3  
Sequence 3, Application US/10062879  
Publication No. US20020127649A1  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang Ling, Hsui-Ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
TITLE OF INVENTION: Polypeptides and Uses Therefor  
FILE REFERENCE: ahp-98089  
CURRENT APPLICATION NUMBER: US/10/062,879  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US/09/178,109  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0

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; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-10-062-879-3

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Query Match Similarity	100.0%	Score 2064;	DB 13;	Length 2064;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2064; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 GATTGGCTGAATCTCACTCAAGCTGGATGGCTGACGCTCGCGGGGCGCGCGCCCAAGA 60  
Db 1 GATTTCCTGAACCTCACTCCAAGCTGGTGTGCTGACGCTCCGCGCGCTCGCGGCCAAGA 60  
QY 61 GCTGAGTCAACATATGGCGGCGCGAAGTTGCGGCGCTAGGCTTTTGGCCGCGGCTGCGAGCC 120



Db 61 GCTGAGATCAATGCGCGCGAGATGTGCGGCTGTGCTTTTGTGCGGCGGCTGCGGCC 120  
Qy 121 ATCGGAGTATGCGCGGAGCAATGCGCCCATGCGCCCTGCGCCCGCGCGCAAGAAACAAG 180  
Db 121 ATCGGAGTATGCGCGGAGCAATGCGCCCATGCGCCCTGCGCCCGCGCGCAAGAAACAAG 180  
Qy 181 CGGAGAGTATGAGTATGTTGTTCTTCAACGTGAGTGGCGGAGGTTTCCAGACTTGAAGACC 240  
Db 181 CGGAGAGTATGAGTATGTTGTTCTTCAACGTGAGTGGCGGAGGTTTCCAGACTTGAAGACC 240  
Qy 241 ACCTGAGAGGCTTACCTCGGACACCTGCTGGGAGCAACGAGAAAGAGTTCTTCTTCAAC 300  
Db 241 ACCTGAGAGGCTTACCTCGGACACCTGCTGGGAGCAACGAGAAAGAGTTCTTCTTCAAC 300  
Qy 301 GAGGACCAAGAGATCTTCTTCAACCGGAGACCCCGAGGTTTCCGCTGCTGCTCAAC 360  
Db 301 GAGGACCAAGAGATCTTCTTCTTCAACCGGAGACCCCGAGGTTTCCGCTGCTGCTCAAC 360  
Qy 361 TTCTACCGGACGCGGAGAGCTGCACTACCGGCTACGAGTGCATCTTGTCTTCAACGAC 420  
Db 361 TTCTACCGGACGCGGAGAGCTGCACTACCGGCTACGAGTGCATCTTGTCTTCAACGAC 420  
Qy 421 GAGCTGCTTCTTACGCGCATCTTCCGAGATCATGCGGAGATCTGCTGCTTCAAGAGTAC 480  
Db 421 GAGCTGCTTCTTACGCGCATCTTCCGAGATCATGCGGAGATCTGCTGCTTCAAGAGTAC 480  
Qy 481 AAGGACCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
Db 481 AAGGACCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
Qy 541 CAGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 CAGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Qy 601 CACACCGAGCAGCTGCGGCTGCTGCTTCTTCACTAGTGCATGCTGCTTCTTCACTGCTG 660  
Db 601 CACACCGAGCAGCTGCGGCTGCTGCTTCTTCACTAGTGCATGCTGCTTCTTCACTGCTG 660  
Qy 661 GTCATCAACCAAGTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Db 661 GTCATCAACCAAGTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 721 CCGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
Db 721 CCGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
Qy 781 TTCAAGCTGAGATACCTGCTGCGGCTTTCGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAG 840  
Db 781 TTCAAGCTGAGATACCTGCTGCGGCTTTCGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAG 840  
Qy 841 AAGGTCATGAGCATGAGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
Db 841 AAGGTCATGAGCATGAGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
Qy 901 ACCAACAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
Db 901 ACCAACAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
Qy 961 ATCTTCAAGTTTTCGCGGCACTCCAGAGGCTGCGGATCTGCGGCTTCAACAAGAGAGC 1020  
Db 961 ATCTTCAAGTTTTCGCGGCACTCCAGAGGCTGCGGATCTGCGGCTTCAACAAGAGAGC 1020  
Qy 1021 TGTGCTCCGAACTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080  
Db 1021 TGTGCTCCGAACTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080  
Qy 1081 ACTGTGATGTTTATGCGAGAGAGGCTCTCTGCGGCAAGAGTTTCAAGAGATCCCTGCC 1140  
Db 1081 ACTGTGATGTTTATGCGAGAGAGGCTCTCTGCGGCAAGAGTTTCAAGAGATCCCTGCC 1140  
Qy 1141 TCGTTTGTGATACCATTTGTACCATGACCAACTGGGATATCGAGAGCATGTGTGCTTAAG 1200  
Db 1141 TCGTTTGTGATACCATTTGTACCATGACCAACTGGGATATCGAGAGCATGTGTGCTTAAG 1200

Qy 1201 ACGATTGACAGGAGAGATCTTCCGCTCATCTGCTCTTGTAGTGGCGTCTGCTTATTTGCC 1260  
Db 1201 ACGATTGACAGGAGAGATCTTCCGCTCATCTGCTCTTGTAGTGGCGTCTGCTTATTTGCC 1260  
Qy 1261 CTGCGAGTCCCTGTGATTTTTCCTTCAACTTTTACCGGATTTTACCAAGATCAAGAGCT 1320  
Db 1261 CTGCGAGTCCCTGTGATTTTTCCTTCAACTTTTACCGGATTTTACCAAGATCAAGAGCT 1320  
Qy 1321 GATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380  
Db 1321 GATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380  
Qy 1381 AGTTGATGATCTTACCTGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
Db 1381 AGTTGATGATCTTACCTGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
Qy 1441 ACGGAGACCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Db 1441 ACGGAGACCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Qy 1501 CATCACTGCTGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560  
Db 1501 CATCACTGCTGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560  
Qy 1561 TTTGAGCAGAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620  
Db 1561 TTTGAGCAGAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620  
Qy 1621 CTGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680  
Db 1621 CTGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680  
Qy 1681 CACCTGCGCAATTTCTTACCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740  
Db 1681 CACCTGCGCAATTTCTTACCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740  
Qy 1741 ATCCATCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
Db 1741 ATCCATCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
Qy 1801 AAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860  
Db 1801 AAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860  
Qy 1861 AGCATCCCACTTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920  
Db 1861 AGCATCCCACTTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920  
Qy 1921 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Db 1921 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Qy 1981 TAAATAATCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040  
Db 1981 TAAATAATCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040  
Qy 2041 GTGAGTGTATTAAGCCGAATTC 2064  
Db 2041 GTGAGTGTATTAAGCCGAATTC 2064

RESULT 2  
US-10-062-879-1  
; Sequence 1, Application US/10062879  
; Publication No. US20020127649A1  
; GENERAL INFORMATION:  
; APPLICANT: Cockett, Mark I.  
; APPLICANT: Dilke, Daniel W.  
; APPLICANT: Chang Ling, Hui-Ping  
; APPLICANT: Sokol, Patricia T.  
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
; TITLE OF INVENTION: Polypeptides and Uses Therefor

```

: FILE REFERENCE: ahp-98089
: CURRENT APPLICATION NUMBER: US/10/062,879
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: US/09/178,109
: PRIOR FILING DATE: 1998-10-23
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2121
: TYPE: DNA
: ORGANISM: human
: US-10-062-879-1

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Query Match	Score	DB	Length
96.8%	1997	13	2121

	Matches	2064	Conservative	0	Mismatches	0	Indels	57	Gaps	1
QY	1	GATTTGCTGA	ACTAACTCC	MAAGCTGGTGTGCTT	AGCGTCGCGCGGCTGCGGCCAAGA	60				
Db	1	GATTTGCTGA	ACTAACTCC	MAAGCTGGTGTGCTT	AGCGTCGCGCGGCTGCGGCCAAGA	60				
QY	61	GCTGGAGTCA	CCATATGCGCGCGGAGTGGGGCTGGCTGGCTTTT	ACC	CGGGGTTGGGGCC	120				
Db	61	GCTGGAGTCA	CCATATGCGCGCGGAGTGGGGCTGGCTGGCTTTT	ACC	CGGGGTTGGGGCC	120				
QY	121	ATCGGGTGA	TGCGCGGTGGCCAACTGCCCCATGCCCCCTTG	CCCCCGGCGCAAGAA	CAAG	180				
Db	121	ATCGGGTGA	TGCGCGGTGGCCAACTGCCCCATGCCCCCTTG	CCCCCGGCGCAAGAA	CAAG	180				
QY	181	CGGCAAGAT	AGCTGATTTCTCTCAACGTGAGTGGCGGAGGTTT	CCAGACTTGAGAGACC	240					
Db	181	CGGCAAGAT	AGCTGATTTCTCTCAACGTGAGTGGCGGAGGTTT	CCAGACTTGAGAGACC	240					
QY	241	ACGCTGAGG	CGCTTACCCGAGCACCCCTGCTGGGAGAGACGGA	AGAAAGATTCTTCC	CTTCAAC	300				
Db	241	ACGCTGAGG	CGCTTACCCGAGCACCCCTGCTGGGAGAGACGGA	AGAAAGATTCTTCC	CTTCAAC	300				
QY	301	GAGGACAC	CAAGAGATTA	CTTCTTGACCGGGAACCCCGAAGTGTTC	CGCTGCTCAAC	360				
Db	301	GAGGACAC	CAAGAGATTA	CTTCTTGACCGGGAACCCCGAAGTGTTC	CGCTGCTCAAC	360				
QY	361	TTCTTAC	CGGACGGGGAGCTGACATACCCGCGCTAC	AGATGTCATCTCTGCTTACAGAC	420					
Db	361	TTCTTAC	CGGACGGGGAGCTGACATACCCGCGCTAC	AGATGTCATCTCTGCTTACAGAC	420					
QY	421	GAGCTGG	CGCTTCTACGGCATCTCCCGAGATCATCGG	GGACTGCTTACGAGAGTAC	480					
Db	421	GAGCTGG	CGCTTCTACGGCATCTCCCGAGATCATCGG	GGACTGCTTACGAGAGTAC	480					
QY	481	AAGGACCG	CAAGAGGAGAACCGCCGACGGCTCATG	AGACGACACGACTTGGAGAAC	540					
Db	481	AAGGACCG	CAAGAGGAGAACCGCCGACGGCTCATG	AGACGACACGACTTGGAGAAC	540					
QY	541	CAGGAGTCA	TGCGCTGCTGACGCTTCCGCGACCATATG	GGGGGCTTTCAGAA	600					
Db	541	CAGGAGTCA	TGCGCTGCTGACGCTTCCGCGACCATATG	GGGGGCTTTCAGAA	600					
QY	601	CACAC	CAGACGCTGGCTGTCTTCTA	CTAGTGA	CTGGCTTTCATCGCTGTG	660				
Db	601	CACAC	CAGACGCTGGCTGTCTTCTA	CTAGTGA	CTGGCTTTCATCGCTGTG	660				
QY	661	GTCATCA	CCAAAGTGTGGAGACGGTGGCTGGGACAG	CGTCCCGGCGACAAAGAGCTG	720					
Db	661	GTCATCA	CCAAAGTGTGGAGACGGTGGCTGGGACAG	CGTCCCGGCGACAAAGAGCTG	720					
QY	721	CGGTGCG	GGAGCGCTACTCGGTGGCTTCTTGCTTGA	CAACGCGCGTGCATGATC	780					
Db	721	CGGTGCG	GGAGCGCTACTCGGTGGCTTCTTGCTTGA	CAACGCGCGTGCATGATC	780					
QY	781	TTTCA	CCGTGAGATACCTCTTGCGGCTTTCGCGGCTT	CCAGCCGCTTACGCTTCA	840					
Db	781	TTTCA	CCGTGAGATACCTCTTGCGGCTTTCGCGGCTT	CCAGCCGCTTACGCTTCA	840					

QY	841	AGCGTAAATGACATCATCGAAGTGTGGCCATATAGCCCTATCTATCCGGTCTGTATG	900
Db	841	AGCGTAAATGACATCATCGAAGTGTGGCCATATAGCCCTATCTATCCGGTCTGTATG	900
QY	901	ACCAACAACGAGGACGTGTCCGGGCGCTTCGTCAAGCTCCGGGCTTCCGGTCTTCAGG	960
Db	901	ACCAACAACGAGGACGTGTCCGGGCGCTTCGTCAAGCTCCGGGCTTCCGGTCTTCAGG	960
QY	961	ATCTTCAAGTTTTCCCGCACTCCCAAGGCGCTGCGATCTGGGCTACACTGAAGAGC	1020
Db	961	ATCTTCAAGTTTTCCCGCACTCCCAAGGCGCTGCGATCTGGGCTACACTGAAGAGC	1020
QY	1021	TGTGCCCTCCCAACGTGGGCTTCTCTCTCTCCCTCAACATGGCATCATCTTTGGC	1080
Db	1021	TGTGCCCTCCCAACGTGGGCTTCTCTCTCTCCCTCAACATGGCATCATCTTTGGC	1080
QY	1081	ACTGTGATGTTTTATGCGAGAAAGGCGCTCCCGGCGAGAACTTCAACAAGCATCCCTGC	1140
Db	1081	ACTGTGATGTTTTATGCGAGAAAGGCGCTCCCGGCGAGAACTTCAACAAGCATCCCTGC	1140
QY	1141	TCGTTTTGGTACACCATTTGTCCACCATGATGACCACTGGGATACGGAGCATGGTGCCTTAAG	1200
Db	1141	TCGTTTTGGTACACCATTTGTCCACCATGATGACCACTGGGATACGGAGCATGGTGCCTTAAG	1200
QY	1201	ACGATTCGAGGGAAGATCTTCGGCTCATCTGTCTCTTGAATGGCGTCTGTATTTGCC	1260
Db	1201	ACGATTCGAGGGAAGATCTTCGGCTCATCTGTCTCTTGAATGGCGTCTGTATTTGCC	1260
QY	1261	CTGCGAGTCCCTGATGTTTTTCCACTTTAAGCGGATTTTACCAACGAAATCAGAGAGCT	1320
Db	1261	CTGCGAGTCCCTGATGTTTTTCCACTTTAAGCGGATTTTACCAACGAAATCAGAGAGCT	1320
QY	1321	GATATAACGACAGGCGACAAAAGAAAGGCCCGCTTGTCCAGATCCCGTGTGGCAAAACAGGC	1380
Db	1321	GATATAACGACAGGCGACAAAAGAAAGGCCCGCTTGTCCAGATCCCGTGTGGCAAAACAGGC	1380
QY	1381	AGTTGGAATGATACCTGTGCACAGCAAGCGAGCGGCTCTCAAGAGGCGCTGAGAGCTG	1440
Db	1381	AGTTGGAATGATACCTGTGCACAGCAAGCGAGCGGCTCTCAAGAGGCGCTGAGAGCTG	1440
QY	1441	ACGGGCAACCCCAAGAAAGAGACATATGGGCAAGCAACCTCACTCATACGAAAGCAGAT	1500
Db	1441	ACGGGCAACCCCAAGAAAGAGACATATGGGCAAGCAACCTCACTCATACGAAAGCAGAT	1500
QY	1501	CATCAACCTGTGCACTGCTGTGAAAAAACCACT-----	1533
Db	1501	CATCAACCTGTGCACTGCTGTGAAAAAACCACT-----	1533
QY	1534	-----AACCAAGATTTATGTATGACAGATGTT	1563
Db	1561	CTGTATCTGTATGAGAACCTCCACCATCAAGAAACACAGATTTATGTATGAGCAGATGTT	1620
QY	1623	GAGCAGAACTGTGATGAGAGTTCAATGCAAGAACTAACCATATCCAAAGATCCTCACTG	1623
Db	1621	GAGCAGAACTGTGATGAGAGTTCAATGCAAGAACTAACCATATCCAAAGATCCTCACTG	1680
QY	1624	TCGAGCAACCCAGGCGCTCACTAACCACTGTGCTCCCGGTGTAGTAAGAAGACCAACAC	1683
Db	1681	TCGAGCAACCCAGGCGCTCACTAACCACTGTGCTCCCGGTGTAGTAAGAAGACCAACAC	1740
QY	1684	CTGCGCAATTTCTAATCTGTGAGATTAATGCGCTGTGGCAGATGCAAGAGCTTCAGACGATC	1743
Db	1741	CTGCGCAATTTCTAATCTGTGAGATTAATGCGCTGTGGCAGATGCAAGAGCTTCAGACGATC	1800
QY	1744	CACATTCAGGGCGATGAGCAGCCCTCCCTCAACAACGATGCGCTTCAGCTTAATTTGAAA	1803
Db	1801	CACATTCAGGGCGATGAGCAGCCCTCCCTCAACAACGATGCGCTTCAGCTTAATTTGAAA	1860
QY	1804	GCAAGACGAGCTGAGACCAAACTGCAAAACATCCAGATACACAGAGCATATGAGC	1863
Db	1861	GCAAGACGAGCTGAGACCAAACTGCAAAACATCCAGATACACAGAGCATATGAGC	1920
QY	1864	ATCCCACTCCCCAGGCTTAACCCCAAGAGGGGAAAGTGGGCCACCCCTTGACAGCCA	1923



Oy		1617	CTCATGTGTCACGCCACCAGCGCTCACTAACACCCGGTGCCTCCGTCGTATGAAGAAGC	1676
Dd		1980	TTCACTGTCTTTCCACAACAAGAGTCCACGACCCTGCTTTCACGACACAAAAAAAAC	2039
Oy		1677	CACACACCTTGCCCAATTCTTAACCTGECGACTACTGSCCTGCGAGCATGACAAGACTCAG	1736
Dd		2040	TTTTTCGATCTCCCAATATGCAATGTATCAAGAAAGCATCAAGTAGTATACAAAGAACTCAG	2099
Oy		1737	CACGATCCACATCCAGGGCAGTGAAGACCCCTCCCTCACAAACAGTGCCTCCAGCCTTAA	1786
Dd		2100	CACGATTCAGATCAGATGTGTGAGAGAAACACTCTGTCTTAACAGCCGATCCAGTTTAAA	2159
Oy		1797	TTTGAAGCACACGACGAGCTGAGACCAAACTGCAAAATCCCAAGATCAGACACGAT	1856
Dd		2160	TGCCAAATGGAAGAGTGTGTTAACTTAACCTGGAACAACTTTATGTGATCTACAGCAT	2219
Oy		1857	CATCAGCATCCCACTCCCCAGCGCTAAACCCACAGAGGGGGAAGATCGGCCA	1908
Dd		2220	AATAAGCATCCCAACACTCTCCAGTAAACACACAGAAAGAAACGATAGGCCA	2271
 RESULT 4 US-10-361-811-253 ; Sequence 253, Application US/10361811 ; Publication No. US20030206918A1 ; GENERAL INFORMATION: ; APPLICANT: Fanger, Gary R. ; TITLE OF INVENTION: FILING, STEVEN P. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; FILE REFERENCE: 210121.484C8 ; CURRENT APPLICATION NUMBER: US/10/361.811 ; NUMBER OF SEQ ID NOS: 293 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 253 ; LENGTH: 2351 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-361-811-253				
 Query Match                48.5%; Score 1000.8; DB 17; Length 2351, Best Local Similarity     72.8%; Pred. No. 1.2e-267; Matches 1348; Conservative    0; Mismatches 492; Indels    12; Gaps    4;				
Oy		66	AGTCAACCATGCGCGCGAGAGTTCGCGCTGCTGCTCTTTTCCCGGCGTGGCCATCGG	125
Dd		423	AGTATCATGCGCGCGGGGGTGGCAGCGTGGCTGCTTTTTCAGAGGGGAGCGCTATCGG	482
Oy		126	GTCGATGCCGCTGGCCCACTGCCCCCATGCCCCCTGGCCCC--GGCCGACAAAGAACAGCG	182
Dd		483	GTCGATGCTGTGCTCTCGGGGCTTAATGCCCGCTCCCCCGAGGACGAGAAAGAAC	542
Oy		183	GCAGATGAGCTGATTTGTCCTCAACGTGAGTGGGGGAGATTCACAGCTGGAGAGACAC	242
Dd		543	CCAAGATGCTCTCAATGTGTGCTGAATGTGATGGCACCCTTCAGACGTGGCAGGACAC	602
Oy		243	GCTGAGCGCTAACCCGACCACTGCTGGCAGACGGAAGAGATGTTCTTTCACACGA	302
Dd		603	CCTGAAGCGTTAACCAAGACCTTAATGCGGCACTTGAAGGAGCATTTTTCACACCC	662
Oy		303	GGAACCAAGAGATCTTCTTCGACCGGAGAACCCGGAAGTGTTCGCTGCGGCTCACTT	362
Dd		663	AGAACTCAGAGATTAATTTCTTTGACCGGACCCAGACATCTTTCGACCATCTGAAATTT	722
Oy		363	CTAACCGACGCGGAGAGCTGCACTAACCCGCTACGAGTGCATCTCTGCTTACGACGCA	422
Dd		723	CTTACCGCACTGGGAAGCTCCACTATCTCTCTCGCACAGATGATCTCTGCTTACATGAAGA	782
Oy		423	GCTGGCCTTTCTAGGCGCATCTCTCCGAGATATATGGGAGCTGCTGCTTACGAGAGTACAA	482
Dd		783	ACTGCGCTTTCTTGTGCGCTCATCCGGAATATATGGGAGCATGCTGTTATGAGAGTACAA	842

QY	483	GGACCCGAAAGGGAGAAACGCCGAGCGGCTCA	TGGAACGACAAACGACTCGAAGAACACA	542
Db	843	GGATTCGACGGCGAGAGAAACGCCGAGCGCTCG	GAGAACGACGACGCGATACCGACACCGCTGG	902
QY	543	GGAG---TCCATGCCCCCTCGCTCAGCTTCCG	CCAGACCAATGTTGGCGGGCCCTTCGAGAACCC	599
Db	903	GGAGAGCGCCCTTGGCCACCACTGACTGCAAG	GAGAGGGGTCTGAGAGGCTTCGAGAACCC	962
QY	600	CCACACGACGACGCTGGCCCTGCTCTTCTACT	ACGTGACGTGACCTTCTCATCGCTGTCTC	659
Db	963	CCACACGACGACGATGCGCCCTGTGTCTACTA	TGTCTACGCGGGGTTTTTTCATGCGCTCTC	102
QY	660	GGTCATCAACCACTGTGTGTGTGAGACGGTGC	CGTGTGCGGCAACGCTGCCGCG---CAGCAAGA	716
Db	1023	TGTATCATCCGATGTGTGTGTGAGAAACGTGC	CGGTGCGGATCAAGCCAGGTCACATTTAAAA	108
QY	717	GCTGCGGTGGGGGAGCGCTACTCGGTGAGCC	CTTCTTGCTCTGGAACAAGGCGGTGAT	776
Db	1083	ACTGCCCCGTGTGAGAGCGGTATGCTGTGAC	CTTCTTGCTTGTGACAACGCGCTGGGTGAT	114
QY	837	CCGACGCTCATGAGCATCATGACGTGTGGCCAT	CAATGCCCTTACTCATCGCTGTGT	896
Db	1203	GCGTAGTGTCTAGTGTATCATCGACGTGTGGC	CAATCGCTTATTAATTTGAGGCGTGT	126
QY	897	CATACCAACAAACGAGAGCGTGTCCGGGCTTGT	GTCAACGTCCGGGTCTTCGGGTCTT	956
Db	1263	GATACACAGACATAGAGAGCTGACGAGGAGCT	TTGTCTACATCCAGATCTTCGGGTCTT	132
QY	957	CAGGATCTTCAAGTTTTTCCCGCCACTCCAG	GGGCTGTGGGATCTGTGGCTACACTGAA	101
Db	1323	CAGGATCTTTAAGTTTTTCCCGCCACTCTCA	AGGCTGTGGGATCTGTGGGTACACTGAA	138
QY	1017	GAGCTGTGCTCCGAACTGGGCTTCTTCTCTCT	CCCTCAACATGACCATCATCATCTT	107
Db	1383	GAGTTGTGCTCAGAAATGGGCTTCTTCTTCT	CTGCTCAACATGACCATCATCATCTT	144
QY	1077	TGCCACTGTGATGTTTTATGCCGAGAAAGGCT	CTCGGCCAGCAAGTTTCAACAAGATCCC	113
Db	1443	CGTCAACAGTTATGTTCTTACGACGAGAAAG	GGGTCTTCGGCTAGCAAGTTTCAACAAGATCCC	150
QY	1137	TGCTCGTTTTGGTACACATTTGCAACATGACA	CCACACTGGGATACGAGACATGATGCC	119
Db	1503	TGCAGCCTTCTGTATATACATGTCATCATGAC	CAACACTAGGGATATGTGTACATGATGCC	156
QY	1197	TAAAGCATTTGCAAGGAAAGATCTTCGGCTCA	TGCTCTTGTGATGTGAGTGGCGTCTGGTCA	125
Db	1563	AAAAACATAGCAAGGAAAGATTTTGTGTTCTA	TCTGTCTGTGTGCTGTGGGCTTGTGTAT	162
QY	1257	TGCCCTGCAAGTCCCTGTGATGTTGTTTCCA	CTTTAGCCGATTTACCAACAGATCAGAG	131
Db	1623	TGCTCTACTGTGTCCGGATTTGTATCAACTCA	ATGATGTCATCTACACAGAAATCAACG	168
QY	1317	AGCTGATTAACGACGGGCAAAAGAGGCCCGCT	TGCCAGAGATCCGTGTGGCCAAAC	137
Db	1683	AGCAGACAAAGAAAGGGGCAAAAGAAAGCTA	GACTGCGCAGAGATCCGGGACGCCAAAG	174
QY	1377	AGGCAAGTTTGCATATCATCTGCAACAGCAAC	CGGCGTCTCTCAACGAGGCGCTGGA	143
Db	1743	CGGAAGGCGCAATGCTTACATGACGAGAGAA	ACGGAATGTGTTATCTCAATATCAGCTGA	180
QY	1437	GCTGACGGGCAACCCGAGAGAGAGACATGGG	CAAGACACTTCACTCATCTGAGAGCCA	149
Db	1803	GTCTCTCAGAGGA---TGAGCAGGCTTTTGT	TATGAGCAAAATCCGCGTCCAGCTTTGAAACCA	185
QY	1497	GCATCATCACTGCTGCACTGCCCTGGAAAAA	ACACTTAACACAGAGTTTATGATGAGA	155
Db	1860	GCATCATCACTGCTTCACTGCTGGAAGAAAA	ACCGAATACAGATGATTTGTGTGACGAACA	191

QY 1557 GATGTTGACGACGACTGCAATGAGAGTTCAATGACGACACTCCATCCACAAAGAGTCC 1616  
DB 1920 AGCTTTTGAAGAAAGCTGACATGAGAGTTGCACTGTTAAATCGTCTTCAAGTCAAGCTCC 1979  
QY 1617 CTACAGTGTCAAGCAACCCAGAGGCTCACTACACCTGCTGCTCCCGTGTAGTAAGAGAC 1676  
DB 1980 TTCACTGCTTTCACACACAGAGAGTCAACAGCACTGCTGCTTTCACAGACGACACAAAAAC 2039  
QY 1677 CACACACTGCCCCAATTTAACTGCGAGCTACTGCGCTGCGAGCAATGACAGAGTCAAG 1736  
DB 2040 TTTTCGATCCCAATATGCAATGATATCAGAGAGCATCAAGATATACAGAGACTCAG 2099  
QY 1737 CAGATCCATATCCAGGAGGAGTGAAGACCCCTCCCTCAACAACAGTGTCTCAGCTTAA 1796  
DB 2100 CAGATTCATGATCAGATGTGTGAGAGACACCTGTGTCTTACAGAGCCGATCCAGTTTAA 2159  
QY 1797 TTTGAAAGCAGACGAGGAGCTGAGACCAACTGCAAAACATCCAGATCAACAGGCAAT 1856  
DB 2160 TGCCTAAATGAAAGAGTGTGTTAACTTAACTGTAACAACTTTATGTGACTACAGCAAT 2219  
QY 1857 CATCAGCATCCCACTCCCGAGGCTTAAACCCAGAGAGGAGAAAGTGGCCA 1908  
DB 2220 AATAGATCCCAACACTCCAGTAAACCAACAGAGAGAGATAGGCCA 2271

## RESULT 5

US-10-369-186-253  
; Sequence 253, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Filing, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 253  
; LENGTH: 2351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-369-186-253

Query Match 48.5%; Score 1000.8; DB 17; Length 2351;  
Best Local Similarity 72.8%; Pred. No. 1.2e-267;  
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 66 AGTCACCATGCGCGCGAGCTTGCGGCTTGCTTTTGCCCGGCTGCGGCATCGG 125  
DB 423 AGTAATCATGGCGGCGGGGTGGCAGGTGCTGCTTTTGCAAGGCGACGGCTATCGG 482  
QY 126 GTGATGTCGGGTGGCCCACTGCCCCCATGCCCCCTGGCCCC--GGCGACAAGAACAGCG 182  
DB 483 GTGATGTCCTGTGGCTCTGGGGCTATGCGGCTCCCCGAGGAGAGGAAAGAGAC 542  
QY 183 GCAGATGAGCTGATTTGCTCAACGTGATGAGGCGGAGGTTCCAGACTGAGAGACAC 242  
DB 543 CCAAGATGCTCTCATTTGTGTGATGTGATGAGGACCCCGCTTCCAGAGTGGCAGGAC 602  
QY 243 GTGAGACGCTACCCGAGACCCCTGCTGGGAGAGCAGAGAGAGGATTTCTTCAACGA 302  
DB 603 CTGGAACGTTAACCCAGACACTACTAGGCGAGTTCTGAGAGGAGACTTTTCTACACC 662  
QY 303 GAGACCAAGAGATCTTTTCCAGCCGGGACCCCGAGAGTGTCCGCTGCGTCAACTT 362  
DB 663 AGAAATCTCAGACAGATTTCTTTGACCGTGAACCCAGAGATCTTCCGCAATCTCGAATTT 722  
QY 363 CTACCGCAGCGGAGAGCTGACATACCGCGCTAGAGTGAATCTCTGCTACAGAGACA 422  
DB 723 CTACCGCAGCTGGAGAGCTTCACTATCTCGCCAGAGATGATCTCTCTTACGATGAGA 782

QY 423 GCTGCGCTTTTACGGCATCTCCCGAGATCATCGGAGACTGTCTGTACAGAGATACAA 482  
DB 783 ACTGGCTTCTTTGGGCTCATCCCGAATATCATCGCGACTGTCTGTATGAGAGATACAA 842  
QY 483 GAGCGCAAGAGGAGAAAGCGCGAGGCTCATGACGACAACAGTATCGGAGAACCA 542  
DB 843 GATTCGACAGGAGAAAGCGCGAGGCTTGCAGAGAGACGCGGATACCGATACCGACCGCTGG 902  
QY 543 GGAG--TCCATGCTCTGCTCAGCTTCCGCGACACATATGTGGCGGCTTTCAGAAACC 599  
DB 903 GAGAGCGGCTTGGCCACATGACTGCAAGGAGAGAGGTGTGAGAGGCGCTTCAGAAACC 962  
QY 600 CCACACAGACGCTGCGCTGTCTTCTACTACATGATGATGCTGCTTCTTACATGCTGTCTC 659  
DB 963 CCACACAGACGATGCGCTGTGTCTTACTATGTCAAGGAGGCTTTTATCATGCGCTCTC 1022  
QY 660 GGTATCACCAACGTGTGTGAGAGCGGTGCGCGGAGCGAGTGGCGGCTTTCAGAAACC 716  
DB 1023 TGTCTATCGGAATGTGTGAAACAGTGGCGGATCAAGCTCCAGGTCACTTAAAGA 1082  
QY 717 GCTGCGGTGGGAGCGCTACTCGGTGGCTTCTTGTGCTGAGACAGCGCGTGCAT 776  
DB 1083 ACTGCGCTGTGAGAGCGGATGTGTGGCTTCTTGTGCTGAGACAGCGCGTGCAT 1142  
QY 777 GATCTTACCGTGAATCTCTGCGGCTCTTCCGCGCTCCAGCGCTTACCTTCAAT 836  
DB 1143 GATCTTACAGTGTGATATTTGCTGCTGCGTGAAGCGCTTATCGATTTTGT 1202  
QY 837 CGCAGCGTATGAGATCATGACGATGAGCATATGCGCTTACATCACTGATCGGTGT 896  
DB 1203 GCTTATGTATGATATCATGACGATGAGTGGCTTATCTTATTAATTTGGCTGT 1262  
QY 897 CATGACCAACAGAGAGGTGTCCGCGCTTGTCAAGCTTCCGCGCTTCCGCGCTT 956  
DB 1263 GATGACAGCAATGAGAGAGTCAAGGAGGCTTGTCACTCGAGTCTTCCGCGCTT 1322  
QY 957 CAGGATCTCAAGTTTCCGCGCATCTCCAGGCGCTGCGATCTGCGCTTACACTGAA 1016  
DB 1323 CAGGATCTTAAATTTTCCGCGCATCTCAAGGCGCTGCGATCTGCGGATACACTGAA 1382  
QY 1017 GAGCTGCGCTCGAAGCTGGGCTTCTGCTCTTCTCCATCAACATGAGGCTCATCTT 1076  
DB 1383 GAGTGTGCTCGAATTTGGCTTCTGCTTCTGCTCAACATGAGGCTTATCACTT 1442  
QY 1077 TGCCACTGTGATTTTATGCGAGAGGAGGCTCTCGCGAGCAAGTTCAAGATCCC 1136  
DB 1443 CGTACAGTATGTTCTAGCAGAGAGAGGCTTGTGGCTAGAGATTTCAACAGATCCC 1502  
QY 1137 TGCTGCTTTTGTATCAACATGTCTACCATGACCACTGGGATTCGAGACATGTGCC 1196  
DB 1503 TGCAGCTTCTGTATACATCTCTCACTGACATGACATAGAGGATATGTATGTGCC 1562  
QY 1197 TAAAGATTTGAGAGGAGAAATCTTGGCTTCATCTCTCTTAAAGTGGCTCTGAT 1256  
DB 1563 AAAAACAATAGCAGGAGAAATTTGTGTCTATCTGTGTGCTAGTGGGCTTGTGAT 1622  
QY 1257 TGCCCTGCGAGTCCCTGTGATTTTCAACTTTAGCCGAGATTTACACCAAGATGAG 1316  
DB 1623 TGCTTACCTGTTCCGCTGATTTGTATCCACTTCACTGATTTACACCAAGATCAAG 1682  
QY 1317 AGCTGATTAACGAGGAGCAAAAGAGCGCGCTTGGCCAGATCTGTGTGCAAAAC 1376  
DB 1683 AGCAGACAAAGAGGAGCAAAAGAGGCTTACATGCGCCAGATCGGCGACCAAAAG 1742  
QY 1377 AGGCAATGGAATGCACTCTGACAGCAAGGCAACGCGCTCTCAAGAGGCGCTGGA 1436  
DB 1743 CGAAGCGCAAAATGCTTACATGCAAGCAAGCAAGGATTTTACTAGTATAGCTGCA 1802  
QY 1437 GCTGACGGGACCCAGAGAGAGGACATGAGGAGACCACTTCACTGAGAGCCA 1496  
DB 1803 GTCTCTAGAGGA---TGAAGAGGCTTTGTATGCAAAATCGGCTTCAAGCTTTGAACCA 1859  
QY 1497 GCATCATCACTGCTGACTGCTGAGAAAAACCACTAACAGAGTTTATGATGACA 1556

Db 1860 GCACCACCACTGGCTTCACTGCTGGAAAAAACCAGATACAGAGTTTGTGGCGAACA 1919

Qy 1557 GATGTTTGAAGAGAACTGATCGATGAGAGTGTTCATGTAGAGAACTAACCATCCAAAGAGTCC 1616

Db 1920 AGCTTTTAAGAAAGCTGATGAGAGTTGGCACTTTTAATGCTCTTCAAGTCACAGTCC 1979

Qy 1617 CTCACTGTCCAGCCACCAGGCTTCATTCACACCTGCTGTCCTCCGTCGTAGTAAGAGAC 1676

Db 1980 TTCACTGTCTTCACACAAGAGATGACACAGACTGCTGTTCAGACACACAAAAAAC 2039

Qy 1677 CACAACCTGCCCCAATTCTAACTGCGAGCTACTGCGCAGCATGCAAGACTCAG 1736

Db 2040 TTTTGGCATCCCAATGCCAAATGATGTACGAAGACCATCAAGTGTATACAAAGAACTCAG 2099

Qy 1737 CACGATCCACATCCAGGGCAGTGAAGACCTCCCTTCACAAACAGTGGCTCCAGCTTAA 1796

Db 2100 CACGATTCAGATCAGATGTGTGAGAGAAACCTCTGTCTTAAACAGCCGATCCAGTTTAA 2159

Qy 1797 TTTGAAAGCAACGACGAGCTGAAGCCAACTGCGAAAACATTCAGATACACACAGCAT 1856

Db 2160 TGCCAAATGGAAGGTGTGTTAAACTTAACTGTGAACAACTTATGTGACTACAGCAAT 2219

Qy 1857 CATCAGATCCCACTCCCGCAGGCTTAAACCCGAGAGGGGGAAGTGGGCCA 1908

Db 2220 AATAAGCATCCCAACCTCCAGTAAACCAACCAAGAAAGACATAGGCCCA 2271

```

RESULT 6
US-10-212-677-252
; Sequence 252, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenaault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-252

Query Match      48.5%; Score 1000.8; DB 15; Length 5333;
Best Local Similarity 72.8%; Pred. No. 1.4e-267;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

Qy      66 AGTACCATGGCGGCCGGAAGTTGGCGCTGTGCCTTTTCGCCGGGTGCGGCATTCG 125
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      959 AGTATCATGGCGGGGGGGGGTGCGACGCTGTGCTGCTTTTGCAAGGGCGAGCTATTCG 1018

Qy      126 GTGGATGCCGTGGCCAACTGCCCATGCCCTGTGGCCCC--GGCCGACAAGAACAAGC 182
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1019 GTGATGCTGTGGGCTGTGGGGGCTTAATGCCGGCTTCCCCGAGCAGAGAGAAAAGAC 1078

Qy      183 GCAGATGACTGATTGTCTTCAACGTGATGGGGGAGGTTTCCAAGCTTGAGAGAAC 242
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1079 CCAAGATGCTTCAATTGTGTAATGTGATGGCACCGCCTTCCAGACGTGGCAGGAC 1138

Qy      243 GCTGAGCGCTACC CGGACACCCCTGCTGGGAGCAGGAGAAGAGTTCTTCAACGA 302
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1139 CTGTGAAGTTTACCAGACACTTAAGTGGCAGTTCTGAGAGGACATTTTCTACACCC 1198

Qy      303 GGAACCAAGAGTACTTCTTGACCGGGAACCCGAGGTGTTCCGCTGCTCAACTT 362
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db	1139	AGAAACTCAGCAGTATTTTCTTTGACCGCTGACCCAGACATCTTCCGCCACATCTGAAATT	1258
Qy	363	CTACCGCAGCGGGAGAGCTGCACTACCCGCGCTACGAGTGCATCTTCTGCTACGACGCA	422
Db	1259	CTACCGCAGCTGGGAAGCTCCACTATCTCCGCAAGAGTGCATCTCTGCTTACGTAGAGA	1318
Qy	423	GCTGGCCTTCTACGGCATCTCTCCGAGATCATCGGGACCTGCTCTACGAGAGTACAA	482
Db	1319	ACTGGCCTTCTTTGGCCTCATCTCCGGAAATCATCGGCACCTGTTATGAGGAGTACAA	1378
Qy	483	GGAACCGCAAGGGAGGAAGCGCGAGCGGCTCATGGAAGACAAACAACCTCGAGAACAA	542
Db	1379	GGATCGCAGCGAGAGAAAGCGCGAGCGCTCAGAGACACCGGATACGACACCGCTGG	1438
Qy	543	GGAG--TCCATGCGCTCGCTCAGCTTCCGCGACACCATGTGAGCGGGCCTTTCAGAAC	599
Db	1439	GGAGAGCGCCCTTGGCCACCACTGACTGCAAGGACAGAGGTCTGAGAGGGCTTCAGAAC	1498
Qy	600	CCACACGACGACGCTGGCGCTGCTTCTACTACGTGACGTGAGCTTTCATGCGCTCTC	659
Db	1499	CCACACGACGACGATGCGCTGCTGTTCTACTAGTACGAGGGTTCATGTCGCTCTC	1558
Qy	660	GCTATCATCCAAGCTGTGTGAGAGCGGTCCGTGGGACGCTCCCGG--CAGCAAGA	716
Db	1559	TGTATCCGAGATGTGTGAGAAAGTGCCTGTGGATCAAGCCAGGTCAATTAAAG	1618
Qy	717	GCTGCGGTGGGGGAGCGCTACTCGGTGGGCTTCTTCTGACCTTGACACGCGGTGCTAT	776
Db	1619	ACTGCCCTGTGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACACGCGCTGCTAT	1678
Qy	777	GATCTTCAACGCTGAGTACTCTGCGGCTTTCGCGGCTCCACGCGTACCGCTTCTAT	836
Db	1679	GATCTTCAAGTGTGATTTTGCTTGGCTGGCTGACGCGCTGATGCTTACGTTTGT	1738
Qy	837	CCGCAAGCTCATGAGCATATCAGACGCTGTGGCATATGCTCCCTTACATCGCTCTGT	896
Db	1739	GCGTAGTGTACTAGATATCATCGACGCTGTGGCATCTGCTTATTAATTTGAGCTGTGT	1798
Qy	897	CATGACCAACAAGGAGCGGTGTCGGGGGCTTGTGTACGCTCCGGGCTTCCGCGTCT	956
Db	1799	GATGACAGACATAGAGAGCTCAGCGGAGCTTGTGTACACTCCGAGTCTTCCGGGTCTT	1858
Qy	957	CAGATCTTCAAGTTCCTCCGCACTCCACAGGCGCTGCGATCTGTGGCTACACATTGAA	1016
Db	1859	CAGATCTTTAAGTTTCCCGCACTGTCAAGGCGTGGGATCTGGGGGTACACATGAA	1918
Qy	1017	GAGCTGTGCTCCGAATCGGGCTTCTTCTTCTTCCCTCACAATGGCATCATCTT	1076
Db	1919	GAGTTGTGCTCACAATTTGGGCTTCTTCTTCTCTCCTCACTATGTGTATCATCATCTT	1978
Qy	1077	TGCCACGTGATGTTTATGCGGAGAGGGCTCTCGGCGACGAAGTTTCAACAATCTCC	1136
Db	1979	CGTACAGTATGTTCTACGCAAGAGAGGGTCTTGCTAGCAAGTTTACACACATCTCC	2038
Qy	1137	TGCTCGTTCGTATACCATTTGTACATATGACACACTGGGATACGAGACATGTGTCC	1196
Db	2039	TGCAGCCTTCTGTATACATCTGTCACTACATACAACTAGGGTATGTGTACATGTGTCC	2098
Qy	1197	TAAAGCATTTGACAGGAAGATCTTGCGCTCATCTGCTCTTATGATGAGCGTCTGTCTAT	1256
Db	2099	AAAAACAATAGCAGGAAGATTTTGTGTTCTATCTGTTCCGTAGTGGGGCTTGTGTCTAT	2158
Qy	1257	TGCCCTGCGAGTCCCTGTGATGTTTCCACTTTTAAAGCCGATTTTACACACAGATCTAGAG	1316
Db	2159	TGCTTACGTGTCCGGATGTATCTCACTTCACTGTCGATCTTACACACGAATCAACG	2218
Qy	1317	AGCTGATTAACGACGGCACAATAAGAGCGCGCTTCGACAGATTCGTGTGCAACAAC	1376
Db	2219	AGCAGACAAAGAGGGGCAAAAAGAAAGTGAACCTGGCCAGATTCGGGGAGCCAAAG	2278
Qy	1377	AGGCAATTCAGATCATCTGCAACGACAGCGCAAGCGGCTCTTCAACGAGCGCTGGA	1436
Db	2279	CGAAGCGCAATCTTACATGACAGACAAACGAAATGTTTATCTAGTATACGCTGCA	2338

Db	1619	ACTGCCCTGTGGAGAGCGGTAATGCTGTGGCTCTTTCGTTGTGACAAAGGCTCGTCAT	1678
QY	777	GATCTTCAACCGTGGAGTACCTCTGCGGCTCTTGCGGCTCCAGCGGCTACCGCTTCAT	836
Db	1679	GATCTTCAACAGTTAAGTAATTGCTTCGCTCGCTGCAAGCGCTAGTGTGTTACGCTTTTGT	1738
QY	837	CGCGAGCGTATGAGCATCATCGAAGTGTGGCCATCATGCGCTACTACATCATCGGCTTGAT	896
Db	1739	GCGTAGTGTCAATGAGTATCATTCAGACGTGTGGCATCTCGCTTTATTCATTTGGGCTGTG	1798
QY	897	CATGACCAACAGAGGACGTGTCCGGCGCCTTGCTACAGCTCCGGGTCTTCCGCGTCTT	956
Db	1799	GATGACAGACAAATGAGGACGTCAACGGAGCCTTTGTCACTCCGAGCTTCCGGGCTCTT	1858
QY	957	CAGATCTCTTCAAGTTTCCCGGCCACTCCAGGGCGTCGGAATCCTGGGGCTACAACTGAA	1016
Db	1859	CAGATCTTTAAGTTTCCCGCCACTCTCAAGGCTGTGGCATCTGGGGGTACAACTGAA	1918
QY	1017	GAGCTGTGCGCTCCCAACTGTGGGCTTCTCTCTCTCCCTCAACATGGCCATCATCTT	1076
Db	1919	GAGTTGTGCGCTCAGAAATTGGGCTTCTTGCTTTCTCGCTCAACATGGGTATCATCATCTT	1978
QY	1077	TGCCACTGTGATGTTTATATGCCGAAAGGCGTCTCGGCGAGCAAGTTACACAGCATCTCC	1136
Db	1979	CGTCAAGTTATGTTCTTACAGCAGAGAAAGGGGTCTTCGGCTAGCAAGTTCAACACATCTCC	2038
QY	1137	TGCCCTCGTTTGTGACACATGTGCAACATGACACAACTGGGATACGGAGCATGTGGCC	1196
Db	2039	TGCAGCCTCTGTGATACCATCGTACCATGACAAACTAGGGTATGGTGTGACATGTGGCC	2098
QY	1197	TAAACAGATTGACAGGGAAGATCTTCGGCTCATCTGTCTCTTGTAGTGGCGTCTGTGCAT	1256
Db	2099	AAAAAACCATACAGGGAAGATTTTTTGTGTTCTATCTGTTTCGCTAGTGGGGTCTTGTGCAT	2158
QY	1257	TGCCCTGCGAGTCCCTGTGATTTGTTTCCAACTTAAAGCGATTTACCAACCAATTCAGAG	1316
Db	2159	TGCTCTACGTGTTCCGGTGTATGTATCAACTTCAGTCGATCTACACCAAGATTCACAG	2218
QY	1317	AGCTGATTAACGACGGGCAAAAGAGAGCCCGCTTGCCAGGATCCGTGGGCCAAAC	1376
Db	2219	AGCAGACAAACGAGGGGCAAAAAGAAAGCTAGCTGGCAGATCCGGGCGCCAAAAG	2278
QY	1377	AGGCAGTTCGAATCATATCTGCAACAGACGCGCAACGGGCTCTCTCAACGAGCGCTGGA	1436
Db	2279	CGAAGGCGAAATCTTACATGACAGACAAACGAAATGGTTTATCTAGTATACGCTGCA	2338

QY	1437	GCTGACGGGCAACCCCAAGAAAGAGAGACACATGGGAGAGACACCTCCTCATCATGAGAGCA	1436
Db	2339	GTCTCTAGAGGA---TGACAGAGCTTTTGTGTAGCAAAATCCGGCTTCAGCTTTGAAACCA	2395
QY	1497	GCATCATCACCTGTCTGCATCTGCTGGAAAAAACACTAACCAAGAGTTATTATGTAGCA	1556
Db	2396	GCACCAACCACTGGCTTCACTGCTGGAAAAAACAAGATCAGAGTTTGTAGAGAAAC	2455
QY	1557	GATGTTTGAAGAGAACTGCATGAGAGATTCAATGAGAACTAACCCATCATCAAGAAAGTCC	1616
Db	2456	AGCTCTTGAAGAAAGCTGCATGAGAAAGTTGACAACTGTTATATGCTCTTCAATGTCACAGTCC	2515
QY	1617	CTCATGTCACACCAACCAGGCTCTCATTAACCACTGCTGCTCCGTCGTAGTGAAGAGAC	1676
Db	2516	TTCACTGCTTTCAACAAGAGAGTCCAGACCTGCTGTTTCAGACGACACAAAAAAC	2575
QY	1677	CACACACCTGCCCAATTCTAACTTCGACGCTACTTCGCTGCGAGCATGCAAGAGCTCAG	1736
Db	2576	TTTTTCGACTCCCAATGCGCAATGTATACGAGAAAGCCATCAAGTGTATACAAAGACTCAG	2635
QY	1737	CACGATTCACATCCAGGGCAGTGAAGACCCCTCCCTCAACAACAGTGGCTCAGGCTTAA	1796
Db	2636	CACGATTTAGATTCAGATGTGTGAAGAGAACCTCTGTCTTAACAGCCGATCAAGTTTAA	2695
QY	1797	TTTGAAGACAGACGACGAGCTGAGACCAAACTGCMAAACATCCAGATCAACACAGCCAT	1856
Db	2696	TGCCAAATATGAAAGATGTGTTTAACTTAATCTGTGAACATCTTATGTGATCAAGCAAT	2755
QY	1857	CATGAGCATCCCACTCCCCACGCGCTAACCCCAAGGGGGAAGTCCGCCA	1908
Db	2756	AATAAGCATCCCAACCTTCAGTAAACCAACCAAGAAAGAACGATAGGCCA	2807

## RESULT 7

```

: Sequence 254, Application US/10212677
: Publication No. US20030129192A1
: GENERAL INFORMATION:
: APPLICANT: Chenault, Ruth A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C7
: CURRENT APPLICATION NUMBER: US/10/212,677
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 254
: LENGTH: 5333
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-212-677--254

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Query Match	48.5%	Score 1000.8;	DB 15;	Length 5333;
Best Local Similarity	72.8%;	Pred. No. 1.4e-267;		
Matches 1348;	Conservative	0;	Mismatches 492;	Indels 12;
				Gaps 4;

Qy	66	GGTCAACATGGGCGGCGGAGATTGGGCGCGGTGCTTTTGGCCGGGCGTGGGCATATGG	125
Db	959	AGTATCATATGGCGGCGGCGGAGCGGTGGCGCTTGTTCATAGGGGACGGCGCTATATGG	1018
Qy	126	GTGATGCGCGGTGGCCAACTGGCCCATGCCCTTGCCCC---GGCCGACAAAGACAAACGG	182
Db	1019	GTGATGCTGTGGCTTCGGGCGCTATCCGGCTCCCCGAGCGAGAGGAAAGAGC	1078
Qy	183	GCAGATGAGCTGATTGTCTCAAGTGAATGGCGGAGATTTCAAGCCTGGAGGACAC	242
Db	1079	CCAGATGCTCTCATTTGTGTGAATGATAGTGGACCGGCTTCCAGACGTGGCAGAGAC	1138

OY	243	CTGGAAGGGCTACCCGGACACCCTGCGGGGACAGAGAAAGAGTTCTTCTCAACGA	302
OY	243	CTGGAAGGGCTACCCGGACACCCTGCGGGGACAGAGAAAGAGTTCTTCTCAACGA	302
Db	1139	CTTGGAAAGTTTATCCAGACACTCTACTGGGAGTTCTTGAAGGGACCTTTTCTACACC	1198
OY	303	GGACACCAAGAGTACTTCTTCCAGCCGGAGACCCCGAGGTGTTCCGTGCGTCAACTT	362
Db	1199	AGAAACTCAGAGATTCTTTTGAACGTGACCAGACATCTTCCGCCACATCTGAATTTT	1258
OY	363	CTTACCGACGGGGAGCTGCACTACCCGCGTACAGATGCATCTCTGCTTACGACAGCA	422
Db	1259	CTACCGACTGGGAAGCTCACTATCCTCCGACAGATGCATCTCTCTTACATGTAAGA	1318
OY	423	GCTGGCCCTTACGAGCACTCCCGGAGATCATCGGGGACGTGCTGCTACAGAGATCAA	482
Db	1319	ACTGGCCCTTCTTGGCCCTCATCCCGGAAATATCGGAGCTGCTGTTATGAGGATCA	1378
OY	483	GGACCGCAAGGGAGAGAACCGCGAGCGGCTCATGAGCAACAGCTCGAGAACACA	542
Db	1379	GGATTCGACGGGAGAGAACCGCGAGCGGCTCGAGAGACAGCGGGATACGACACGCTG	1438
OY	543	GGAG--TCATGCGCTCGCTCAGCTTCCGACAGCAATGTGCGGGCTTCGAAACC	599
Db	1439	GGAGAGCGCCCTTGGCCCACTGACTGCAAGGACAGAGGTCTGGAGGGCCCTCGAAACC	1498
OY	600	CCACACACAGACGCTGGCGCCCTGCTCTACTAGTACGTGGGCTTCTTCACTGCTGCTC	659
Db	1499	CCACACACAGACGAGTGGCCCTGGTGTCTACTAGTACAGGGAGTTTTCATGCGCTCC	1558
OY	660	GGTCATCAACCACTGGTGGAGACGGTGCCTGCGGACGGTCCCGGG--CAGCAAGA	716
Db	1559	TGTATCGCGAATGTGTGGAAACAGTGCCTGGGATCAAGCCAGGTCACTTAAAGA	1618
OY	717	GCTGCGGTGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGGACACGCGTGCCTCAT	776
Db	1619	ACTGCGCTGGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACACGCGCTCGCTCAT	1678
OY	777	GATTTTACCGTGGAGTACCTCTCGGGGCTCTTGGCGGCTCCGACCGGCTACCGCTTCAT	836
Db	1679	GATCTTCAACAGTTAAGTATTTGCTTGGCTGGCTGACAGCGCTAGTGTGTTATCCGTTTGT	1738
OY	837	CCGACGCGTCAATGAGCATCATGACGTTGGTGGCATATGCGCTTACTACATCGGCTGGT	896
Db	1739	GCGTAGTGTCAATGAGTATCATGACGTTGGTGGCATCTGCTTATTAATGGGGTGGT	1798
OY	897	CATGACCAACACAGAGACGTGTCCGGCGCCTTGTGCACGTCCGGGCTTCCGCGCTT	956
Db	1799	GATGACAGACATAGAGACGTCAACGGAGCCTTGTGCACTCCGAGCTTCCGGGCTT	1858
OY	957	CAGAGTCTTCAAGTTTCCCGCACCTCCAGAGGCGTGGGATCTTGGGCTTACACATGAA	1016
Db	1859	CAGAGTCTTAAAGTTTCCCGCACCTCAAGAGGCGTGGGATCTTGGGCTTACACATGAA	1918
OY	1017	GAGCGTGGCCCGGAACTGGGCTTCTTCTCTCCCTCAACAGGCAATCATCATCTT	1076
Db	1919	GAGTTGGCTTCAAGATTGGGCTTCTTCTTCTCTCAACAGGCTATCATCATCTT	1978
OY	1077	TGCCACTGTGATGTTTATGCGGAGAGGGCTCCTCGGCGACGAAGTTTCAACAGATCCC	1136
Db	1979	CGCTACAGTATGTTCTACGAGAGAGGGGCTTCCGGCTAGCAAGTTTCAACAGATCCC	2038
OY	1137	TGCTCGTTTGGTACACATTTGTCAACATGACACACTGGGATACGGAGCATGTGTCC	1196
Db	2039	TGCAGCCCTTCTGTATACATCTGTACCATATGACAACTAGGGTATGTGACATGTGCC	2098
OY	1197	TAAACGATTTGCAAGGAATCTCCGCTGCATCTGCTCTTATGATGGCGTCCGTGAT	1256
Db	2099	AAAAACATACAGAGGAATTTTGTGTTATCTGTCTTCCGTGAGTGGGCTTGTGTAT	2156
OY	1257	TGCCCTGCACTCCCTGTGATTTGTTTCCAACTTTAGCGGATTTACACAGAAATCAGAG	1316
Db	2159	TGCTCTACTCTTTCGGGTATTTGATTCGAATTTCACTGATGTGATCTACACAGAAATCAGAG	2218
OY	1317	AGCTGATTAACGAGGGACAAAGAGCCCGCTTGCAGAGTCCGTGTGGCCAAAC	1376



Db	2219	AGCAGACAAACGAAAGGCGACAAAGAAAGCTTAGACTGCGCAGAGATCCGGGCGACGCAAAAG		22787
Qy	1377	AGGCAgTTGCAATGCAATACCTTGCAcAGcAGAGCGCAACGGGCTCTTCAACGAGGCGCTTGA		14368
Db	2279	CGGAAGCGCAATGCTTTCATATGCAAGAGCAAAAGAAATGTTTACTCATTAATCAGCTGCA		23388
Qy	1437	GCTGACGGGCAcCCCGAAGAGAGACATGggCAAGAcCAACTCTCATCTGAGAGCCA		14960
Db	2339	GTCTCTCAGAGGA---TGAGCAGGCTTTTGTTAGCAAAATCCGGCTCAGCTTTGAAACCCA		23959
Qy	1497	GCATTCATACCTGCTGTCAGCTGCTGGAaaaaCCATACACGAGTTTATTGATGAGCA		15566
Db	2396	GCACCACACCACTGCTTTCATCTGCTGGAAAAAACCAcGATCAcGAGTTTGTCAGCAACA		24555
Qy	1557	GATGTTTGAAGAGAACTGcATGAGAGAGTTCAATGAGAACTAACCTATCCACAAGAAATCC		16161
Db	2456	AGCTCTTTGAAGAAAGCTGcATGAGAAgTTGCAACTGTTTATGCTCTTCAATGTCACAGTCC		25151
Qy	1617	CTCACTGTCCAGGCACCCAGGCGCTCACTACCAcCTGcGTCTCCGGTGTAGTAAAGAAAGAC		16766
Db	2516	TTTCACTGTCTTTCACAAcAAGAGATCCAGCAcCTGCTGTTCACACGACACAAAAAAC		25757
Qy	1677	CACACACCTGGCCCAATTCTAACTTGcAGCTACTGCTCGGcAGAGATGACAAAGACTCAG		17361
Db	2576	TTTTTGcATCTCCCAATGcCAATGATATCAGAAAGCATTAAGTATGATACAAAGAACTCAG		26351
Qy	1737	CACGATCCACATCCAGGGCAGTgAGACAGcCCTCCCTCAcAAcCAAGTGCCTCAGACTTAA		17961
Db	2636	CACGATTCAGATTCAGATGTGTGAGAGAAcCACTCTGTCTTAACAGCGATCCAGTTTAAA		26951
Qy	1797	TTTGAAAGCAGACGACGAGCTGAGACCAATCTGCaaaaCATCTCCAGATACCAAGCCAT		18561
Db	2696	TGCCAAATATGAAAGATGTGTTTAAACTAAACTGTGACAAACTTATGTGACTACAGCAAT		27551
Qy	1857	CATCAGCATCCCACTCCCGACGCGCTTACCCCAAGAGGGGAAAGTGGGCCA		1908
Db	2756	AATATAGATCTCCAAcCACTCTCGATTAACCAcCAcCAAGAAAGAAcGATAGGCCA		2807

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RESULT 8
US-10-361-811-252
Sequence 252, Application US/10361811
Publication No. US20030206918A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Flinn, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361.811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 252
LENGTH: 5333
TYPE: DNA
ORGANISM: Homo sapiens
US-10-361-811-252

Query Match          48.5%; Score 1000.8; DB 17; Length 5333;
Best Local Similarity 72.8%; Pred. No. 1.4e-267;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY      66 AGTCACCACTGCGCGCCGGAGTTGCGGCGCTGCGTCCCTTTTGCCTCCCGGCGTGGCGGCATCG 125
Db      959 AGTATCATCATGCGCGCGCGGGGCTGGGACGACGTGCTGCTCCTTTTCAAGGGGCGAGCGCTATCG 1018

QY      126 GTGATATGCGCGGTGGGCAACTGCCCCCATGCCCCCTGGCCCC---GGCCCGACAAAGAACAGCG 182
Db      1019 GTGATATGCTGTGGGCTTGGGGGCTTAATGCCGGCTTCCTCCCGAGCGACGAGAGAAAGGAC 1078

QY      183 GCAGATAGACTGATTGTCTCTCAACGTGATGGCGGAGAGTTTCCAGACTTGAGAGACAC 242

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Db	1079	CGAAGATCTCTCATTGTGCTGAATGTAGTGGCAACCCGCTTTCAGACGTGACAGACAC	1138
Oy	243	GCTGGAGGCTAACCCGGACACCTGTGCTGGAGACGAGAGAAAGAGTTCTTCTTCAACGA	302
Db	1139	CCTGGAAAGTTAACCAAGACACTCTACTGTGGCAGTTCTGAGAGGGACCTTTTCTACACCC	1199
Oy	303	GGACACCAAGAGTACTTCTTTCGACCCGGAGACCCCGAGGTGTTCCGCTGCGTGTCACTT	362
Db	1199	AGAAACTCAGACGATATTTCTTGTGACCCGGAACCCAGACATCTTCCGCCACATCTCGAATTT	1258
Oy	363	CTACCGCACGGGGAAAGCTGCACTACCCGGCTTACGAGTGCATCTCTGTCTACAGACGA	422
Db	1259	CTACCGCACTGGAAGCTCCACTATCTCTGCGCAGAGTGCATCTCTGTACGATGAAGA	1318
Oy	423	GCTGGCCCTTTCACGGCATCTCTCCGGAGATCATCGGGACGTGCTGTCAAGAGTACAA	482
Db	1319	ACTGGCCCTTCTTGGCTCTATCCGGAAATCATCGGCGACTGCTGTATGAGAGTACAA	1378
Oy	483	GGACCGCAAGAGGAGAAACCGCGAGCGCTCATGACACACGACTTCGAGAACCAACCA	542
Db	1379	GGATCGCAGCGAGAGAAACGCGAGCGCTGTCAAGACGACCGGATACCGACACGCTGG	1438
Oy	543	GGAG---TCCATGCCCTGCTCAGCTTCCGCAAGACATGTGGGGGCTTCGAAACCC	599
Db	1439	GGAGGCGCCCTTGGCCACACATGACTGCACAGGACAGAGGGTCTGAGAGGGCTTCGAAACC	1498
Oy	600	CCACACCGACGACGCGGCGCCGTCTTCTTACTAGGTGATGGAGCTTTCATCGCTGTCC	659
Db	1499	CCACACGACGACGATGGCCCTGTGTTCTTATATGTCAAGGGGTTTTTCAATTGGCCGTTC	1558
Oy	660	GGTCATCAACCAAGCTGTGTGAGAGACGATGCCCTGTGGCGACGATCCCGAG---CAGCAAGCA	716
Db	1559	TGTATATGCGAATGTGGTGAAGAACAGTGGCCGTGGAGATCAAGCCAGGTCAATTAAAGA	1618
Oy	717	GCTGCCGTGCGGGAGCGCTACTCGTGGCTTCTTCTGCTGTGACACGGCGTGTGAT	776
Db	1619	ACTGCCCTGTGGAAGGCGGTATGCTGTGGCCTTCTTGTGCTTGTGACACGGCGTGTGAT	1678
Oy	777	GATCTTCAACCGTGAAGTACCTCCGCGGGCTTGTGGCGGCTCCGAGCGGTACCGCTTCAT	836
Db	1679	GATCTTCAACATGATGATTTTGTCTTCCGCTGGCTGACAGCGCTATGCTTACCGTTTGT	1738
Oy	837	CCGACGCGTCAATGAGCATCATCGACGTGTGGCCATCATGGCTCTTACTACATCGGTCTGGT	896
Db	1739	GGTAAAGTGTATGATGATCATCGACGTGTGGCCATCGTGTCTTATTAATTTGGGGCTGT	1798
Oy	897	CATGACCAACACGAGGACGTGTCCGGCGCTTGTGTAAGCTCCGGGTCTTCCGCGTCTT	956
Db	1799	GATGACAGACATGAGACGTCACGCGAGCGCTTGTGTCACTCCGAGCTTCCGGGCTTT	1858
Oy	957	CAGGATCTTCAAGTTTCCCGCCACTCCCGAGGGCTGCGATCTCTGGGCTTACACATGAA	1016
Db	1859	CAGGATCTTCAAGTTTCCCGCCACTCTCAAGGCTGTGCGATCTCTGGGCTTACACATGAA	1918
Oy	1017	GAGCTGTGCCCTCCGAACGAGGCTTCTTCTCTCTCCCTACCAATGGCATCATCTT	1076
Db	1919	GAGTTGTGCTCAGAAATTTGGGCTTCTTGTCTTCTCTGCTACCATGGCTATCATCTT	1978
Oy	1077	TGCCACTGTGATGTTTATGCGGAAAGGCGCTCTCGGACAGCAAGTTTACAMGATCTCC	1136
Db	1979	CGTACAGTATATGTTTACGAGAGAAAGGGGTCTTGGGTGTGCAAGTTTACACGATCTCC	2038
Oy	1137	TGCTCGTGTGTTGTGACACATTTGTACACATGACACACTGTGGATACGAGACATGTGGCC	1196
Db	2039	TGACGCGCTTCTGTGATACATGTGCACATGACAAACTAGGGATATGTGACATGTGGCC	2098
Oy	1197	TAAACGATTCAGAGGAAGATCTTCGGCTCATCTGTCTCTTGAATGGCGTCTGTGAT	1256
Db	2099	AAAAACCATAGCAGAGGAAGATTTTGTGTTCTATCTGTTCCGTAGTGGGGCTTGTGAT	2158
Oy	1257	TGCCCTGCAGTCCCTGTGATGTTTTCAACTTTAGCCGAGATTTACACAGAAATCAAG	1316

Db 2159 TGCTCTACTGTTCCGGTGTGTTATTCCTCACTTCACTGTCATACCAACCAATCAACG 2218  
QY 1317 AGCTGATTAACGACGAGGACAAAAAGAGCCCGCTTGCAGAGATCCGTGTGGCAAAAC 1376  
Db 2219 AGCAGACAAACGAAAGGACCAAAAAGAGTACCTGGCAGAGATCCGGGACAGCAAAAG 2278  
QY 1377 AGCAGTTTCAATGATGATCTGCAACGAAAGCGACGGGCTCTCTCAACGAGCGCTGGA 1436  
Db 2279 CGAAGGCGCAAAATGCTTACATGACAGCAAAACGAAATGTTTACTCATGTAATCAGCTGCA 2338  
QY 1437 GCTGACGGGACCCCGAAGAGAGACATGGGCAAGACACCTCATCTCATGAGAGCA 1496  
Db 2339 GTCTCTAGAGAA--TGACAGAGCTTTTGTAGCAAAATCCGGCTTCACGCTTGAACCA 2395  
QY 1497 GCATCATCACTGCTGCTGCTGCTGGAAGAAACCACTAACCAAGATTATGATGACA 1556  
Db 2396 GCACACCACTGCTTCACTGCTGGAAGAAACCAAGATTCAGAGTTTGTGACGACAA 2455  
QY 1557 GATGTTTGAAGACATGCTGATGAGAGTTCAATGACAGACTTACCATCAACAAGAGTCC 1616  
Db 2456 AGCTTTGAAGAAAGCTGACATGAGAGTTGCACTGTAAATGTCCTTCAAGTCAAGTCC 2515  
QY 1617 CTGACTGTGACGACACCCAGGCTCACTACACCTGCTGCTCCCTGTGATGAAGAGAC 1676  
Db 2516 TTCACTGTCTTCAACAAAGAGAGTACACAGACCTGCTGTTCAAGACGACACAAAC 2575  
QY 1677 CACACCTGCGCAATTTCTAAGCTGCGAGCTACTGCTGCTGCGAGCATGAGAGCTCAG 1736  
Db 2576 TTTTGGATCCCAATATCCATATGATGAGAGAGCATCAAGATATGATTAAGAACTCAG 2635  
QY 1737 CAGATTCACATTCAGGGGAGTGAAGAGCCCTCTCTCAACAAGTGTCTCAGCTTAA 1796  
Db 2636 CAGATTCAGATGATGATGTGAGAGAACACCTCTGTCTTAACAGCCGATCCAGTTTAA 2695  
QY 1797 TTTGAAGACGAGAGAGGACGACGACCAACTGTGAACCAATCCAGATCAACAGCAT 1856  
Db 2696 TGGCAAAATGAAAGATGTGTAACTTAACGTGAACCACTTATGTGACTACAGCAAT 2755  
QY 1857 CATCAGCATCCCACTCCCGAGCGCTAACCCGAGAGGGGAAAGTGGGCA 1908  
Db 2756 AATTAAGATCCCAACACTTCAATACCAACGAGAGAGATAGGCA 2807

RESULT 9  
US-10-361-811-254

; Sequence 254, Application US/10361811  
; Publication No. US20030206918A1  
; GENERAL INFORMATION:  
; APPLICANT: Panger, Gary R.  
; APPLICANT: Filing, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.484C8  
; CURRENT APPLICATION NUMBER: US/10/361.811  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 254  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-361-811-254

Query Match 48.5%; Score 1000.8; DB 17; Length 5333;  
Best Local Similarity 72.8%; Pred. No. 1.4e-267;  
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

QY 66 AGTCACCATGCGCGCGAGGTGCGGCTGCTGCTTTTGGCCGCGCTGCGGCATCG 125  
Db 959 AGTAATCATGCGCGCGGCGGCGGCTGCGGCTTTTGGCAAGGCGAGGCTATCG 1018  
QY 126 GTGATGCGGCTGCGCACTGCGCCATGCGCCCTGCGCC--GGCGACAAAGACG 182

Db 1019 GTGATGCTGTGCGCTCGGGGCTATATGCGGCTCCCGAGGACGAGAGAGAAAAAGAC 1078  
QY 183 GCAGATGATGATGATGCTCTCAACGTAAGTGGGCGAGATTTCAGACTGAGAGACAC 242  
Db 1079 CCAAGATGCTCTATTTGTGTGATGTAGTGGCACCGGCTTCAGACGTGGAGAGACAC 1138  
QY 243 GCTGAGCGCTACCCGAGACACCTGTGGGACAGACGAGAAAGAGTCTTCTTCAACA 302  
Db 1139 CCGGAACCTTACCCAGACACTTACTGCGGAGTTTGAAGAGGACTTTTTCACACCC 1198  
QY 303 GGAACACCAAGAGTATTTCTTGAGACCGGAGACCCGAGGTTCCCGTGGTGTCAACTT 362  
Db 1199 AGAACTTCAGAGTATTTCTTGAACCGTACCCAGACATCTTCCGACATCTGAAATTT 1258  
QY 363 CTACCGCAGGGGAACTGCACTACCGGCTTACAGATGATCTGTGCTTACAGACAGCA 422  
Db 1259 CTACCGCAGGGGAACTGCACTATCTTCCGACAGATGATCTGTGCTTACAGTAAAG 1318  
QY 423 GCTGGCTTTCTACGGGATCTTCCGAGATCATGCGGGAATGCTGTCTACGAGAGTACA 482  
Db 1319 ACTGGCTTTCTTGGGCTCATCCGGAATCATCGGAGACTGCTGTATGAGAGATACAA 1378  
QY 483 GGAACGCAAGAGAGAGAGAGAGCGGAGGCTCATGACGACAAAGACTCGGAGAACACA 542  
Db 1379 GATTCGACGAGAGAGAGAGAGCGGAGGCTGACAGAGCAGCGGATACCGACCGCTG 1438  
QY 543 GGAG--TCCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599  
Db 1439 GAGAGACGCTTGGCCACATGATGATGATGATGATGATGATGATGATGATGATGATG 1498  
QY 600 CCAACACGAGAGCTGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 659  
Db 1499 CCAACACGAGAGCTGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1558  
QY 660 GGTATCACCAACGTTGTGAGAGAGCGTGTGCGGCGGAGAGTGTGCGGCGG--CAGCAAGA 716  
Db 1559 TGTTCATGCGAGATGTGTGAGAGAGAGTGTGCGGAGATGAGCGGATCACTTAAAG 1618  
QY 717 GCTGCGGCGGAG 776  
Db 1619 ACTGCGCTGTGAG 1678  
QY 777 GATCTTACCGTGAAGTACTCTGCGGCTCTTGTGCGGCTCTTGTGCGGCTCTTGTG 836  
Db 1679 GATCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1738  
QY 837 CGGAGCGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896  
Db 1739 GGTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1798  
QY 897 CATGACCAACAG 956  
Db 1799 GATGACAGACATGAG 1858  
QY 957 CAGGATCTTCAAGTTTCCCGCAGCTTCCAGAGGCTGCGAGATCTTGGGCTTACAC 1016  
Db 1859 CAGGATCTTCAAGTTTCCCGCAGCTTCCAGAGGCTGCGAGATCTTGGGCTTACAC 1918  
QY 1017 GAGCTGTGCTCGGAG 1076  
Db 1919 GAGTTGTGCTCGGAG 1978  
QY 1077 TGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1136  
Db 1979 CGCTTACAGTTATGTTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2038  
QY 1137 TGCTGTGTTTGTGATACCATGTCACATGACACACTGGAGTACGAGAGATGTTGCC 1196  
Db 2039 TGCAGCTTCTGATATACATGTCACATGACACACTGAGGATGATGATGATGATGATG 2098  
QY 1197 TAAGAGATTTGAGAGAGAGATCTTGGCTTCATGCTCTTGAAGTGGCTCTGCTCAT 1256  
Db 2099 AAAACCATAGCAGGAGAGATTTTGTCTTATCTGTGCTGAGTGGGCTTGTGCTCAT 2158

QY 1257 TGCCCTGCAGTCCCTGATGTTTCCAACTTTAGCCGAGTTTACCAACAGATCAGG 1316  
DB 2159 TGCTTACTGTTCCGGTGATTTGTAATCCAACTTCACTGATGATCTCAACCAATACTACG 2218  
QY 1317 AGCTGATTAACGACGAGGACCAAAAGAGCCCGCTTGCAGAGATCCGTGTGAGCAAAAC 1376  
DB 2219 AGCAGACAAACGAGAGGACCAAAAGAGATGATGAGCGCAGATCCGGGAGCCAAAAG 2278  
QY 1377 AGGCACTTGAATGATACCTGACACAGCAAGCGCAACGGGCTCTCAACGAGGCGCTGGA 1436  
DB 2279 CGGAAGCCCAATGCTTACATGACAGCAAAAGGATGTTTACTAGTAATCACTGCA 2338  
QY 1437 GGTACGCGGACCCGAGAGAGACATAGGGCAAGACCACTCACTCATGAGAGCA 1496  
DB 2339 GTTCTCAAGAGA--TGAGCAGGCTTTTGTATGCAAAATCCGGCTCAGCTTGAAACCA 2395  
QY 1497 GCATCATCACTGCTGACATGCTGAGAAAAAACAATAACAAGATTATGATGACA 1556  
DB 2396 GCACACACACCTGCTTCACTGCTGAGAAAAACAAGATCAAGATTGTGAGAGACA 2455  
QY 1557 GATGTTGACGAACTGCAATGAGAGATTCAATGCAAACTAACCATTCACAAAGATCC 1616  
DB 2456 AGCTTTGAGAGAAAGCTGATGAGAGATTGCAACTGTATCGTCTTCAAGTCACAGTCC 2515  
QY 1617 CTCACCTGTCAGCCACCCAGGCTCACTAACCACTGCTGCTCCGCTGATGAGAAAGAC 1676  
DB 2516 TTCACTGCTTTCACAAAGAGATCAACAGCACTGCTGTTTCAACAGCAACAAAAAAAC 2575  
QY 1677 CACACACCTGCCCAATTTCTAACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736  
DB 2576 TTTTTCGATCTCCAAATGCAATGATATCAGGAAGCATCAAGTATATACAGAACTCAG 2635  
QY 1737 CAGCATTCACATTCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1796  
DB 2636 CACATTCAGATGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695  
QY 1797 TTTGAAAGACAGACGAG 1856  
DB 2696 TGCCAAATGAG 2755  
QY 1857 CATGAGCATCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCC 1908  
DB 2756 AATAGCATCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCCCACTCC 2807

RESULT 10  
US-10-369-186-252  
; Sequence 252, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 252  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-369-186-252

Query Match 48.5%; Score 1000.8; DB 17; Length 5333;  
Best Local Similarity 72.8%; Pred. No. 1.4e-267; Indels 12; Gaps 4;  
Matches 1348; Conservative 0; Mismatches 492;

QY 66 AGTACACATGCGCGGAGGAGTTCGCGCTGCTGCTTTTGGCCGGAGCTGCGGCATCGG 125  
DB 959 AGTATCATGCGCGGAGGAGTTCGCGCTGCTGCTTTTGGCCGGAGCTGCGGCATCGG 1018

QY 126 GTGATGCGGAGGAGCACTGCCCCCATGCCCCCTGCGCCCC--GGCCGACAAAGAACAGCG 182  
DB 1019 GTGATGCTGTGCTGCGGAGGCTTCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078  
QY 183 GCAGATGAGCTGATTTGCTCAACGATGAGTGGCGAGGAGTTCAGACCTGAGAGAGAGAG 242  
DB 1079 CCAAGATCTCTCATTTGTGCTGAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138  
QY 243 GCTGAGGCTTACCCGAGACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302  
DB 1139 CTGGAAGCTTACCCAGACCTTACTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198  
QY 303 GGAACCAAGAGATCTTCTTCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362  
DB 1199 AGAACTCAGAGATTTTCTTGAACCTGAGCCAGACATCTTCCGCACTCTGAAATTT 1258  
QY 363 CTACCGCAGGAG 422  
DB 1259 CTACCGCAG 1318  
QY 423 GCTGAGCTTCTTCAAGGATCTTCCGAGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAG 482  
DB 1319 ACTGAGCTTCTTGGGCTCATCCGAGAAATCATGCGAGATGCTGTATGAGAGATCAAA 1378  
QY 483 GGAACGAG 542  
DB 1379 GGAATCGAG 1438  
QY 543 GGAAG--TCCATGCGCTGCTCAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
DB 1439 GGAAG 1498  
QY 600 CCAACAG 659  
DB 1499 CCAACAG 1558  
QY 660 GGTATTCACCACTGCTGAG 716  
DB 1559 GTGATCGAG 1618  
QY 717 GCTGCGGAG 776  
DB 1619 ACTGAGCTGTGAG 1678  
QY 777 GATCTTCACTGAGAGATCTCTGCGAGCTTCTGCGAGCTTCCAGCCGCTTCACTCCGCTT 836  
DB 1679 GATCTTCACTGAGATTTTGTCTTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1738  
QY 837 CCGAGAGCTTATGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896  
DB 1739 GCGTATGCTATGATGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1798  
QY 897 CATGACCAAG 956  
DB 1799 GATGACAGACATAG 1858  
QY 957 CAGATCTTCAAGTTTCCGAG 1016  
DB 1859 CAGATCTTCAAGTTTCCGAG 1918  
QY 1017 GAGCTGTGCTCGAG 1076  
DB 1919 GAGTTGTGCTCAAGATTTGGCTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1978  
QY 1077 TGCCACTGTGATGTTTATGCGAG 1136  
DB 1979 CGCTACAGTATGTTTCAAG 2038  
QY 1137 TGCCCTGTTTGTGACCACTTGTACATGACCACTGAGATGAGAGAGAGAGAGAGAGAGAG 1196  
DB 2039 TGCAAGCTTCTGATATCACTGACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2098



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Db 2039 TGCAAGCCCTTGTGTATACATGTCACCATGACAAACATAGGATATGATGATGTC 2098
Qy 1197 TAAAGCATTTGAGGAGAAATCTTGGCTCCATCTGCTCTTGAAGTGGCTCTGCTAT 1256
Db 2099 AAAAAACATACAGAGGAAATTTTGTGTTATCTGTTCTGCTGAGTGGGCTCTTGCTAT 2158
Qy 1257 TGCCCTGCACTCCCTGATGTTGTTTCAACTTATGCGGATTTTCCACCAAGATACAG 1316
Db 2159 TGCTCTACTCTTTCGGATGATGTTATCCAACTTCAAGTGCATCTACACCAAGATCAAG 2218
Qy 1317 AGCTGATTAAGCGAGGAGCAAAAGAAAGCCCGCTTCCAGAGATCCGCTGTCGCAAAAC 1376
Db 2219 AGCAGACAAAGAGAGGAGCAAAAGAAAGCTAGATGCGCCAGATCCCGGAGCCAAAG 2278
Qy 1377 AGCAGATTCGATGATCACTGACAGCAAGCGCAAGCGGCTCTTCAAGAGCGCTGGA 1436
Db 2279 CGGAAGCGCAATATGCTTACATGACAGCAAGCAAGGATGTTTACTCAGTAATCAGCTGA 2338
Qy 1437 GCTGACGGGACCCCGAGAGAGAGACATGAGGCAAGACCACTTCACTCATCTGAGAGCA 1496
Db 2339 GTCCCTCAAGAGA--TGAGAGGCTTTTGTAGCAAAATCCGCTCCAGCTTTGAAACCA 2395
Qy 1497 GCATCATCACCTGCTGACCTGCTGAAAGAAACCACTAACCAAGATTTATGATGAGA 1556
Db 2396 GCACCAACCACTGCTTCACTGCTGAAAGAAAGCAAGATCAGAGTTTGTGAGAGCA 2455
Qy 1557 GATGTTTGAAGAGAACTGATGAGAGATTCATGAGAACTAACCCATCCACAGAAATCC 1616
Db 2456 AGCTTTTGAAGAAAGCTGATGAGAGATTCATGAGAACTGATGATGCTTCAAGTCAAGTCC 2515
Qy 1617 CTCACTGTCAGCAAGCCAGAGCTTCACTACCACTGCTGCTCCGCTGATGAGAAAGAC 1676
Db 2516 TTCACTGCTTCAAGCAAGAGTCAACGACACCTGCTGTTTCAACAGCAACCAAAAGAAC 2575
Qy 1677 CACACACCTGCGCAATTTAACTGCGAGTACTGCGCGGAGAGAGAGAGAGAGAGAGAG 1736
Db 2576 TTTTGGCATCCCAATGTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2635
Qy 1737 CAGCATTCACATCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1796
Db 2636 CACGATTCAGATCAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695
Qy 1797 TTTGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
Db 2696 TGCCAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2755
Qy 1857 CATCAGCATCCCGCACTCCCGAGGCTAACCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1908
Db 2756 AATAAGCATCCCAACCTCCAGTACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807

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## RESULT 12

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US-10-121-746-9
; Sequence 9, Application US/10121746
; Publication No. US2003003648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US2003003648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT FILING DATE: US/10/121,746
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K-Hnov12
US-10-121-746-9

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Query Match 40.9%; Score 843.2; DB 14; Length 3424;
Best Local Similarity 68.2%; Pred. No. 8.7e-224;
Matches 1287; Conservative 1; Mismatches 559; Indels 39; Gaps 7;

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Qy 65 GAGTCACCATGAGCGGCGGAGAGTGGCGGCTGAGCTGCTTTTGGCCGGGCTGGCCATCG 124
Db 249 GTGGCAGATGAGCGGCGGAGGCTGGCCAGAGTGGCTTTTGGCGGAGAGAGAGAGAGAG 308
Qy 125 GGTGATGCGGATGCGCAATGCGCCATGCGCCCTGCGCCCGGCGGAGCAAGAGCGGC 184
Db 309 GGTGATGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
Qy 185 AGATGAGCTGATGCTCTCAAGTGAAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
Db 369 GAGATGAGCTGATGCTCTCAAGTGAAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 428
Qy 245 TGAGCGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
Db 429 TGAGCGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
Qy 305 ACACCAAGAGATGCTTCTTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 489 ACTAGAGAGATGCTTCTTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
Qy 365 ACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 549 ACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
Qy 425 TGCGCTTCAAGAGATGCTTCTTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
Db 609 TGCGCTTCAAGAGATGCTTCTTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
Qy 485 ACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
Db 669 ACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
Qy 545 AGTCATGCTCTGC-----TGAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
Db 729 AGCGCCAGCGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
Qy 596 ACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
Db 789 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
Qy 656 TCTGCTCATCAGCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
Db 849 TGTGCTCATCAGCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
Qy 711 -CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
Db 909 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
Qy 770 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829
Db 969 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
Qy 830 GCTTCATCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889
Db 1029 GCTTCATCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1088

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QY 890 GTCTGTCATGACCAACAGAGAGCTGTCCGGCGCTTCGTACGCTCCGGGCTTCC 949  
DB 1089 GCGTTTGGTGGCCCAAGAGAGAGTGTCTGGCGCTTTGTGACCCCTGCTGTGTTCC 1148  
QY 950 GCGTCTTCAAGATCTTCAAGTTTCCCGCACTCCAGGGCGCGGATCTCGGGCTACA 1009  
DB 1149 GGGTGTGTCGATCTTCAAGTTTCTCCAGGCACTCACGGGCTTGAGGATTTGGGCTACA 1208  
QY 1010 CACTGAAGAGCTGTGCTCCGAACTGGGGCTTCTCTCTCTCTCCCTCACCATGGCCATCA 1069  
DB 1209 CACTCAAGAGCTGTGCTCTGAGCTGGGCTTCTCTCTCTTCTCCCTCAACATGGCCATCA 1268  
QY 1070 TCACTTTTGGCACTGTGATGTTTTATGCCAGAAAGGCTCTCGGCCAGAGTTCAAA 1129  
DB 1269 TCACTTTTGGCACTGTGATGTTTTATGCCAGAAAGGCTCTCGGCCAGAGTTCAAA 1328  
QY 1130 GCATCCCTGCTGTTTTGGTTATACCATTTGTCAACATGACACACTGGGATAGGAGACA 1189  
DB 1329 GCATCCCTGGGCTTCTGGTTATACCATTTGTCAACATGACACAGCTGGCTACGGAGACA 1388  
QY 1190 TGGTGCCTAAGACGATTCAGAGGAAGATCTTGGGCTCATCTGCTCCTTGAGTGGGCTCC 1249  
DB 1389 TGGTGCCTAAGACGATTCAGAGGAAGATTTGGGGTCACTGTCTCACTGAGTGGCTCT 1448  
QY 1250 TGGTCACTTGGCTTGGCCAGTCCCTGTGATGTTTCAACTTTAAGCCGATTTACCAACA 1309  
DB 1449 TGGTCACTTGGCTTGGCCAGTCCCTGTGATGTTTCAACTTTAAGCCGATTTACCAACA 1508  
QY 1310 ATAGAGAGGTGATTAACGAGGAGCAACAAAGAGGCGGCTTGGCAGAGATCCGTGTG 1369  
DB 1509 ACCAGCGGGCTGACAGCGCGGAGACAGAGAAAGGCGCTTGGCAAGAGTCGATTTGG 1568  
QY 1370 CCAAAACAGGCAAGTTCGATGATCTTGTGACAGACGCGCAACGSGCTCTCAACGAG 1429  
DB 1569 CAAAGAGTGTACCAACATGCTCTCTGAGTACAGAGAAAGGAGGCGCTTGA----- 1623  
QY 1430 CGCTGAGCTGACGGGACCCCAAGAGAGACATGGGCAAGACCACTCACTCATCG 1489  
DB 1624 ----GGACAGCGGAGTGGGAGAGACAGGCTTTGTGACAGAAACGTTTGGCTTTG 1679  
QY 1490 AGAGCCGATCATCACTGCTGACCTGCTGAGAAAACCACTAACAGAGATTTATG 1549  
DB 1680 AACAGCAACATCACTTGTCTGCTGCTGAGTGAAGAGACAGTGCATGAGTTTCAAG 1739  
QY 1550 ATGAGCAGATGTTT--GAGCAGAACTGATGAGATTCATGACGAACTACCATCCACA 1608  
DB 1740 ATGAGCTCACTTCAGTGAAGCCCTGGGAACCGTCTGGCGGGTGGCCGACAGCCGTA 1799  
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; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
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; PRIOR FILING DATE: 2000-04-25  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 08:07:28 ; Search time 6052.92 Seconds  
(without alignments)  
12579.627 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_ges1: \*  
9: gb\_ges2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1643.8	79.6	1911	9	AY419309 Mus muscu
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5	985.6	47.8	2997	3	AK032268 Mus muscu
6	960	46.5	1893	9	AY406812 Homo sapi
7	944.6	45.8	1893	9	AY406814 Mus muscu
8	842	40.8	1944	9	AY408063 Homo sapi
9	798	38.7	1956	9	AY408065 Mus muscu
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#### ALIGNMENTS

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            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED     14671302
REFERENCE   2 (bases 1 to 1911)
            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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COMMENT     These sequences were made by sequencing genomic exons and ordering
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 1 (bases 1 to 1911)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
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 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1911)  
AUTHORS Clark,A.G., Gnanowskij,S., Nielson,R., Thomas,P., Kejariwal,A.,  
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Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
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VERSION AY419309.1 GI:39775266  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1911)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1911)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
SUBMITTED (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
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Matches 1744; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

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DB 361 TATGGATCTCTCCCGAGATCATCGGGGACTGTGTCTAGAGAGATCAAGAACCCCAAG 420  
QY 493 AAGGAGAGCCGAGGCGCTCATGAGCAACAAGTCTGGAAGCAACCGAGAGTCCATG 552  
DB 421 CCGGAGAGATGCGAGGCGCTCATGAGTGAATGACTTGAAAAACAACGAGATCATAG 480  
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 LOCUS AK033962 3730 bp mRNA linear HTC 03-APR-2004  
 DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length  
 enriched library, clone:9330129C02 product:potassium voltage-gated  
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 ACCESSION AK033962.1 GI:26329580  
 VERSION AK033962.1  
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kitsuwa, T., Tashiro, H., Itoh, M.,  
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Yonish-Rouss, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watanabe, M.,  
 Fuyukawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 JOURNAL 20530913  
 MEDLINE 11076861  
 PUBMED  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6  
 AUTHORS Adachi, J., Aizawa, K., Akiyama, T., Hara, A., Hashizume, M.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kaga, I., Kasukawa, T.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.  
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 DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length

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ACCESSION AK032268.1 GI:26328092  
 VERSION AK032268  
 KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
 Mammalian; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 2 Carninci, P. and Hayashizaki, Y.  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)

REFERENCE 3  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 4  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Komno, H., Akiyama, J., Niehi, K., Kitsuami, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Iehi, Y., Nakamura, S., Hazama, T., Nishine, T., Harada, A.,  
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J.,



TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-pipet sequencing pipeline with 384 multichannel sequencer	Genome Res. 10 (11), 1757-1771 (2000)	20030913		
11076861				
4				
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	5		
The RIKEN Genome Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 2997)		
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizmoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)				
COMMENT				
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers				
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SOURCE				
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Best Local Similarity	72.0%	Pred. No. 8,7e-218			
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QY	113	CTGCGCCCATCGGTGATGCGCGGTGCGCACTGCCCCATGCCCCCTGGCCCCCGCCGACA	172		
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QY	173	AGACACACCG---CAGATGAGCTGATTTGCTCAACTGATAGTGGCGGAGTTCCAGA	229		
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QY	230	CCTGGAGGACACACGTGGAGGCGTACCCCGGACCCCTGCTGGGGACGACGCGAAGAGGT	289		
Db	1142	CATGGCAAGACACCTTGAGAGATACCCAGACACTGTCTGGATGTTCTGAGAGACT	1201		
QY	290	TCTTCTTCAACGAGGACACCAAGGAGTACTTTCGACCGGGACCCCGAGGTTCGCT	349		
Db	1202	TTTTTCAACCCAGAGACCCACATATCTTTTGACCGTGAACCCGACATCTTCGCG	126		
QY	350	GCGTCTCAACTTCTACCGCACGCGGGAAGTGCATACCGCGCTGACAGTGCATCTGTG	409		
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QY	410	CTTACGACGACGAGTGGCTTTTCAACGCACTCTCCCGAATCATCGGGAGTCTGCT	469		
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QY	707	G---CAGCAAGAGCTGCGTGGCGGGAGCGCTACTCGGTGACCTTCTTGTGCTGACA	763		
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QY	764	CGGCGTGCATGATTTTCAACGATGAGTACTCTTGCGGCTCTTTCGGGCTCTCCAGCC	823		
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QY	884	ACATCGCTGTGATGACCAACAACAGAGACGTGCTCGGCGCTTCTGTCACGCTCCGGG	943		
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QY	944	TCTTCCGCGTCTTCAAGATCTTCAAGTTTTCGCGCACTCCACGGGCTGGGATCTTGG	1003		
Db	1862	TCTTTGAGTCTTCAAGATCTTTAAGTTTTCGCGCACTTCAAGGGCTGGGTATACGG	1921		

OY	1004	GCTACACCTAAAGAGCTGTGCTCCGAACTGGGGCTTCTCTGTCTCCCTCAACATGG	1063
Db	1922	GGTACACCTTAAGAGCTGTGATCAAGACTGGGCTTCTGTCTCTCTCTCAACATGG	1961
OY	1064	CCATCATCATCTTGGCCACTGTGATGTTTATGCGAGAAAGGGCTCTCGGCCAAGT	1123
Db	1982	CTATCATCATTTTGGCTTACCGTTATGTTCTAGCGAGAAAGGGCTTTCAGCAAGCAAGT	2041
OY	1124	TCACAAGCATCCCTGCTCTGTTTGGTACACCATTTGTACCATATGACCACTGGGATACG	1183
Db	2042	TCACCAAGCATCCCGGACGCTTCTGGTACACCATGTCTACCATATGCAACACTGGGGATATG	2101
OY	1184	GAGACATGTGTCTAAGACGATTTGACAGGAAAGATTTTGGGCTCCATCTGCTCTTGGATG	1243
Db	2102	GGCAGATGTATCAAAAACCATAGCAGGAAAGATTTTGGGTCCATCTGTCTACTGACG	2161
OY	1244	GCGTCTGGTCAATGCTCCCTGCGAGTCCCTGTGATTTGTTCCAACTTTAGCCGGAATTAAC	1303
Db	2162	GAGTCTTGGTCAATGGCTGATCCCGTGCTGTGATGTGTCCAGCTTGAGTGGATCTAAC	2221
OY	1304	ACCAGATTCAGAGAGCTATTAAGCGCAGGGCACAAAAGAGGCCCTTGCCAGATCC	1363
Db	2222	ACCAAAACCAACGAGCACAACCAAGAGGCAACAAAGAAAGCCGCTGGCCAGATCC	2281
OY	1364	GTGTGGCCAAAACAGGCGAGTTGGAATGATTCCTGCAAGCAAGGCGCAACGGGCTCCCA	1423
Db	2282	GAGCAGCCAAAAGCGGAGGTGCAATGCTTACATGCAAGCAAGCGAATGGCTACTAGCA	2341
OY	1424	ACGAGCGCTGAGAGCTGAACGGGCAACCCAGAAAGAGAGCAATGGGCAAGACCACTTAC	1483
Db	2342	GCAACACAGCTGAGTCTCGGAGGAT--GAACGGGCTTCAATAAGCAAACTGGATCCA	2398
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Db	2399	GCTTTGAGACACAGCACCAACCACTGCTTCACTGCTGGAGAAAAACAAGAACATGAGT	2458
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Db	2459	TTGTGATGAACAGTCTTTTGAAGAACTGTGATGAAGTTGGCCACCGTCAATGGCCAT	2518
OY	1604	CCACAAGAGTCCCTCACTGTCTAGGCAACCGAGGCTCATTAACAACCTGTGCTCCGTC	1663
Db	2519	CAAGTCAAGTCCCTCTCTCTCTCAACAAGAGATCAACGACACTTGTGTCTACGGA	2578
OY	1664	GTAAGTAAGAGACACACACCTGCGCAATTCTAACCTGCCAGCTACTGCTGCGACGA	1723
Db	2579	GACACAAAAGACTTTCGCACTTCTTAATGCAATGTGCGGAAGCATAGAGGCAAGTG	2638
OY	1724	TGCAAGAGCTCAGACAGATCCACATCCAGGCGAGTGAAGACGCCCTCCCTCAACACATC	1783
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OY	1784	GCTCAGGCTTAAATTTGAAGCAGACGAGCTGAGACCAAACTGCAAAAATATCCAGA	1843
Db	2699	GATCCAGCTTAAATCCCAAAATGGAAGAGTGTGTTAACTTAACTGTGAACAACCTTAAG	2758
OY	1844	TCACCACGCCATCATCAGCATCCCACTCCCGACGCGCTAACCCAGAGGGGAAAATC	1903
Db	2759	TGACCACAGCATATATTAAGCATCCCAACACTCTCAGTAACACCCCAAGAGGCGACGA	2818
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LOCUS	1993 bp DNA linear GSS 15-DEC-2003
DEFINITION	Homo sapiens KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION	AY406812
VERSION	AY406812.1 GI:39762783

KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Interfing nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1893)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
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Query Match	46.5%; Score 960; DB %; Length 1893;
Best Local Similarity	69.6%; Pred. No. 7,2e-212;
Matches 1285; Conservative	0; Mismatches 548; Indels 12; Gaps 4;
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QY	133 CCGGTGGCACTGCGCCCATGTCCTTGGCCCC--GGCCGACAGAACACGCGCAGAT 189
DB	61 CCGTGGCTCGGGGCTTATGCCGCTCTCCCGAGGCGAGAGAAAGACCCAAAT 120
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QY	250 CGTACCCCGACACCCCTGTGGGAGGACGAGAGAGAGTCTTTCTTCAAGAGACACC 309
DB	181 CGTTACCCAGACACTTACTGGGAGTCTTGAAGGACCTTTTCTACCAACCGAAACT 240
QY	310 AAGAGTACTTCTTGACCGGAGACCCCGAGGTGTTCCGCTCGTGTCACTTCAACGC 369
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QY	667	ACCAACGTGTGTGAGACGGTGCCTGTGCGGACCGGTCCGGG- - -CAGCAGAAGACTGGCG	723
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QY	1204	ATTGACAGGAAGATCTTCGGCTCCATCTGTCTCTTGAATGGCGTCTGTGATTTGCCCTG	1263
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QY	1384	TGCAATGATATCCCTGCACAGCAAGCGCAAGGGCTCCCTCAACAGAGGCGTGTGABCTGAC	1443
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QY	1684	CTGCCCAATTCTAACCCTGCCAGCTACTGCGCTGGCGAGCATGCAAGAGCTCAGACATC	1743		
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Db	1678	CAGATTCAGATGTGTGGAGAGAAACACTCTGTCTTAACAGCGCATTCAGTTTAAAGCCAAA	1737		
QY	1804	GCAGACGACGAGCTGAGACCAAACTGCAAAAATCCAGATCACCAAGCATATATAGC	1863		
Db	1738	ATGGAAGAGTGTGTTAAACTAACTGTGAACAACCTTATGTGACTTACAGCAATATATAGC	1797		
QY	1864	ATCCCACTCCCCGAGCGCTTAACCCGACGAGGGGAAAGTCGGCCA	1908		
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DEFINITION	Mus musculus KCND2 gene, VIRUTAL TRANSCRIPT, partial sequence,				
ACCESSION	AY406814	genomic survey sequence.			
VERSION	AY406814.1	GI:39762785			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.				
AUTHORS	1 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smnisky,D.J., Adams,M.D. and Cargill,M.				
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene tricos				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smnisky,D.J., Adams,M.D. and Cargill,M.				
AUTHORS	Direct Submission				
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
COMMENT	Location/Qualifiers				
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gene	/gene="KCND2"				
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ORIGIN					
Query Match	45.8%;	Score 944.6;	DB 9; Length 1893;		
Best Local Similarity	69.1%;	Pred. No. 2,7e-208;			
Matches 1275;	Conservative 0;	Mismatches 557;	Indels 12; Gaps 4;		
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QY	133	CCGGTGGCAACTGCCCCCATGCCCCCTGGCCCCGCGCGACAAACAAGCGG---CAGAT	189		
Db	61	CTGTTCCTTCCTGGGCGCTATGCGTGGCGCCCCCAAGACAGAGAGAAAAGAAAGACTCAGAC	120		
QY	190	GAGCTGAATTGTCTCAACGTGAGTGGCGGAGGTTCCAGACTTGGAGAACCAAGCTGGAG	249		
Db	121	GCTCTGATGATGCTGGAACGTGAGTGGGACCCGTTTCCAGACATGGCAAGACACACCTGGAA	180		

OY	250	CGCTAACCCGGAACACCTCTCTG3GAGACGGAGAAGAGGTTCTTCTTCAACGAGGACACC	309
Db	181	CGATGCCAGACACTCTGCTGGGTAATTTCTAGAGAGACTTTTCTTACACCCAGAGACC	240
OY	310	AAGAGTACTTCTTTCGACCGG3GACCCCGAGGTGTTCGCTCGTCTCACTTTCAC	369
Db	241	CAACAATCTCTTGTGACCGTGACCCGGACACTTTCGCGCACATCTTCAATCTTTCACCGC	300
OY	370	ACGGGGAAGCTGACCTACCCGCGCGTACGAGTGACATCTCTGCTCAACGAGACTGGCC	429
Db	301	ACGGGGAAGCTTCACTATCCCGCGCATGAGTCACTTCGCTTTATGATGAAGAACTGGCC	360
OY	430	TTCTACGGCATCTTCCCGAGATCATCGG3GACTGTGCTTACGAGAGTACAGACCGC	489
Db	361	TTCTTTGGCTTCATCCGAGAAATTATGGCACTGCTGTATGAGAGTACAGACCGC	420
OY	490	AAGAGGAGAACCGCGAGCGGCTCATGAGACACACACTCGGAGAACACACAGAGT--	547
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OY	548	-CCATGCCCTGCTCAGCTTCCGCGACACATGTGCGGGGCTTTCAGAACCCCGCACAC	606
Db	481	GCGCTGCCACATGACTGTGAGGACAGAGGCTTGGCGGCTTTGAGAACCCCGCACCC	540
OY	607	AGCAGCTGGCCCTGTGCTTCTTACTACGTGACTGGCTTTCATGCTGTCTCGATC	666
Db	541	AGCAGCAATGGCCCTGTGCTTCTTACTATGTGACTGGGTTCTTCATTTGCGTCTCAGTATC	600
OY	667	ACCAACGTGTGAGAGACGATGCGCGGAGGACCGTCCCGG---CAGCAAGACCTTCGG	723
Db	601	GCGATGTGTGAGAACATTCCTCATGTGGGTCTAGCCAGGCACATTAAGAACTGCT	660
OY	724	TGCGGGAGCGCTACTCGGTGGCTTCTTCTGCTGACACAGCGGTGCGTATGATCTTC	783
Db	661	TGTGGGAGAGATGTATGCGGTGGCTTCTTCTGTTGAAATACCGCTGTGTCATGATCTTC	720
OY	784	ACCGTGAATACCTCTCGGGCTCTTGGCGGCTCCAGCCGCTACCGCTTATCCGACGC	843
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OY	844	GTCATGACATCATCATGAGTGTGGCCATCATGCGCCCTTACATTCGAGTGTATGACC	903
Db	781	GTCATGATATCATCATGAGTGTGGCCATCTCAACCTTATCATTTGGGCTGTGATGACA	840
OY	904	AAACAAGAGAGCTGTCCGGCGCTTGTGTACAGCTCGGGGTCTTCGCTTTCAGATC	963
Db	841	GACATGTAGAGATGTCAGTGAGACCTTTGTACACTCCAGTCTTTCGAGTCTTCAGATC	900
OY	964	TTCAAGTTTCCCGCACTCCACAGGGGCTGGGGATCCGTGGGCTTACACTGAAAGCTGT	1023
Db	901	TTTAAAGTTTCCCGCACTTCCAGAGGCTGGGTATCTGGGGTACCCCTTAAGAGCTGT	960
OY	1024	GCTTCCGACTGGGCTTCTTCTTCTCCCTCAACATGAGGCATCATCTTTTGCACAT	1083
Db	961	GCATCAGAACTGGGCTTCTGTGCTTTTCTCTCACAATGGGTATCATTTTGGTAC	1020
OY	1084	GTCATGTTTATGCGGAGAAAGGCTCTCGGCGACAGAGTTCAACAAGATCCCTGCTCG	1143
Db	1021	GTTATGTTTATGCGGAGAAAGGCTCTTACACAAAGATTACACAGATCCCGGCAACC	1080
OY	1144	TTTTGTATCACCATTTGTACATGACACACTGGGATCTAGGAGACATGTGCTTAAAGC	1203
Db	1081	TTTGTGTATCACCATGTGACCATGACAACTGCGGGTATGGCGACATGTATCAAAAAAC	1140
OY	1204	ATTGCAAGGAAAGATTTGCGCTCATCTGTCTTGAATGCGCGTCTGTCAATTGCGCTG	1263
Db	1141	ATAGCAGGGAAGATTTTGGGCTCATCTGTCACTAGACCGGAGTCTTGTGATTTGCGCTA	1200
OY	1264	CGAGTCCCTGATTTGTTTCCACTTTTACCGGATTAACAACGAATACAGAGGCTGAT	1323
Db	1201	CCCGTCTGTGATGTGTGCACTTCACTGATGAGATCTTACACCAAAACAAACGAGCAAC	1260

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Db	1321	GCAAAATGCTCATGACAGAGCAAGCGGAATGGGTCTATGAGCAACAGCT---GAGANN	1377
OY	1444	GGCACCCCAAGAGAGAGCACATGGGCAAGACCACTCATCTCATGAGAGCCAGCATCAT	1503
Db	1378	NN	1437
OY	1504	CACCTGCTGCACCTGCTGGAAAAACAACCTAACACAGAGTTATGTAGCAGATGTTT	1563
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OY	1804	GCAGACGACGAGCTGAGACCAAACTGCAAAACATCCAGATCACCAAGCCATCATGAC	1863
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DEFINITION	Homo sapiens KCND1 gene, VIRUTAL TRANSCRIPT, partial sequence.				
ACCESSION	AY408063				
VERSION	AY408063.1	GI:39764034			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1944)				
REFERENCE	Clark,A.G., Gliadowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T. J., Sninsky, J. J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1944)				
AUTHORS	Clark,A.G., Gliadowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T. J., Sninsky, J. J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them on alignment.				
FEATURES	Location/Qualifiers				

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DB 121 GTTCTGGTGAAGTGAAGCGGAGCGGCTTTGAGACTTGAAGATACGCTGGACGCG 180
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RESULT 9  
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LOCUS  
DEFINITION Mus musculus KCNDB1 gene, VIRUTAL TRANSCRIPT, partial sequence,

genomic survey sequence.  
ACCESSION AY408065  
VERSION AY408065.1 GI:39764036  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 1956)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,D.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source location/Qualifiers  
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Best Local Similarity 68.1%; Pred. No. 3e-174;  
Matches 1257; Conservative 0; Mismatches 550; Indels 39; Gaps 9;  
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LOCUS	AY06813
DEFINITION	Pan troglodytes KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY06813
VERSION	AY06813.1
KEYWORDS	GI:39762784
SOURCE	GSS.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Pan troglodytes Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Pan.
AUTHORS	1 (bases 1 to 1893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trices
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1893)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
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QY	133 CCGGTGGCGCAACTGCCCATGCCCTGGCGCCC---GGCCGACAGAAACGCGGAGAGAT 189       
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QY	310	AAGAGTACTTCTTTCGACCGGGAACCCGAGGTTCCGCTGCGTCAACTTCTTACCGC	369
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QY	370	ACGGGGAAGCTGACCTACCCGCGCTACGAGTGATCTTGCTTACGACGACGACTGGCC	429
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Db	841	GACATATGAGACGTCAAGGAGCTTTGTCAACTCGAAGTCTTCGGGTCTTCAGATC	900
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Db	1021	NN	1080
QY	1144	TTTTTGTAACCAATTGTCAACCATACCAACTGGGATTCGGAACATGTGTCTTAAGCG	1202
Db	1081	NN	1140
QY	1204	ATTGACAGGAAGATCTTCGCTCATCTGCTCTTGAATGCGTCTGTCAATGGCCCTG	1262
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Db      1201 CCGGTCCTGGTGTATGATCACTTCACTGATCAACCAAGATCAACAGCAGAC 1260
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DEFINITION Pan troglodytes KCDN1 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION AY408064
VERSION AY408064.1 GI:39764035
KEYWORDS GSS.
SOURCE  Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
REFERENCE 1 (bases 1 to 1939)
AUTHORS  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
        Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
        Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,
        Adams,M.D. and Cargill,M.
        Inferring nonneutral evolution from human-chimp-mouse orthologous
        gene trios
        Science 302 (5652), 1960-1963 (2003)
JOURNAL 14671302
PUBMED  2 (bases 1 to 1939)
REFERENCE  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
AUTHORS  Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
        Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,
        Adams,M.D. and Cargill,M.
        Direct Submission
        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
        Rockville, MD 20850, USA

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COMMENT  This sequence was made by sequencing genomic exons and ordering
FEATURES  them based on alignment.
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ORIGIN
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Best Local Similarity 56.1%; Pred. No. 4,1e-146;
Matches 1053; Conservative 0; Mismatches 786; Indels 39; Gaps 6;

Qy      73 ATGGCGGCGGAGTGGGCGCTGGCTCTTTGGCCGGGCTGGCGGCAATCGGATGAG 132
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Qy      133 CCGGAGCAACTGCCCCATGCCCCCTGGCCCGGCGGCAAGAAAGAGAGATGAG 192
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Qy      193 CTGATTGCTCAAGTGAAGTGGGCGGAGGTTCAAGCTGAGAGCAAGCTGAGCGC 252
Db      121 GTTCTGTGTGAACGTGAGCGGACCGCTTTGAATGGAAGATAGCTGAGCCG 180
Qy      253 TACCGGAGACCCGTGGGGAGAGAGGAGGAGGATTTCTTCAACAGAGCAACAAG 312
Db      181 TACCAAGATACCTTGGGAGAGCTGGAGAGGAAATTTCTTCAAGATGTGACTAGG 240
Qy      313 GAGTACTTCTGACCGGAGACCCCGAGTGTTCGCTGCTGCTCAATTTCAACGAG 372
Db      241 GAGTACTTTTGTGATGGACACCTGACATGTTCCGCAATGTGTGAATTCNAACGAG 300
Qy      373 GGAAGCTGACTACCCGGGCTAGAGATGATCTGTGCTTACAGACAGAGCTGGCTTC 432
Db      301 GGGCGGCTGACTGCGCAAGGAGATGATCAAGGCTTCAAGCAAGAGCTGGCTTTC 360
Qy      433 TAGGATCTCTCCGAGATCATCGGGGAC-----TGCTGTACGAGAG 477
Db      361 NNNNNNCGGTTCCAGAGTGTGTCGTTGACNNNNNNNNNNNNNNNNNNNNNNNNNN 420
Qy      478 TACAAGACCGCAAGAGGAGAAAGCGGAGGCTCATGAGCAACAAGCTCGAGAAC 537
Db      421 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480
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Db      481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540
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Db      841 GTGCCAAGAGAGAGATGTCTGTGGCCGCTTTGTCACCCCTGCTGTGTCCGGGTGTT 900
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Db      901 CGCATCTTCAAGTTTCCAGGACCTCACAGGGCTTGAGGATCTGGGGCTACACACTCAAG 960
Qy      1018 AGCTGTGCTCCGAGCTGGGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1077
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Qy      1378 GGCAGTTGATGATCTTACCTGACAGCAGCAGCGGCTCTCAACGAGCGCTGGAG 1437
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Qy      1438 CTGACGGGACCCGAGAGAGAGAGACATGGGCAAGACCACTCACTATGAGAGCCAG 1497
Db      1372 AGCGGAGTGGCGAGGAAAGAGGCTTTTGTGTGACGAAACGTTCTGCTTTGAAAGCA 1431
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RESULT 12

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LOCUS      AK033805      3302 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
            library, clone:9230112B12 product:potassium voltage-gated channel,
            Shal-related family, member 1, full insert sequence.
ACCESSION  AK033805
VERSION    AK033805.1 GI:26329482
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS    Carninci, P. and Hayashizaki, Y.
TITLE      High-efficiency full-length cDNA cloning
JOURNAL    Meth. Enzymol. 303, 19-44 (1999)
MEDLINE    99279253
PUBMED     10349636

REFERENCE
AUTHORS    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
            Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL    Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE    20499374
PUBMED     11042159

REFERENCE
AUTHORS    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
            Kono, H., Akiyama, J., Nishi, K., Kitenai, T., Tashiro, H., Itoh, M.,
            Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A.,
            Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,
            Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohta, B., Watanabe, M.,
            Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J.,
            Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multipillar sequencer
JOURNAL    Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE    20530913
PUBMED     11076861

REFERENCE
AUTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE      Functional annotation of a full-length mouse cDNA collection
JOURNAL    Nature 409, 685-690 (2001)
MEDLINE    11706861
PUBMED     11076861

REFERENCE
AUTHORS    The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE      Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL    Nature 420, 563-573 (2002)
MEDLINE    12000000
PUBMED     12000000

REFERENCE
AUTHORS    Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
            Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
            Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
            Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
            Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
            Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
            Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
            Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
            Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
            Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
            Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
            Muramatsu, M. and Hayashizaki, Y.
TITLE      Direct Submision
JOURNAL    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216]
COMMENT    cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:<http://genome.gsc.riken.jp/>  
URL:<http://fantom.gsc.riken.jp/>

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## ORIGIN

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QY	1458	GGAGCCATATGGGGCAAGAACCACTCACTCATCGAGGCGAGCATCATACCTGCTGCACTG	1517
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QY	1869	CACCTCCCCCAGCGCTAACCCCAAGG	1894
Db	1375	CACCCCCCTGCGCAACAGCCAGATG	1400

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED		
1	Roest Croollius,H., Jalllon,O., Dasliya,C., Bouneau,L., Fisher,C., Bernot,A., Fzames,C., Wincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissbach,J.	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence	Nat. Genet.	25 (2), 235-238	(2000)	2	Roest Croollius,H., Jalllon,O., Dasliya,C., Ozouf-Costez,C., Fzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	Genome Res.	10 (7), 939-949	(2000)		
3	(bases 1 to 993)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
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399	GTGCATCTCTGCTCAACGAGACGAGAGTGGCTTCTACGAGCATCTCCCGAGATCATCGG	399	GTGCATCTCTGCTCAACGAGACGAGAGTGGCTTCTACGAGCATCTCCCGAGATCATCGG	399	GTGCATCTCTGCTCAACGAGACGAGAGTGGCTTCTACGAGCATCTCCCGAGATCATCGG	399	GTGCATCTCTGCTCAACGAGACGAGAGTGGCTTCTACGAGCATCTCCCGAGATCATCGG	399	GTGCATCTCTGCTCAACGAGACGAG				

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Dd		576	TACGGCCAATGATAAAACAAGTCCGTGTGAAGAACCGCTACACGGTAGCGTTCTTTCAT	517
Oy		759	GCA CAGCAGCGGCGCTCATMGATCTTTCACCGTAAGAGTACTCTCTGGGCGCTTTCCGAGCTCC	818
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Oy		819	CAGCCGGCTACCGCTTTCATCCGCAACCGTCATGAGCATCATGACGTGTGGCCATCATGCC	878
Dd		456	TAGCCGTTTACCGCTTTATGCGCTCGGTGATGAGATCATTTGACGTGATGGCANTCGGCC	397
Oy		879	CTACTCATATGGTCTGTGATCATGACCAAACAAGAGACGTGTCCGGCGCTTTCGTACGCT	938
Dd		396	CTACTCATATGGCTGTGTGATGACCAAACAAGAGACGTGAGCGGCGCTTTCGNTNC-NI	338
Oy		939	CCGGGCTTCOCGCGTTCACGAGATCTTCAGTTTTTCCCAGCACCTCCAGGGGCGTGGCGAT	998
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Oy		999	CTTGGGCTAACACACTGAAAGCTGTGGCTCCGA ACTGGGCTTTCTTCTTCTCCCTCAC	1058
Dd		277	CTTGGGCTAACACGCTCAAAAAG-TGGCGCTGGAGCTGGGCTTCTGCTCTTCTCCCTCAC	219
Oy		1059	CATGGCATCATCATCTTTTGGCACTGTGATGTTTATATGCGAAGAGGGCTTCTGGCGAG	1118
Dd		218	CATGGCATCATCATCTTCCGCACCGCTACGATGTTCTACGCGAAGAAAGATCCAGCTCCAG	159
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Dd		98	GTGAGTA 92	
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM		AL267651 AL267651.1 GI:7989467  GSS; genome survey sequence. Tetradon nigroviridis Tetradon nigroviridis Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percnomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetradodon.		
REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED		1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesse,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)		
AUTHORS		2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Co스타z,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,U. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
JOURNAL MEDLINE PUBMED		20359837 10899143 3 (bases 1 to 1054) Genoscope. Direct Submission		
REFERENCE TITLE		3 Genosope. Direct Submission		

**JOURNAL**

Submitted (12-APR-2000) Genoscope - Centre National de séquençage  
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequefgenoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetraodon>.

## FEATURES

**Bouyce**

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Db	830	RACGGGCTCATATCTCTCAACGTGAGCGGAGCAAGTTTCAGAGTGTGGCAACACTTTGG	771
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Db	710	ACGAATGAGTACTTTTTCGACCGGACCCCGACATCTTTAGGACATCTGAATTTTTC	651
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QY	427	GCCTTCAGGGCATCTCCCGGAGTCAATCGGGGACGTGCTGTACGAGAGTCAAGAGAC	486
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RESULT 15	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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		CH230-39G12, genomic survey sequence.					
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			Bz203918				
			Bz203918.1	GI:23861970			
			GSS.				
			Rattus norvegicus (Norway rat)				
			Rattus norvegicus				

## FEATURES

**Source**

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Pietter de Jong"

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**ORIGIN**

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|||||  
|||  
**Dd** 2 GGCGAATTGCTGCTTAGAGAGATCAA-TACCGCAAGCGGGAGAAAGCTGAAGCGGCTCATG 60  
|||||  
|||  
**Oy** 517 GACGACAAAGATCTCGGAGAACAAACCGAGAGTTCATGCCCCCTCGCTCAGCTTCGCGCAGACC 576

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Db	121	ATGTGGCGGGCTTTGAGAAACCCCAACGACGCTGGCCCTGGCTTTCTACTAGTG	180
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Db	181	ACAGGCTTCTCATGCTGTCTGGGTATCAACGATGGTGGAGACGGTGGCCATGCGGC	240
Qy	697	ACGGTCCCGGAGCAAGAGCTGGCGGAGCGCTACTCGGTGACCTTCTTCTGC	756
Db	241	ACGGTCCCGGAGCAAGAGCTGGCGGAGCGCTACTCGGTGACCTTCTTCTGC	300
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Db	301	CTGACACAGGCGGTGCTATGATCTTCAACGATGACCTTCTGGGCTTTCCGGGCA	360
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Job time : 6059.92 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:58:11 ; Search time 107.56 Seconds  
(without alignments)  
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Title: US-10-062-879-2

Perfect score: 3412  
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Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Issued Patents AA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
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2	3403	99.7	US-09-142-791A-4	Sequence 4, Appli
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4	3291.5	96.5	US-09-142-791A-2	Sequence 2, Appli
5	3265.5	95.2	US-09-142-791A-6	Sequence 6, Appli
6	2498.5	73.2	US-09-949-016-6828	Sequence 6828, Ap
7	2102	61.6	US-09-336-643A-10	Sequence 10, Appli
8	846	24.8	US-09-949-016-8327	Sequence 8327, Ap
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APPLICANT: Cockett, Mark I.									
APPLICANT: Dilks, Daniel W.									
APPLICANT: Chang Ling, Hwai-ping									
APPLICANT: Sokol, Patricia T.									
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and									
FILE REFERENCE: ahp-98089									
CURRENT APPLICATION NUMBER: US/09/178,109									
CURRENT FILING DATE: 1998-10-23									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: Patent In Ver. 2.0									
SEQ ID NO 2									
LENGTH: 655									
TYPE: PRT									
ORGANISM: human									
US-09-178-109-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 2e-318;									
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QY	1	MAAGVAAWLPFARAALIGMW	FPARAAIGMFPVANC	PMPLADADKXKODELIV	NVSGRRFQWRTTLER	60			
DB	1	MAAGVAAWLPFARAALIGMW	EVANCPMLADADKXKODELIV	NVSGRRFQWRTTLER	60				
QY	61	YPTDILGSTEKEFPENDEK	YFPDRDDEVRCVLPFRGK	LHYPRECI	SAVDELAF	120			
DB	61	YPTDILGSTEKEFPENDEK	YFPDRDDEVRCVLPFRGK	LHYPRECI	SAVDELAF	120			
QY	121	YGILPEIIGDCVEYEDRKE	NAERLMDDDSENNOESM	PSLFFQRTMRAFENP	HTST	180			
DB	121	YGILPEIIGDCVEYEDRKE	NAERLMDDDSENNOESM	PSLFFQRTMRAFENP	HTST	180			
QY	181	LALVYYVTGTFVAVITN	VEVTPCGTVGSKELP	CGERYVAFFCLDTAC	WIFVE	240			
DB	181	LALVYYVTGTFVAVITN	VEVTPCGTVGSKELP	CGERYVAFFCLDTAC	WIFVE	240			
QY	241	YLALFPAASRYRIRSV	MSIIDVAIMPYIGV	WNNNEVDVSAFVTL	RVRFRJFKF	300			
DB	241	YLALFPAASRYRIRSV	MSIIDVAIMPYIGV	WNNNEVDVSAFVTL	RVRFRJFKF	300			
QY	301	SRHSQGRILIGYTLKSC	ASELGLFLFSLTMAI	IIIFATVFAEKGSSAK	STSIIPASFWY	360			
DB	301	SRHSQGRILIGYTLKSC	ASELGLFLFSLTMAI	IIIFATVFAEKGSSAK	STSIIPASFWY	360			

Qy	36	TIYMTTLTIGDMVPTIAGKIFGSI	CSLSGYVLALPVPIVNSFSTIYHONRADKR	420
Db	361	TIYMTTLTIGDMVPTIAGKIFGSI	CSLSGYVLALPVPIVNSFSTIYHONRADKR	420
Qy	421	AOKKARIARIVAKTSSNAYLH	SKRGNLNALELTGTPREEHMGKTTSLIESQHLL	480
Db	421	AOKKARIARIVAKTSSNAYLH	SKRGNLNALELTGTPREEHMGKTTSLIESQHLL	480
Qy	481	HCEKTTGSLYVDDPLSVRTSTI	KNEFIDEQFEDQNCMESSMONTSPRSPSLSSHP	540
Db	481	HCEKTTGSLYVDDPLSVRTSTI	KNEFIDEQFEDQNCMESSMONTSPRSPSLSSHP	540
Qy	541	GLTTTCCSRRSKKTTHLPNSNL	PATRLRSMOELSTIHIQGSBQPSLTTSRSLSLKADKG	600
Db	541	GLTTTCCSRRSKKTTHLPNSNL	PATRLRSMOELSTIHIQGSBQPSLTTSRSLSLKADKG	600
Qy	601	LRPNCKTSOITTLIISITPPAL	LPREGSRPPASPGNTNIPSTISVNVVYSVL	655
Db	601	LRPNCKTSOITTLIISITPPAL	LPREGSRPPASPGNTNIPSTISVNVVYSVL	655

## RESULT 2

```

US-09-142-791A-4
Sequence 4, Application US/09142791A
Patent No. 6368823
GENERAL INFORMATION:
APPLICANT: Antoine Michel Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Fais
APPLICANT: Jean-Luc Jayve
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 655
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-4

```

Query Match	99.7%	Score 3403	DB 3	Length 655
Best Local Similarity	99.7%	Pred. No. 1.6e-317		
Matches 653	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

Qy	MAAGVAAAMLPBAAAALIGMMVPANCGMPLAPADKXKRODELVLVNSGRRCQMTTLR	60
Db	1 MAAGVAAAMLPBAAAALIGMVPANCMPLAPADKXKRODELVLVNSGRRCQMTTLR	60
Qy	YPTDLGSTEKEFPENEDTKEYEFPDRPVEFVCVINFYRTGKLHYPREYCISAAYDELAIF	120
Db	61 YPTDLGSTEKEFPENEDTKEYEFPDRPVEFVCVINFYRTGKLHYPREYCISAAYDELAIF	120
Qy	YGLPELIIIGBCCYEKYDKRREBAERLMDNDSENNOSEMPLSFRCQMMAPAFENPHST	180
Db	61 YGLPELIIIGBCCYEKYDKRREBAERLMDNDSENNOSEMPLSFRCQMMAPAFENPHST	180
Qy	YGLPELIIIGBCCYEKYDKRREBAERLMDNDSENNOSEMPLSFRCQMMAPAFENPHST	180
Db	121 YGLPELIIIGBCCYEKYDKRREBAERLMDNDSENNOSEMPLSFRCQMMAPAFENPHST	180
Qy	LAAYFYVYTGFLAVSVIYNVETVPCGVPSKELPCGERISVAFPCFLDPAACMIPTVE	240
Db	181 LAAYFYVYTGFLAVSVIYNVETVPCGVPSKELPCGERISVAFPCFLDPAACMIPTVE	240
Qy	YLLRLFAAPSRYAFIRISVMSIIDVVAIMDYIIGLVMTNNEDVSGAFVTLRAFRVFRLEPKF	300

Db	241	YLLRLFAARSRRPFRISWMSIIDVALMPYIIGLVWNINNEDVSAFVTLNVPVFRIFKE	300
Qy	301	SRHSQGLRIILGTYLLKSCASELGEFLLSLTMAIIIPATVMTAEKGSASAKFTSIPASFWY	360
Db	301	SRHSQGLRIILGTYLLKSCASELGEFLLSLTMAIIIPATVMTAEKGSASAKFTSIPASFWY	360
Qy	361	TIYVMTTLTGVMVWPKTAGKIFGSGISGLSVLIALPVPIVSNFRIRIHNORADKRR	420
Db	361	TIYVMTTLTGVMVWPKTAGKIFGSGISGLSVLIALPVPIVSNFRIRIHNORADKRR	420
Qy	421	AQKKAFLAIRVAKTGSSNAYLHSHRNQILNEALELGTPEEHEMGKTSILIESQHHL	480
Db	421	AQKKAFLAIRVAKTGSSNAYLHSHRNQILNEALELGTPEEHEMGKTSILIESQHHL	480
Qy	481	HCLKTKTGLSYLVDDPLLSVSTSIKNEHFIDEQMFQNCMESSMUNYPSIRSPSLSPH	540
Db	481	HCLKTKTGLSYLVDDPLLSVSTSIKNEHFIDEQMFQNCMESSMUNYPSIRSPSLSPH	540
Qy	541	GLTLTTCSSRSKKTTHLPNSNIPARLASMDELSTIHQSGEOPSLTTSRSSLNLRADDG	600
Db	541	GLTLTTCSSRSKKTTHLPNSNIPARLASMDELSTIHQSGEOPSLTTSRSSLNLRADDG	600
Qy	601	LRPNCKTSQITTAIISIPTPPALTPEGESRPPAPSPGNTNIPISITSNVAVSVL	655
Db	601	LRPNCKTSQITTAIISIPTPPALTPEGESRPPAPSPGNTNIPISIANVAVSVL	655

### RESULT 3

```

US-09-178-109-4
: Sequence 4, Application US/09178109
: Patent No. 6395477
: GENERAL INFORMATION:
: APPLICANT: Cockett, Mark I.
: APPLICANT: Dilks, Daniel W.
: APPLICANT: Chang, Ling, Hui-Ping
: APPLICANT: Sokol, Patricia T.
: TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
: FILE OF INVENTION: Polypeptides and Uses Therefor
: FILE REFERENCE: ahp-98089
: CURRENT APPLICATION NUMBER: US/09/178,109
: CURRENT FILING DATE: 1998-10-23
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 636
: TYPE: PRT
: ORGANISM: human
US-09-178-109-4

```

Query Match	96.7%	Score 3300.5	DB 3	Length 636
Best Local Similarity	97.1%	Pred. No. 1.1e-307		
Matches 636, Conservative	0	Mismatches 0	Indels 19	Gaps 1

Qy	1	MAGVAAAMLPEPRAAALIGMPYANCPMLAPADKKODELITYANSGRRPQMTTLER	60
Dp	1	MAGVAAAMLPEPRAAALIGMPYANCPMLAPADKKODELITYANSGRRQMTTLER	60
Qy	61	YPDTLTGSTEKEKEFFFNEDTEKEFFPQDEVEPRCVLNFRTGKJLHPREYCISAYDELAF	120
Dp	61	YPDTLTGSTEKEKEFFFNEDTEKEFFPQDEVEPRCVLNFRTGKJLHPREYCISAYDELAF	120
Qy	121	YGLLPETIDGCCYEEKKDKRKRNARLMDNDSENKQSSMPSLSFRQTMRAPENPHTST	180
Dp	121	YGLLPETIDGCCYEEKKDKRKRNARLMDNDSENKQSSMPSLSFRQTMRAPENPHTST	180
Qy	181	LALVFYVYTGFFIAVSVINVEVETPCGVSGSKELPCGERYSVAFFCLDTCACMIPTVE	240
Dp	181	LALVFYVYTGFFIAVSVINVEVETPCGVSGSKELPCGERYSVAFFCLDTCACMIPTVE	240
Qy	241	YLRLRLAASRRFRFRSVNSIIDVAALMPYITGLVMTNNEVSGAFPLRFRFRFLFKF	3000
Dp	241	YLRLRLAASRRFRFRSVNSIIDVAALMPYITGLVMTNNEVSGAFPLRFRFRFLFKF	3000

```

Qy 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIFATMFAEKGSSASKFTSIPASFWY 360
|
Db 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIFATMFAEKGSSASKFTSIPASFWY 360
Qy 361 TIVMTTLGYDMPVKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
|
Db 361 TIVMTTLGYDMPVKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
Qy 421 AOKARLARIRVAKTGSSNAYLHRSKRGLEALFELGTPEEHMGKTTSLIESQHLL 480
|
Db 421 AOKARLARIRVAKTGSSNAYLHRSKRGLEALFELGTPEEHMGKTTSLIESQHLL 480
Qy 481 HCEKTTGLSVLDVDPILSVRTSTIKNHEFIDEQMFONCMESSMONTPTSRPSLSHP 540
|
Db 481 HCEKTTGLSVLDVDPILSVRTSTIKNHEFIDEQMFONCMESSMONTPTSRPSLSHP 521
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSLNLKADG 600
|
Db 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSLNLKADG 581
Qy 601 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGNTNIPSTSNVAVSVL 655
|
Db 582 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGNTNIPSTSNVAVSVL 636

```

RESULT 4  
US-09-142-791A-2  
Sequence 2, Application US/09142791A  
Patent No. 6368823

```

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmejs
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-2

```

Query Match 96.5%; Score 3291.5; DB 3; Length 636;  
Best Local Similarity 96.8%; Pred. No. 7.9e-307;  
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

```

Qy 1 MAAGVAAAMLPPARAALIGMVPVANCMPMLAPADKNKRODELIIVNVSGRRQTRTTLER 60
|
Db 1 MAAGVAAAMLPPARAALIGMVPVANCMPMLAPADKNKRODELIIVNVSGRRQTRTTLER 60
Qy 61 YPDTLLGSTEKEPFENEDTEKEYFFDRDDEVEFRCVLNFRTGKLHYPRYECISAYDELAIF 120
|
Db 61 YPDTLLGSTEKEPFENEDTEKEYFFDRDDEVEFRCVLNFRTGKLHYPRYECISAYDELAIF 120
Qy 121 YGIIPEITIGDCCYEYKORKEBNARLMDNDSENNSQMSPLSRQTMFAFENPHTST 180
|
Db 121 YGIIPEITIGDCCYEYKORKEBNARLMDNDSENNSQMSPLSRQTMFAFENPHTST 180
Qy 181 LALFVYVTVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTCVMIPTVE 240
|
Db 181 LALFVYVTVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTCVMIPTVE 240

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Db 181 LALFVYVTVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTCVMIPTVE 240
|
Qy 241 YLNLFPAPSRIRYRIRSYMSIIDVAIMPYITGLVMTNNEVSGAFYTLRFRFRIFKE 300
|
Db 241 YLNLFPAPSRIRYRIRSYMSIIDVAIMPYITGLVMTNNEVSGAFYTLRFRFRIFKE 300
Qy 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIFATMFAEKGSSASKFTSIPASFWY 360
|
Db 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIFATMFAEKGSSASKFTSIPASFWY 360
Qy 361 TIVMTTLGYDMPVKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
|
Db 361 TIVMTTLGYDMPVKTIAGKIFGSI CSLSGVLVIALPVPIVSNFSRIYHONQADRR 420
Qy 421 AOKARLARIRVAKTGSSNAYLHRSKRGLEALFELGTPEEHMGKTTSLIESQHLL 480
|
Db 421 AOKARLARIRVAKTGSSNAYLHRSKRGLEALFELGTPEEHMGKTTSLIESQHLL 480
Qy 481 HCEKTTGLSVLDVDPILSVRTSTIKNHEFIDEQMFONCMESSMONTPTSRPSLSHP 540
|
Db 481 HCEKTTGLSVLDVDPILSVRTSTIKNHEFIDEQMFONCMESSMONTPTSRPSLSHP 521
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSLNLKADG 600
|
Db 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEQPSLTTSRSLNLKADG 581
Qy 601 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGNTNIPSTSNVAVSVL 655
|
Db 582 LRPNCKTSQITTAIISIPTPPALTPEGESRPPASPGNTNIPSTSNVAVSVL 636

```

RESULT 5  
US-09-142-791A-6  
Sequence 6, Application US/09142791A  
Patent No. 6368823

```

GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmejs
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-6

```

Query Match 95.7%; Score 3265.5; DB 3; Length 636;  
Best Local Similarity 96.2%; Pred. No. 2.5e-304;  
Matches 630; Conservative 1; Mismatches 5; Indels 19; Gaps 1;

```

Qy 1 MAAGVAAAMLPPARAALIGMVPVANCMPMLAPADKNKRODELIIVNVSGRRQTRTTLER 60
|
Db 1 MAAGVAAAMLPPARAALIGMVPVANCMPMLAPADKNKRODELIIVNVSGRRQTRTTLER 60
Qy 61 YPDTLLGSTEKEPFENEDTEKEYFFDRDDEVEFRCVLNFRTGKLHYPRYECISAYDELAIF 120
|
Db 61 YPDTLLGSTEKEPFENEDTEKEYFFDRDDEVEFRCVLNFRTGKLHYPRYECISAYDELAIF 120
Qy 181 LALFVYVTVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTCVMIPTVE 240
|
Db 181 LALFVYVTVGFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFCLDTCVMIPTVE 240

```

Qy	12	YGLPEIIGDCCCEBXKDKRENAERLMDNDSENNKSSMPSLSPROMWPAFENPNTST	160
Db	121	YGLPEIIGDCCCEBXKDKRENAERLMDNDSENNKSSMPSLSPROMWPAFENPNTST	160
Qy	181	LALVFFVYVYGFIAVSITNVVEITVPDGTVPDGSKELPCEERYSAVAFCLDTACVMIETVE	240
Db	181	LALVFFVYVYGFIAVSITNVVEITVPDGTVPDGSKELPCEERYSAVAFCLDTACVMIETVE	240
Qy	241	YLLRLFAPEBYAFIRSVMSIIDVAIMPYUIGLMTNNEDSGAFVTLRFRVYERFLFK	300
Db	241	YLLRLFAPEBYAFIRSVMSIIDVAIMPYUIGLMTNNEDSGAFVTLRFRVYERFLFK	300
Qy	301	SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIPATVWFAEKSSASKETSIPASFWY	360
Db	301	SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIPATVWFAEKSSASKETSIPASFWY	360
Qy	361	TIYMTMTLIGDMPVPTIAGKI FGSICSLGYVALRVPVYVSPSTIYNONRADRR	420
Db	361	TIYMTMTLIGDMPVPTIAGKI FGSICSLGYVALRVPVYVSPSTIYNONRADRR	420
Qy	421	AOKKARLARIRAVAKTSSSNAYLHYSKKNGLNLEALFELGTPEBEHNGKTTSLIESQHNL	480
Db	421	AOKKARLARIRAVAKTSSSNAYLHYSKKNGLNLEALFELGTPEBEHNGKTTSLIESQHNL	480
Qy	481	HCELEKTTGSLVLDDELVSVRTSTIKNHFIDBQMFQONCMHSSMONTPTSTRSSLSHP	540
Db	481	HCELEKTT-----NHFIDBQMFQONCMHSSMONTPTSTRSSLSHP	521
Qy	541	GLTWTCCSRKSKTTHLPNSNLPATRLRMOELSTIHIQGSBQPELITRSLSLMLKADG	600
Db	522	GLTWTCCSRKSKTTHLPNSNLPATRLRMOELSTIHIQGSBQPELITRSLSLMLKADG	581
Qy	601	LRPNCKTSQTTTAAIISITPPPALTPBGESEPPPAAPGPTNIPSTSNVAVYSVL	655
Db	582	LRPNCKTSQTTTAAIISITPPPALTPBGESEPPPAAPGPTNIPSTSNVAVYSVL	636

```

RESULT 6
US-09-949-016-6828
Sequence 6828, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6828
LENGTH: 630
TYPE: PRT
ORGANISM: Human
US-09-949-016-6828

```

Query Match	73.2%;	Score 2498.5;	DB 4;	Length 630;
Best Local Similarity	73.6%;	Pred. No. 1.1e-230;		
Best Match	486;	Conservative 69;	Mismatches 70;	Indels 35;
				Gaps 7;

QY 1 MAAGAAAMLPFARAAAIIGMVPANCMPLAPADKNR - ODEI.VLVNLSGRFPTMRTTLE 59  
DB 1 MAAGAAAMLPFARAAAIIGMVPANCMPLAPADKNR - ODEI.VLVNLSGRFPTMRTTLE 60  
QY 60 RYPTDILGSTETKEFFPNEDTKETFFPRDDEVFVCVNFRTGKLTHTPRYCISATYDELA 119  
DB 61 RYPTDILGSTETKEFFPNEDTKETFFPRDDEVFVCVNFRTGKLTHTPRYCISATYDELA 120

QY	120	YUGLPEIIGOCCEEYEDRKRENERLMDUDSNMOS -NPSLSFRTIMRAFENPRT	178
Db	121	FFGLIPETIGOCCEEYEDRRRENNERLODDADDTDTAGESALPMTARQVRVRAFENPRT	180
QY	179	STLAVFYVYTGFFIAVSITNVVETVPQGVPS -KELPCGERYSVAFFCLDTACWTF	237
Db	181	STMLAVFYVYTGFFIAVSIVIANVVEVTPCGSSPGHKEIPCEBRYAVALFCLDTACWTF	240
QY	238	TVEYLLRFEAPSRPRFIRSVMSIIDVAALMPLYGYGLWNTNEDVSGAFVTLRVFPVPI	297
Db	241	TVEYLLRFLAAAPSRPRFIRSVMSIIDVAALPYIYGLWNTNEDVSGAFVTLRVFPVPI	300
QY	298	EKFSHHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAS	357
Db	301	EKFSHHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPAA	360
QY	358	FMYTIVMTTIGYGMVPKTTAGTKFGSICSLGYLVIALPVPVIVSNSRILYHONORD	417
Db	361	FMYTIVMTTIGYGMVPKTTAGTKFGSICSLGYLVIALPVPVIVSNSRILYHONORD	420
QY	418	KRAQOKKARLARIRVAKTGSSNAVLHSKRNGLNTALBELTGPPEEHMKTSLTLESQHN	477
Db	421	KRAQOKKARLARIRVAKTGSSNAVWQSKRNGLSNLOQ -SSDEQOFAVSKGSGSFETOHN	479
QY	478	HLHLEKTTGLSYVDPLSVKSTIKNHFIFIDQMEQOMESBMONYSTBSPIS	537
Db	480	HLHLEKTT-----NHFVEQVFEBSCEMAVATNRPSPHSBPS	520
QY	538	SHPGITTTCCSRRSKKTHLPNSNLPATRLRSMOELSTIHQSGSEOPSLTTRSSJNLKA	597
Db	521	SQGVATSTCCSRRHKHTFRIPAVANSVGHQSGIOELSTIQICVERTPLSNSRSSLNAM	580
QY	558	DDGLRPNCKTISOITAIISIPPPALTBEGSERP--PRASBPGRNIPISITSNVAVYSVL	655
Db	581	EECVATNOEQPVYTAIISIPPPVTTBEGDPRSPSPVSG-----NIVAYSAL	630

```

RESULT 7
US-09-336-643A-10
/ Sequence 10, Application US/09336643A
/ Patent No. 6399761
/ GENERAL INFORMATION:
/ APPLICANT: Miller, Andrew P.
/ APPLICANT: Curran, Mark Edward
/ APPLICANT: Hu, Ping
/ APPLICANT: Rutter, Marc
/ APPLICANT: Wang, Jian-Wang
/ TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
/ FILE REFERENCE: SEQ-15P
/ CURRENT APPLICATION NUMBER: US/09/336,643A
/ CURRENT FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 60/076,687
/ PRIOR FILING DATE: 1998-08-07
/ PRIOR APPLICATION NUMBER: 60/116,448
/ PRIOR FILING DATE: 1999-01-19
/ PRIOR APPLICATION NUMBER: PCT/US99/03826
/ PRIOR FILING DATE: 1999-02-22
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 646
/ TYPE: PR1
/ ORGANISM: H. sapiens
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(646)
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-10

```

Query Match	61.6%	Score 2102	DB 3	Length 646
Best Local Similarity	63.3%	Pred. No. 1.3e192		
Matches 488	Conservative	116	Indels 54	Gaps 14

```

Qy 1 MAAGVAAWLPFARAAAGMMPVANCMPPLAPADKXKRODELLIVANSGRRPOTWTTTLER 60
Db 1 MAAGIATLPLPRAKAAVGMPLPAPQOPLPAPGVKASRGDXVLVAVVSGRRPOTWTTTLER 60
Qy 61 YPDTLLGSTEKEFFENEDTKEYFPDRDPEVPRCVLNFYRTGKLHYPRYECISAYDELAIF 120
Db 61 YPDTLLGSTEKEFFADSDGEFFDRDPDMFRHVLNFRTGKLHCPROECTIOAPBELAIF 120
Qy 121 YGILPEITGDCCYEYKQKKEKNAERLMDNDSENNOGSMESL----SPROTMAFAFNP 176
Db 121 YGILPEITGDCCYEYKQKKEKNAERLMDNDSENNOGSMESL----SPROTMAFAFNP 179
Qy 177 HTSTALAFYVYVTFEIVAVITNVETVPC--GTVPSKELPCGERSVAFECIDTACV 234
Db 180 HTSTALAFYVYVTFEIVAVITNVETVPC--GTVPSKELPCGERSVAFECIDTACV 239
Qy 235 MIFVEYLLRLFAAPSRVFRSVMISIDVVAIMPYVIGLVMTNNEDEVSAGFVTLRVPRV 294
Db 240 LIFGEYLLRLFAAPSRVFRSVMISIDVVAIMPYVIGLVMTNNEDEVSAGFVTLRVPRV 299
Qy 295 FRIFESHSGQRLIGYTLKSCASELGPLLPSLTMAIIPATVNFVAEKSSASKETSI 354
Db 300 FRIFESHSGQRLIGYTLKSCASELGPLLPSLTMAIIPATVNFVAEKSSASKETSI 359
Qy 355 PASFYVITVMTTIGYGMVPRKTAGKIFGICSLGVLVIALPVPVIVNSFRSYHONO 414
Db 360 PASFYVITVMTTIGYGMVPRKTAGKIFGICSLGVLVIALPVPVIVNSFRSYHONO 419
Qy 415 RADKRAQKARLARIRVAKTSSNAVYHSKRNGLNEALETGTPEEHHM-GKITSLE 473
Db 420 RADKRAQKARLARIRVAKTSSNAVYHSKRNGLNEALETGTPEEHHM-GKITSLE 475
Qy 474 SQHHHLHLEKTTGLSYLVDPDLLSVRTSTIKNHEFIDEQMFECNCESSMONTYSTRS 533
Db 476 QOHHLHLLEKTTGLSYLVDPDLLSVRTSTIKNHEFIDEQMFECNCESSMONTYSTRS 515
Qy 534 PLSLSHP-----GLTTCCSRRSK-KTTHLPNSNLPATLRSMOELSTHIGOSEPSLT 588
Db 516 TVSSSQPQPSGLSSCCPRRAKRAIRLANSTASVS-RGMOELDM--LAGLRSHAPQ 572
Qy 589 SRSSINLAKDGLRPNCKTSQITTAIISIPTPALTPGESRPPAPSPG----- 637
Db 573 SRSSINLAKDGLRPNCKTSQITTAIISIPTPALTPGESRPPAPSPG----- 629
Qy 638 PNTNIPSTNSNVKVS 653
Db 630 SSLGTPCLFPETVKIS 645

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RESULT 8
US-09-949-016-8327
; Sequence 8327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: RastSeq for Windows Version 4.0
; SEQ ID NO 8327
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Human

```

```

US-09-949-016-8327
Query Match 24.8%; Score 846; DB 4; Length 260;
Best Local Similarity 60.0%; Pred. No. 1,1e-72;
Matches 174; Conservative 35; Mismatches 49; Indels 32; Gaps 4;
Qy 368 LGYGMVPRKTAGKIFGICSLGVLVIALPVPVIVNSFRSYHONORADRRKQKARL 427
Db 1 LRGDMVPKTIAGKIFGICSLGVLVIALPVPVIVNSFRSYHONORADRRKQKARL 60
Qy 428 ARIRVAKTSSNAVYHSKRNGLNEALETGTPEEHHMGTSLIESQHHLHLEKETT 487
Db 61 ARIRVAKTSSNAVYHSKRNGLNEALETGTPEEHHMGTSLIESQHHLHLEKETT 119
Qy 488 GLSYLVDPDLLSVRTSTIKNHEFIDEQMFECNCESSMONTYSTRSPLSHPGLITTC 547
Db 120 -----NHFPVDEQVFEESSCMEVATVNPSSHSPSLSSQGVTSYCC 160
Qy 548 SRSKKTHLPNSNLPATLRSMOELSTHIGOSEPSLTSSRLNKKADGRLPNCKT 607
Db 161 SRHKKTFRIPNANVSGHSGIOELSTIQRCYERKTPLSRSRLNKKADGRLPNCKT 220
Qy 608 SQITTAIISIPTPALTPGESRP--PPASGPNTNIPSTNSNVKVSVL 655
Db 221 PYVTTAIIISIPTPALTPGESRPESPEYSG-----NIVRSAL 260

```

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RESULT 9
US-09-833-466-13
; Sequence 13, Application US/09833466
; Patent No. 6727353
; GENERAL INFORMATION:
; APPLICANT: Jedia, Timothy James
; TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.2
US-09-833-466-13

```

```

Query Match 22.5%; Score 767; DB 4; Length 806;
Best Local Similarity 27.5%; Pred. No. 2,7e-64;
Matches 223; Conservative 115; Mismatches 243; Indels 230; Gaps 27;
Qy 27 MFLPAD--KKKRODELLIVANSGRRPOT-WRTTLERYPDTLLG-----STEKEFF---- 74
Db 20 LPPRPVILIRSKTCSRKRVKINVGILNHEVLMR-TLDRLPRTLKLDKDCVTHESLBYCD 78
Qy 75 -FNDTKEYFPDRDPEVPRCVLNFYRTGKLHYPRYECISAYVDDLAHYGLPELIGCCY 133
Db 79 DYNLNENEYFPDRDPEVPRCVLNFYRTGKLHYPRYECISAYVDDLAHYGLPELIGCCY 138
Qy 134 EYVDK-----RENAERLMDNDSENNOGSMESLSPROTMAFAFNPSTLALVY 186
Db 139 ARYHQKQNMWELRRAETMRDGEPEPNTCCPDR--AKKLDLLEKPNSSVAAKTIA 196
Qy 187 YVTFEIVAVITNVETVPC--GTVPSKELPCGERSVAFECIDTACVMTFTV 239
Db 197 IVSILFTVLTALSTLMTPELOETDERGQINDRQLA-----HVEAVCIAMFTM 246
Qy 240 EYLLRLFAAPSRVFRSVMISIDVVAIMPYVIGLVMTNN-----EDVSGAFVTLRVF 292

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Db 247 EYLLRFSSPPKKMKFFGPNLVNIDLALIPYYVITFLESNNKSVLQFQVRBRVQJPRIM 306
Qy 293 RVFFIFEFPSRHSQGLRILGTYLKSASBELGFLPSLTMAIIPATYMPFAEKGSSAKST 352
Db 307 RILRILILAKHSSTGLSLGFTLRSSVNELOLLILFLAMGMIMFSSLVFPAEKOEDBATKPT 366
Qy 353 SIPASFYTYVYMTTGLSYGDMVPRTAGKIFGSIIGSLGVLVYALBPVYISNFSRIYQ 412
Db 367 SIPASFMYATITMTTVYIGDIYFKTLIGKIVGGICCIAGVLYALBPIIYVNNFSEFYK 426
Qy 413 NORADKRAOKKARLARIRVAKTS-----SNAYLHSKRNGULNEALELGT-----T 459
Db 427 QKQKEK---AIKREALERAKNGSIVSMVLKDAFARSMH-LIDVAVEKAGSANTKOS 481
Qy 460 PEEHMGKTTSLBSQHHHLHCLKTKTGSLYVDDPLSIVRTSTIKMHEFIDEOMFEO- 518
Db 482 ADDMH-----LSPSFKMKARKALSETS-----SNKSFENKYOEVSQKSHEDL 524
Qy 519 -NCMESSMNVPSRSPSL-----SSHPC-----LTTTCCSR 550
Db 525 NNTFSSPPHLSAQKLEMLYNEITKQPHSHPNPDQEKPERPSAYEEIEEMEYVVCPE 584
Qy 551 S-----KKT-----THLNSNLPATRLSMOELSTIHQSEQ-- 583
Db 585 QLAVAQTEVIVDMKSTSSIDSPSCANDPFIETERSPLPPPSASHLQMKPTDLPGTEHQ 644
Qy 584 -----PSLITTSR-----SSL 593
Db 645 RARGPPELTLSREKGPARDOTLEAVAPDITVNLDAAGSQCGLHSPLOQDNATDPSKSL 704
Qy 594 -----NLKADDGLRPCKTS-----QITTAIISTPPAL-----TPBEE 628
Db 705 KGSNPLKSRSLKVNFKENKGSAPOTPESTARPLPVTTADFSLTPPHISTILLETBPSQG 764
Qy 629 SRP-----PPASPGENTNI 642
Db 765 DRPCWALRFQRLVADLEPKGCPBPFSANCSL 795

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RESULT 10  
US-09-833-466-12

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; Sequence 12, Application US/09833466
; Patent No. 6727353
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv1.1, a No. 6727353el Voltage-Gated Potassium Channel From
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.1
; US-09-833-466-12

```

Query Match	21.8%;	Score	742.5;	DB	4;	Length	854;	
Best Local Similarity	29.1%;	Pred. No.	6.7e-62;					
Matches 194;	Conservative	115;	Mismatches	213;	Indels	143;	Gaps	20

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OY      27 MLLAPAD-KNKQDELIYANSGRRFQT-WRTLEPYDTLTG-----STEKEFF----- 74
Db      12 LPPPEMVEIISKACSRRLVNVGLAHEVLWR-TLDRLPRTLGLKRDONTHDSLLEYCD 70
OY      75 -FNEDTKEYFPDRDPEVFRCVLNFYRGTKLHYRVCEISAYNDELAFYGLIPETIGDCCY 133
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Dd 71 DYSLDNDNEFFDRHPGAFSTSLNFYRTRGLHMMEMCALSFSGQEDLWNGIDEBIYESCCQ 130
Qy 134 BEYDRKRENNERLMDNDNSENNQE-----SMPLSFQOTMRRARENHTSLALVFYVY 188
Dd 131 ARYHQKQOMNEELKREARELTREBBGEFNDTTCBAEKKKQKJLDLEKPNSSAAAKILAIT 190
Qy 189 TGFEIASVTINNVETVPCGTVPQSGKEBPCGERYSVA-----FFCLDPAWVIFVEYDL 243
Dd 191 SIMTIVISTILSLNTLP-----ELQSIDEFQGSIDNQGLAHVAEAVCIAMFMEBYL 242
Qy 244 RLPAAPSRYPFIRSVMSIIDVAIMPYITGLVMTN-----EDVSGAFVTLRVFRVFR 296
Dd 243 RFLSPKMKWKFQGPLNADILALIPYVITFLTESNKSVLQFQVVRVRYOJFRIMRILR 302
Qy 297 IFRSRSQGLRILIGYTLKSCASEGLPFLSLTMAIIFATVMPFYAKGSSASKFTSIPA 356
Dd 303 ILKARSHSTGLQSGFTLRRSYNELGILLPLANGIMFSSVLFPAEKDEDDEDTKKSIPA 362
Qy 357 SFWTYITVMTLGYGDWVPKTIAGKIFGSI CSLSGVLYALPVPIVANSFRKIYHONORA 416
Dd 363 SFWMATIMTIVGVGDIYPKTLILGKIYGLCLCIGVLYALPIPIIVNNFSFYMEQKRQ 422
Qy 417 DXRPAQKKARLARIRVAKTGSSNAYLSKRGCL-----NEALELTGPREEBH 464
Dd 423 EKAKIRREA-LEP-----AKRNGSIVSNMKDAFARSIEMDIVVERKNGN 467
Qy 465 MGTITSLIESOHHLHLEKTYTGLSYLVDPBLSVPTSIKNHFIDEQMEQNCMESS 524
Dd 468 MGKDKDV---ODNHLSPPWKMKWTKRT-----LS-ETSSSKS-----FETK 503
Qy 525 MONYPSTRSPSLSHPGLLTTCSCSRRSKKTTHLPNSNLPAFLRSMOELSTHIOGSEOP 584
Dd 504 EQGSPBK-----ARSSSPQHL-----NVQGLEDMVYNKTAKTQSQP 539
Qy 585 SLTTRSSSLNKADGGLRPNCKTSQITTAIISIPPLATPBGESRPPASGCPMNTIYS 644
Dd 540 ILNKTESAQSKPKREL-----EMESISFVPAP-----LPT 570
Qy 645 ITSNVY 650
Dd 571 RTEGVI 576

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RESULT 11  
US-09-275-252A-6  
; Sequence 6, Application US/09275252A

```

: Patent No.6664197
: GENERAL INFORMATION:
: APPLICANT: Mackinnon, Roderick
: APPLICANT: The Rockefeller University
: TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
: TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
: TITLE OF INVENTION: Channel Proteins, and Uses Thereof
: FILE REFERENCE: 018512-002901US
: CURRENT APPLICATION NUMBER: US/09/275, 252A
: CURRENT FILING DATE: 1999-03-24
: PRIOR APPLICATION NUMBER: US 09/045, 529
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: US 09/054, 347
: PRIOR FILING DATE: 1998-04-02
: PRIOR APPLICATION NUMBER: WO PCT/US99/06307
: PRIOR FILING DATE: 1999-03-22
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 858
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-275-252A-6

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Query Match	21.8%	Score 742.5	DB 4	Length 858
Best Local Similarity	29.1%	Pred. No. 6.7e-62		
Matches 194	Conservative 116	Mismatches 213	Indels 143	Gaps 20

```

QY 27 MFLPAD--KXKQDELIVLVSGRRPQT-WRTLLERYPDLLG-----STEKEFF----- 74
DB 16 LPPEMEIVLRKASRRRLVNGVLAHEVLMR-TLDRLPRLRLKDCNTHDSLLEYCD 74
QY 75 -FNEDTKEVFPDRDPEVFRVCLNFYRTGKLHYPRYECISAYDDELAIFYGILPEIIGDCCY 133
DB 75 DYSLDNNEVFPDRHGAFTSLINFRIGRLHMEMECALSSQELDVYGIIDEIYESCCQ 134
QY 134 EBYDKRRENAERLMDNDSENNOE-----SNPISLFRQTMRAFENPHSTLALVFFYV 188
DB 135 ARYHQKEQNMKEBKRBAETLREREGGEFDMTCCAEKSKKMLDLEKPNSSVAAKILAI 194
QY 189 TGFPIAVSVTNVETVPCGVPSKELPCGERYSVA-----FCLDPAQWIFVEYLL 243
DB 195 SIMFIVSTIALSNLTP-----ELQSLDEFGQSTDNPOLAHEVAVCIAMFMEYLL 246
QY 244 RLFAAPSRFRFRSVMSIIDVVAIMPYIIGLVMTNN-----EDVSGAFVTLRFRVFR 296
DB 247 RLFSPPKMKKFFKGPLNADILALIPYVITFLTESNKSVDLOFQVRRVVOQIFRIMRLR 306
QY 297 LFKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPA 356
DB 307 ILKLARHSTGLQSIGFTLRRSYNELGILLFLAMGIMIFSSLVFPAEKDEDDTKFKSIPA 366
QY 357 SFWYTIYMTLIGYDGMVPKTIAGKIFSGISLSGVVIALPVPIYVNSFRITHQONORA 416
DB 367 SFWYTIYMTVGYDIPKTLIGIVGLCCICAGVIALPIPIVNNFSEFYKEOKRQ 426
QY 417 DKRAOKKARLARIVAKTSSNAYLHSGRNGLL-----NEALELTGPPEEH 464
DB 427 EKAKRREA-LER-----AKRNGSIVSMNMKDAFARSIMMOIVVEKNGEN 471
QY 465 MGTTSLSIESQHHLHLCLEKTTGLSYLVDDPLLSVTSITIKNHEFIDEQMFQONCMSS 524
DB 472 MGKDKV---QDNHLSPKMKWTKRT-----LS-ETSSSKS-----PFTX 507
QY 525 MONTPTSRPSLSHPGLTTCCSRKSKTTHLPNSNIPATRLRMQELSTIHIQSSQP 584
DB 508 EOGSPER-----AKSSSSPQHL-----NVQOLEMNYMKMAKTOSQP 543
QY 585 SLTTSRSSILNKADGLRPNCKTSQITAIISIPTPALTPGESRPPASGPENTIPS 644
DB 544 ILNKESAAQSKPEEL-----EMESIPSPVAD-----LPT 574
QY 645 ITSNV 650
DB 575 RTEGVI 580

RESULT 12
US-08-464-340A-13
; Sequence 13, Application US/08464340A
; Patent No. 5710019
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,340A

```

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; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-464-340A-13

Query Match 21.2%; Score 724; DB 1; Length 539;
Best Local Similarity 33.0%; Pred. No. 1.9e-60;
Matches 163; Conservative 98; Mismatches 165; Indels 68; Gaps 13;

QY 27 MFLPAD--KXKQDELIVLVSGRRPQT-WRTLLERYPDLLG-----STEKEFF----- 74
DB 15 LPPEMEIVLRKASRRRLVNGVLAHEVLMR-TLDRLPRLRLKDCNTHDSLLEYCD 73
QY 75 -FNEDTKEVFPDRDPEVFRVCLNFYRTGKLHYPRYECISAYDDELAIFYGILPEIIGDCCY 133
DB 74 DYSLDNNEVFPDRHGAFTSLINFRIGRLHMEMECALSSQELDVYGIIDEIYESCCQ 133
QY 134 EBYDKRRENAERLMDNDSENNOE-----SNPISLFRQTMRAFENPHSTLALVFFYV 189
DB 134 ARYHQKEQNMKEBKRBAETLREREGGEFDMTCCAEKSKKMLDLEKPNSSVAAKILAI 193
QY 190 GFTFAVSVTNVETVPCGVPSKELPCGERYSVA-----FCLDPAQWIFVEYLLR 244
DB 194 IMFIVSTIALSNLTP-----ELQSLDEFGQSTDNPOLAHEVAVCIAMFMEYLLR 245
QY 245 LFAAPSRFRFRSVMSIIDVVAIMPYIIGLVMTNN-----EDVSGAFVTLRFRVFR 297
DB 246 FLSSPPKMKKFFKGPLNADILALIPYVITFLTESNKSVDLOFQVRRVVOQIFRIMRLR 305
QY 298 LFKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKSSASKFTSIPA 357
DB 306 ILKLARHSTGLQSIGFTLRRSYNELGILLFLAMGIMIFSSLVFPAEKDEDDTKFKSIPA 365
QY 358 SFWYTIYMTLIGYDGMVPKTIAGKIFSGISLSGVVIALPVPIYVNSFRITHQONORA 417
DB 366 SFWYTIYMTVGYDIPKTLIGIVGLCCICAGVIALPIPIVNNFSEFYKEOKRQ 425
QY 418 KRAOKKARLARIVAKTSSNAYLHSGRNGLL-----NEALELTGPPEEH 465
DB 426 KAKRREA-LER-----AKRNGSIVSMNMKDAFARSIMMOIVVEKNGEN 470
QY 466 GKTTSLSIESQHHL 479
DB 471 GKDKV---QDNHL 481

RESULT 13
US-09-336-643A-4
; Sequence 4, Application US/09336643A
; Patent No. 639761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Ruter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 639761el Human Potassium Channels

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FILE REFERENCE: SEQ-15P  
CURRENT APPLICATION NUMBER: US/09/336,643A  
CURRENT FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 60/076,687  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 60/116,448  
PRIOR FILING DATE: 1999-01-19  
PRIOR APPLICATION NUMBER: PCT/US99/03826  
PRIOR FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 601  
TYPE: PR1  
ORGANISM: H. sapiens  
US-09-336-643A-4

Query Match 21.1%; Score 720.5; DB 3; Length 601;  
Best Local Similarity 31.8%; Pred. No. 4,9e-60;  
Matches 192; Conservative 102; Mismatches 221; Indels 89; Gaps 15;

40 ELIVLVNSGRFRQWRTTLERYPDTLL-----GSTKEFFFNEDTKEYF 83  
8 EKIIIVGGRHREYRSTLTLPETRLAMLADPDGGRPEPTDGGVSSSGGCGCEFF 67  
84 FDDDEVEYFCVNLFFRTGKLHYPRYECISAYDELAFFYGLPELIGDCYEEYKRRREN 143  
68 FDRHGVFAVVLNYYRTGKLHCPADVCGPLFEEELAFWGLDETDEVCMMYV--RQHRD 125  
144 AERLM-----DDNSEN-----NQESMPSLS-----FRQTMRAFEN 175  
126 AERLADIFETPDLLIGDPGDEDLAAKRLGIEDAAGGDPGSGKGRMRRLQPRMMLFED 185  
176 PHTSTLALVYVYVYGFPIAVSVITNVETVPCGVSPSKELPCGERYSV-----A 225  
186 PYSSRAARFAFASLFFILVSIITTCLETHAFAIVAKTEPVINGSVLQYEIETDPA 245  
226 PFCIDTACWIFVVEYLLRLFAAPSRYRFRSVMSIIDVVAIMPYI-----GLVMTNNE 280  
246 LTVYEGVCVWFPEFELVRLVFSNKLFIKLNLIIDFVALIPFYLEVGLSGLSKAAK 305  
281 DVGAFATLAVFRVFRFKFSRHSQGLRIIGYTKASASLGLFBSLTMALIIIFATVMF 340  
306 DVGFLRVFRVRLRIFKLRHFVGLRVGLHTLRASITNEFLLIIFLAGVLIIFATMIY 365  
341 YAEK-----GSSASKFTSIPASFWYTIIVMTTGYGDMVPKTIAGKIPSGISLGS 391  
366 YAEVGAQPDPSASEHTQFNKLPIDGFWAVVMTTILGIDMTPTQISGLVGLCALAG 425  
392 LVVIALFVPIVSNFRIYHONRADRRARQAKRLARIRVAKTGSSNAYLSHRKGLLN 451  
426 VLTAMFVPIVNNFG--MYSLAMAKQKLPKRKK--HIPAPASSPTCKTELMNACN 482  
452 EALBELTPEEEMHAKTSLIESQHHLHLEKTTGLSTLVDDP--LLSVRTSTIKNHEF 510  
483 -----STQSDTCIGKDNRLLE--HNRSVLSGSDSTSEPLPRLPRRSSTRDKNR 534  
511 IDEOMF-----EQNCMESSMOWNPSTRSPSLSHPGLTTCGSRRSKKTTHLPPNSNPAT 565  
535 RGETCFLLTTGDTYTCASDGGIRKYEKRSILNLAGLN--ALRLSPVTSPTNSPCPLR 592  
566 RLRS 569  
593 RSRs 596

RESULT 14  
US-09-275-252A-4  
Sequence 4, Application US/09275252A  
Patent No. 6641997  
GENERAL INFORMATION:  
APPLICANT: MacKinnon, Roderick  
APPLICANT: The Rockefeller University

TITLE OF INVENTION: Assays for Screening Compounds which Interact With  
TITLE OF INVENTION: Cation Channel Proteins, Mutant Probabiotic Cation  
TITLE OF INVENTION: Channel Proteins, and Uses Thereof  
FILE REFERENCE: 018512-002901US  
CURRENT APPLICATION NUMBER: US/09/275,252A  
CURRENT FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: US 09/045,529  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: US 09/054,347  
PRIOR FILING DATE: 1998-04-02  
PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
PRIOR FILING DATE: 1999-03-22  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 616  
TYPE: PR1  
ORGANISM: Drosophila melanogaster  
US-09-275-252A-4

Query Match 21.0%; Score 715.5; DB 4; Length 616;  
Best Local Similarity 31.7%; Pred. No. 1.5e-59;  
Matches 173; Conservative 105; Mismatches 153; Indels 115; Gaps 15;

40 ELIVLVNSGRFRQWRTTLERYPDTLLGSTKEF--FNEEDTKEYFPDDEVEYFCVNLFF 98  
97 ERVIVNSGLREBETQRLTINQPDLLGDPARLRFRYDLRHEFFDRSRPSFDALYY 156  
99 RT--GKLHYPRYECISAYDELAFFYGLPELIDGCCYEEYKRRKRAELMDNSENNO 157  
157 QSGGRLLRPVNPDLVFSSEIKFYB-----LGDQALNKRE-----DEGFIKEE 201  
158 ESMPSLSFRQTMRAFENPHTSTLALVYVYVYGFPIAVSVITNVETV-----206  
202 RPLPDHEKRWKWLFEYBESSQAARVVAIIISFVLLSIVIFCLETLEBFHXYKVENTT 261  
207 -CGTVPSKELPCGERYSVAFCLDTACWIFVVEYLLRLFAAPSRYRFRSVMSIIDV 265  
262 TNGTKIEDEVP---DITDPFELIETLCIWFTEFELTVFLACPKNLNCRDVMNVIDI 318  
266 AIMPYIIGLV-----WNNEDVSGARV--TLRVFRIRIFKFSRH 303  
319 AIIPIYITLAVVAREEDTLNPKAVSPQDKSSNQAMSLALIRVLRVFRIFLGRH 378  
304 SOGLRIIGYTKASASLGLFBSLTMALIIIFATVMFVAEKSSASKFTSIPASFWYTI 363  
379 SKGLQILGHTLAKAMELGLIIFELFIVGLVSSAYFAFASSENSFFSIPDAFWAVY 438  
364 TMTTGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPIVSNFRIYHONRADRRARQ 423  
439 TMTTVGYGDMTPVGFNGKIVGSLCVIAGVLTIALPVPIVSNFNYFYHREADREEMQSON 498  
424 KALARIIRVAKTGSSNAYL-----HSKRNGL-----INELBELTPEEEMHAKT 468  
499 FNVH-----TSCSYLPGALGOHLKKSJSESSSDIMDDGDATTPGLTDTGR 548  
469 TSLIESQHHLHLEKTTGLSTLVDDPPLSVRTSTIKNHEFIDEOMFQNCMESSMOWN 528  
549 -----HMV-----PFL--RT-----QGSFEKQQLQDLQLO 572  
529 PSTRSP 534  
573 QGQOSP 578

RESULT 15  
US-09-949-016-8164  
Sequence 8164, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastseq for windows Version 4.0
; SEQ ID NO 8164
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8164

```

```

Query Match      20.9%; Score 713.5; DB 4; Length 552;
Best Local Similarity 33.9%; Pred. No. 2e-59;
Matches 167; Conservative 96; Mismatches 160; Indels 69; Gaps 12;

```

```

QY 18 GMPVANC-----EMP--LAPADKKRDELIVANSGRPPQWRTTIERYPDTLL 66
Db 48 GAPQGGCGGGCGCDRYEPLPSLPAAAGQDCGGERVINISGLRFETOLKTLCPETLL 107
QY 67 GSTEKEF-FENEDTKEYEFDSDPEVRCVLPNRYRT-GKLHYPRYECISAYDELAFYGL 124
Db 108 GDPKRRMYFDFPLNRNPSFDALYYQGGRIIRPVNPVIDIFSEIRFYQ-- 165
QY 125 PEIIGDCCYEYKDKRENARLMDNDSENNQESMPSLSPROTWMRAFENPHTSLALV 184
Db 166 ---LGEEMKEFRE-----DEGFLREERPLPRRDFOQVWLLFEYPSSGPARG 212
QY 185 FYYVTGFFIAVSVTNNVETVPCGTVPSKELPC-----GER----YSV 224
Db 213 IAIYSVILILISIVFCLETLP--EPRDEKDYPASTQDSFEAGNSTSGRAGASPSFD 270
QY 225 AFPLCDTACVMIFTEVEYLLRLPAASRYRFRSVMSIIDVVALMPYIIGLVW-----T 277
Db 271 PFVVEITCIIMFSEFELLVRFACPSKATFSRNIMNLIIDIVALIPYFITLGTELAERQGN 330
QY 278 NNEDEVGAFV-TLRVFRVRIFFKFSRHSQGLRIIGYTLKSCASELGFLLFSITMAIIIPA 336
Db 331 GQQAASLAILRLVIRLVRFRIFFKLSRHSKGLIIGQTLKASRELGLIFFLFIVILFS 390
QY 337 TWMFYAEKSSASKFTSIPASFWYTIVTMTLGYGDMVPKTIAGKIFGSIKSLGVLVIA 396
Db 391 SAVYFAEADDEPTSGFSSIPDAFMWAVVMTVTGYGDMHPVTIGKIVGSLCAIAGVLTIA 450
QY 397 LEPVPIVSNFSRIYHONRADKRR-----AQKKARLARIYVAKTGSSNAYLHSHK 445
Db 451 LEPVPIVSNFNYFYHRETEGEGSQYMHVGSQHLSSAEBLRKARNSNTLSKSEYVIE 510
QY 446 RNLGLNLEALLET 457
Db 511 EGGMNHSAFPQT 522

```

Search completed: April 6, 2005, 07:21:28  
 Job time : 110.56 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: April 6, 2005, 00:35:45 ; Search time 497.211 Seconds  
(without alignments)  
509.498 Million cell updates/sec

Title: US-10-062-879-2  
Perfect score: 3412  
Sequence: 1 MAAGVAAWLPFRARAAATGWM.....RGPNTNPSITSNVKVSVL 655

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3412	100.0	655	5	ABB79584 Human Kv4
2	3403	99.7	655	2	AAW79590 Human Kv
3	3403	99.7	655	8	ADFE91398 Wild-type
4	3396	99.5	655	7	ADD48188 Rat Prote
5	3395	99.5	655	4	ADSI16294 Human vol
6	3391	99.4	655	4	AAAB86321 Human Kv4
7	3300.5	96.7	636	5	ABB79585 Human Kv4
8	3291.5	96.5	636	2	AAW79589 Human Kv
9	3265.5	95.7	636	2	AAW79591 Human Kv
10	3035.5	89.0	611	7	ADBE61252 Rat Prote
11	2498.5	73.2	630	7	ADMI0929 Human O64
12	2498.5	73.2	630	7	ADMI0928 Human O64
13	2498.5	73.2	630	7	ADMI0930 Human O64
14	2498.5	73.2	630	7	ADMI0927 Human O64
15	2498.5	73.2	630	8	ADJ11257 Human ova
16	2498.5	73.2	630	8	ADJ11260 Human ova
17	2498.5	73.2	630	8	ADJ11258 Human ova
18	2498.5	73.2	630	8	ADJ11259 Human ova
19	2498.5	73.2	630	8	ADJ11256 Human ova
20	2498.5	73.2	630	8	ADM43520 Human ova
21	2498.5	73.2	630	8	ADM43519 Human ova
22	2498.5	73.2	630	8	ADM43521 Human ova
23	2496.5	73.2	630	8	ADM43518 Human ova
24	2493.5	73.1	629	4	AAV13523 Amino aci
25	2113	61.9	647	4	AAAB86319 Human Kv4
					AAAM25597 Human pro

26	2108	61.8	646	4	AAAB86318 Human Kv4
27	2102	56.6	646	2	AAV34123 Human pot
28	1937.5	51.8	571	4	ABB71722 Drosophi1
29	894	26.2	217	4	AAAB86320 Human Kv4
30	869	25.5	214	2	AAV13524 Amino aci
31	825	24.2	255	7	ADMI0926 Human O64
32	825	24.2	255	8	ADJ11256 Human ova
33	825	24.2	255	8	ADM43517 Human ova
34	767	22.5	806	7	ADJ79875 CIRA_huma
35	755.5	22.1	911	7	ADJ69676 Human hea
36	748.5	21.9	985	8	ADJ30147 Drosophi1
37	748.5	21.9	985	8	ADJ30143 Drosophi1
38	746	21.9	149	8	ADJ25645 Voltage-g
39	742.5	21.8	854	6	ABP58354 Human pot
40	742.5	21.8	854	7	ADJ79874 CIRA_huma
41	742.5	21.8	858	2	AAV32015 Human cat
42	742.5	21.8	858	5	AAO17058 Human KCN
43	742.5	21.8	858	5	ADJ38328 Human cat
44	742.5	21.8	985	4	ABB57774 Drosophi1
45	741	21.7	853	7	ADBE63538 Rat Prote

## ALIGNMENTS

RESULT 1  
ABB79584  
ID ABB79584 standard; protein; 655 AA.  
XX  
XX ABB79584;  
XX  
XX 01-OCT-2002 (first entry)  
XX  
XX Human Kv4.3 potassium channel (long form).  
XX  
XX Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;  
XX  
XX nootropic; neuroprotective; cardiac; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US6395477-B1.  
XX  
XX 28-MAY-2002.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX (AMHP) AMERICAN HOME PROD CORP.  
XX  
XX Cockett MI, Dilks DW, Ling HC, Sokol PT;  
XX  
XX WPI; 2002-556093/59.  
XX  
XX N-PSDB; ABB84400.  
XX  
XX New isolated polynucleotide encoding human Kv4.3 potassium channel  
XX  
XX polypeptide, useful as probe in a diagnostic method for detecting nucleic  
XX  
XX acid encoding human Kv4.3, and for treating Alzheimer's and heart  
XX  
XX diseases.  
XX  
XX Claim 1; Col 16-20; 19pp; English.  
XX  
XX The present sequence is the protein sequence of the long isoform of novel  
XX  
XX human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been  
XX  
XX identified: the present full-length form (hKv4.3 long); and a second form  
XX  
XX (see ABB79585), which has a deletion of 19 amino acids in the carboxy  
XX  
XX domain after the predicted sixth transmembrane domain (hKv4.3 short).  
XX  
XX Human heart primarily expresses hKv4.3 long, whereas human brain contains  
XX  
XX both forms. The invention provides Kv4.3 polypeptides, polynucleotides,  
XX  
XX and methods for producing these polynucleotides. The Kv4.3 polypeptides  
XX  
XX and polynucleotides are useful in the diagnosis, treatment and screening  
XX  
XX of human diseases relating to an excess or deficiency of hKv4.3 activity,  
XX  
XX including Alzheimer's disease and heart disease

XX Sequence 655 AA;  
SQ

Query Match 100.0%; Score 3412; DB 5; Length 655;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGVAAALPFAARAAALGMPPVANCMPPLAPADKKNKRODELIYLVNSGRRFQRTWRTLLER 60  
DB 1 MAAGVAAALPFAARAAALGMPPVANCMPPLAPADKKNKRODELIYLVNSGRRFQRTWRTLLER 60

QY 1 YPDTLLGSTEKEEFFNEDTKKEYFFDRDPEVFRCLNPFRTGKLHYPRYCISAYDDELAF 120  
DB 61 YPDTLLGSTEKEEFFNEDTKKEYFFDRDPEVFRCLNPFRTGKLHYPRYCISAYDDELAF 120

QY 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNQESMPSLSFQRTWRAENPHST 180  
DB 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNQESMPSLSFQRTWRAENPHST 180

QY 181 LALVFYVYTGFFIAVSVITNVVETVPCGTVPGSKELPCGERSVAFFCLDTACVMIFTYE 240  
DB 181 LALVFYVYTGFFIAVSVITNVVETVPCGTVPGSKELPCGERSVAFFCLDTACVMIFTYE 240

QY 241 YILRLFAAPSRPRFIRSVMSIIDVVAIMPYYIGLVMTNNDVSGAFVTLRFVFRIFKE 300  
DB 241 YILRLFAAPSRPRFIRSVMSIIDVVAIMPYYIGLVMTNNDVSGAFVTLRFVFRIFKE 300

QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360

QY 361 TIVMTTLGVDWVPKTIAGKIFGSIKSGVLVIALPVPVIYNSFRIVHONQADKRR 420  
DB 361 TIVMTTLGVDWVPKTIAGKIFGSIKSGVLVIALPVPVIYNSFRIVHONQADKRR 420

QY 421 AOKKARLARIKVAKTGSSNAYLHSKRNGLANEALTLGTPEEBHMGKTTSLIESQHHL 480  
DB 421 AOKKARLARIKVAKTGSSNAYLHSKRNGLANEALTLGTPEEBHMGKTTSLIESQHHL 480

QY 481 HCELEKTTGLSYLVDPLSVRTSTIKNHEFIDEOMFQNCMESSOMYPTSTRSPSLSSHP 540  
DB 481 HCELEKTTGLSYLVDPLSVRTSTIKNHEFIDEOMFQNCMESSOMYPTSTRSPSLSSHP 540

QY 541 GLTITCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEBPSLTSTRSSINLKADG 600  
DB 541 GLTITCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQSEBPSLTSTRSSINLKADG 600

QY 601 LRPNCKTSQITTAIISITPPALTPBEGSRPPASPGPNTNIPSTISNVKVSYL 655  
DB 601 LRPNCKTSQITTAIISITPPALTPBEGSRPPASPGPNTNIPSTISNVKVSYL 655

RESULT 2  
AAW79590  
ID AAW79590 standard; protein; 655 AA.  
XX  
AC AAW79590;  
XX  
DT 11-JAN-1999 (first entry)  
XX  
DE Human Kv potassium channel hkv4.3 (longer isoform).  
XX  
KM Potassium channel; Kv; hkv4.3; human; Alzheimer's disease; arrhythmia;  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 488..506  
XX /note="extra residues of longer hkv4.3 isoform"  
PN W09842833-A2.  
XX

PD 01-OCT-1998.  
XX  
XX 23-MAR-1998; 98WC-EF001901.  
PR 27-MAR-1997; 97GB-00006377.  
PR 09-DEC-1997; 97BP-00402971.  
PR 11-DEC-1997; 97EP-00403007.  
XX  
XX (SMIX ) SMITHKLINE BEECHAM LAB PHARM.  
PI Br11 AMa, Calmele TPG, Falvire JSP, Javre J, Rouanet S;  
XX  
XX WPI, 1998-542277/46.  
DR N-PSDB; AAV61572.  
XX  
XX  
XX New potassium channel polypeptides, hkv4.3 - and hkv4.3-encoding  
PT polynucleotide(s) useful in the treatment of disorders including cardiac  
PT arrhythmias and Alzheimer's disease.  
XX  
XX  
XX Claim 2; Page 26-27; 47pp; English.  
XX  
XX This is the amino acid sequence for an isoform of human Kv potassium  
CC channel hkv4.3. The sequence was deduced from an isolated hkv4.3  
CC polynucleotide (see AAV61572), and has 97% identity with rat Kv4.3.  
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all  
CC Kv family related proteins. A shorter isoform (see AAW79589) has been  
CC identified, which lacks amino acid residues 488-506 of the longer  
CC isoform. The invention relates to hkv4.3 polypeptides and  
CC polynucleotides, and to methods for producing such polypeptides by  
CC recombinant techniques. hkv4.3 polypeptides can be used to identify  
CC agonists and antagonists of hkv4.3 and to raise specific antibodies. Also  
CC claimed are methods for utilizing such agonists and antagonists for the  
CC treatment of subjects in need of enhanced or reduced activity or  
CC expression of hkv4.3 polypeptide. These include the treatment of cardiac  
CC arrhythmias and Alzheimer's disease. The invention can also be used to  
CC detect disease associated with inappropriate hkv4.3 expression or  
CC activity  
XX  
SQ Sequence 655 AA;  
Query Match 99.7%; Score 3403; DB 2; Length 655;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAGVAAALPFAARAAALGMPPVANCMPPLAPADKKNKRODELIYLVNSGRRFQRTWRTLLER 60  
DB 1 MAAGVAAALPFAARAAALGMPPVANCMPPLAPADKKNKRODELIYLVNSGRRFQRTWRTLLER 60

QY 61 YPDTLLGSTEKEEFFNEDTKKEYFFDRDPEVFRCLNPFRTGKLHYPRYCISAYDDELAF 120  
DB 61 YPDTLLGSTEKEEFFNEDTKKEYFFDRDPEVFRCLNPFRTGKLHYPRYCISAYDDELAF 120

QY 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNQESMPSLSFQRTWRAENPHST 180  
DB 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNQESMPSLSFQRTWRAENPHST 180

QY 181 LALVFYVYTGFFIAVSVITNVVETVPCGTVPGSKELPCGERSVAFFCLDTACVMIFTYE 240  
DB 181 LALVFYVYTGFFIAVSVITNVVETVPCGTVPGSKELPCGERSVAFFCLDTACVMIFTYE 240

QY 241 YILRLFAAPSRPRFIRSVMSIIDVVAIMPYYIGLVMTNNDVSGAFVTLRFVFRIFKE 300  
DB 241 YILRLFAAPSRPRFIRSVMSIIDVVAIMPYYIGLVMTNNDVSGAFVTLRFVFRIFKE 300

QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360

QY 361 TIVMTTLGVDWVPKTIAGKIFGSIKSGVLVIALPVPVIYNSFRIVHONQADKRR 420  
DB 361 TIVMTTLGVDWVPKTIAGKIFGSIKSGVLVIALPVPVIYNSFRIVHONQADKRR 420

QY 421 AOKKARLARIKVAKTGSSNAYLHSKRNGLANEALTLGTPEEBHMGKTTSLIESQHHL 480

```

Db 421 AOKKARLARIRIVAKTSSNAYLHRSKNGLNLEALGTGPBEHMGKTTSLIEQHHL 480
Qy 481 HCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSQONTPTSTRSPSLSSHP 540
Db 481 HCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSQONTPTSTRSPSLSSHP 540
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSGSEOPSLTTSRSSLNKADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSGSEOPSLTTSRSSLNKADG 600
Qy 601 LRPNCKTSQITTAIISITPPALTPREGSRPPSPGPNNTIPSTSNVVKVSVL 655
Db 601 LRPNCKTSQITTAIISITPPALTPREGSRPPSPGPNNTIPSTSNVVKVSVL 655

```

RESULT 3  
ID ADF91398 standard; protein; 655 AA.

AC ADF91398;  
DT 26-FEB-2004 (first entry)  
DE Wild-type hkv4.3 #SEQ ID 5.

XX Antiarhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
XX trianquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;  
XX nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
XX blocker; pharmacological; agrochemical; veterinary; arrhythmia;  
XX tachycardia; congestive heart failure; epilepsy; stroke;  
XX traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
XX Parkinson's disease.

XX Homo sapiens.  
XX OS  
XX WO2003097682-A1.

XX 27-NOV-2003.

XX PF 14-MAY-2003; 2003WO-1B002453.

XX PR 15-MAY-2002; 2002GB-00001123.

XX PR 15-MAY-2002; 2002US-0378076P.

XX PR 15-MAY-2002; 2002US-0378131P.

XX PA (DEVG-) DEVGEN NV.  
XX PI Kaletta TJ, Dewulf NE, Plaetinck GKM;

XX WIPI; 2004-061981/06.

XX DR N-PSDB; ADF91397.

XX New nematode worm expressing a heterologous nucleotide sequence encoding  
PT a functional voltage-gated potassium channel of the Kv4 family, useful  
PT for determining compounds that interact with the voltage-gated potassium  
PT channel.

XX Example 1; SEQ ID NO 5; 82pp; English.

XX The invention relates to a nematode worm that expresses a heterologous  
CC nucleotide sequence encoding a functional voltage-gated potassium channel  
CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,  
CC part or fragment. The nematode worm is useful in determining whether a  
CC compound interacts with the voltage-gated potassium channel of the Kv4  
CC family or whether a compound is an agonist, antagonist, opener and/or  
CC blocker of the voltage-gated potassium channel expressed by the nematode  
CC worm. The methods are used for identifying and developing compounds that  
CC interact with voltage-gated potassium channels of the Kv4 family. The  
CC compounds may be used in the development and/or preparation of  
CC compositions for pharmaceutical, agrochemical and/or veterinary use.  
CC These may be used in preparing compositions for preventing or treating  
CC diseases or conditions such as arrhythmia, tachycardia, congestive heart

CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,  
CC Alzheimer's disease or Parkinson's disease. The current sequence  
CC represents wild-type hkv4.3.

XX Sequence 655 AA;

Query Match 99.7%; Score 3403; DB 8; Length 655;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 MAAGVAAWLPRAAAGIOMPEVANCPEPLADKXKQDELIIVNLSGRFRQWTTTLER 60
Db 1 MAAGVAAWLPRAAAGIOMPEVANCPEPLADKXKQDELIIVNLSGRFRQWTTTLER 60
Qy 61 YPDTLLSGTEKEFFPNEDTKYFFDRDPEVRCVLFNFRGKLHYPRFECTSAYDELAF 120
Db 61 YPDTLLSGTEKEFFPNEDTKYFFDRDPEVRCVLFNFRGKLHYPRFECTSAYDELAF 120
Qy 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSPROTMMRAFENPHST 180
Db 121 YGILPEIIGDCCYEYKDKRENAERLMDNDSENNOESMPSLSPROTMMRAFENPHST 180
Qy 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVPGSKEPLCGERYSAVAFCLDTACVMIPTVE 240
Db 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVPGSKEPLCGERYSAVAFCLDTACVMIPTVE 240
Qy 241 YLRLFAAPSRKRYRIRSYMSIIDVAIMPYITGLVMTNNEVSGAFVTLRFRFRIRIKF 300
Db 241 YLRLFAAPSRKRYRIRSYMSIIDVAIMPYITGLVMTNNEVSGAFVTLRFRFRIRIKF 300
Qy 301 SRHSGRLIIGVTLKSCASELGFLLFSLTMAIIFATVMPFAEKSSASKFTSIPASFWY 360
Db 301 SRHSGRLIIGVTLKSCASELGFLLFSLTMAIIFATVMPFAEKSSASKFTSIPASFWY 360
Qy 361 TIVMTTLGYGDMVPKTIAGKIFGSIKSGVLVIALPVPYIVSNFSRIYHONRADRR 420
Db 361 TIVMTTLGYGDMVPKTIAGKIFGSIKSGVLVIALPVPYIVSNFSRIYHONRADRR 420
Qy 421 AOKKARLARIRIVAKTSSNAYLHRSKNGLNLEALGTGPBEHMGKTTSLIEQHHL 480
Db 421 AOKKARLARIRIVAKTSSNAYLHRSKNGLNLEALGTGPBEHMGKTTSLIEQHHL 480
Qy 481 HCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSQONTPTSTRSPSLSSHP 540
Db 481 HCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSQONTPTSTRSPSLSSHP 540
Qy 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSGSEOPSLTTSRSSLNKADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSGSEOPSLTTSRSSLNKADG 600
Qy 601 LRPNCKTSQITTAIISITPPALTPREGSRPPSPGPNNTIPSTSNVVKVSVL 655
Db 601 LRPNCKTSQITTAIISITPPALTPREGSRPPSPGPNNTIPSTSNVVKVSVL 655

```

RESULT 4  
ID ADD48188 standard; protein; 655 AA.

AC ADD48188;  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX Rat Protein AAB53321, SEQ ID NO 13886.  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX Rattus norvegicus.  
XX OS  
XX Unidentified.  
XX WO2003016475-A2.

```

XX 27-FEB-2003.
PD 14-AUG-2002; 2002MO-US025765.
XX
PF 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX (PARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Coetigan M,
XX
XX WPI; 2003-268312/26.
XX GENBANK; AAB53321.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 655 AA;
SQ
Query Match 99.5%; Score 3396; DB 7; Length 655;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 652; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 241 YLRLFAAPSRFRFRSWSIIDVVAIMFYIIGLWMTNEDVSGAFVTLRVRVRIKFX
XX
QY 301 SRHSGRLIGYTLKSCASELGFLLPSLTMATIIIFATWVFYAKGSSASKFSPISAFXY 360
DB 301 SRHSGRLIGYTLKSCASELGFLLPSLTMATIIIFATWVFYAKGSSASKFSPISAFXY 360
QY 361 TIVMTTLLGYGDMVPKTIAGKIFGSI CSLGVLTALPVVIVSNFSRIYHONQADKR 420
DB 361 TIVMTTLLGYGDMVPKTIAGKIFGSI CSLGVLTALPVVIVSNFSRIYHONQADKR 420
QY 421 AOKKARLARIYAKGSSNAYIHSKRNGLNLAELITGPPEEHNGKTSLESQHHL 480
DB 421 AOKKARLARIYAKGSSNAYIHSKRNGLNLAELITGPPEEHNGKTSLESQHHL 480
QY 481 HCLEKTGSLYVDDPLSVRTSTIKNHEFIDEOMEFOKCMSSMQNYSTSPSLSHP 540
DB 481 HCLEKTGSLYVDDPLSVRTSTIKNHEFIDEOMEFOKCMSSMQNYSTSPSLSHS 540
QY 541 GLTTCCSRRSKKTHTLPNSNLPATRLRSMOELSTIHIGSBOPLITRSSSLNKADG 600
DB 541 GLTTCCSRRSKKTHTLPNSNLPATRLRSMOELSTIHIGSBOPLITRSSSLNKADG 600
QY 601 LRPNCTTSQITTAIISIPFPALTPGEGSRPPSPGPTNIPISITSNVYKSVL 655
DB 601 LRPNCTTSQITTAIISIPFPALTPGEGSRPPSPGPTNIPISITSNVYKSVL 655

RESULT 5
ADSI6294
ID ADSI6294 standard; protein; 655 AA.
XX
AC ADSI6294;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human voltage-dependent potassium channel (HsapKv4.3) protein.
XX
XX Voltage-dependent ion channel; drug candidate;
XX aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
XX anticonvulsant; antiarrhythmic; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region /note="Hydrophobic region (S1)"
FT Region /note="Hydrophobic region (S2)"
FT Region /note="Hydrophobic region (S3)"
FT Region /note="Hydrophobic region (S3)"
FT Region /note="Hydrophobic region (S4)"
FT Region /note="Hydrophobic region (S5)"
FT Region /note="Hydrophobic region (S5)"
FT Region /note="Pore region (P)"
FT Region /note="Hydrophobic region (S6)"
XX
PN US2004175761-A1.
XX
PD 09-SEP-2004.
XX
PF 01-MAR-2003; 2003US-00377139.
XX
PR 01-MAR-2003; 2003US-00377139.
XX
PA (MACK/) MACKINNON R.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX

```



PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
 XX WPI; 2004-642122/62.  
 DR GENBANK; AF120491.  
 XX Screening drug candidates that target voltage dependent ion channel  
 PT protein, involves contacting screening protein with chemical compound,  
 PT which is drug candidate and determining whether chemical compound binds  
 PT to screening protein.  
 XX Disclosure; SEQ ID NO 6; 61pp; English.  
 XX  
 CC The invention relates to the composition of matter suitable for use in  
 CC identifying chemical compounds that bind to voltage-dependent ion channel  
 CC proteins. The composition comprises a screening protein that consists of  
 CC an ion channel voltage sensor domain of the ion channel protein  
 CC immobilised on a solid support. The invention is useful for identifying  
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
 CC channel proteins. The drug candidate of the invention is utilised for  
 CC treating a condition mediated by aberrant electrical activity that  
 CC initiates uptake or release of neurotransmitters and contraction of  
 CC muscles. The drug candidate of the invention is also utilised for  
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-  
 CC dependent potassium (Kv) channel protein.  
 CC  
 XX Sequence 655 AA;  
 SO  
 Query Match 99.5%; Score 3395; DB 8; Length 655;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MAAGVAAALPPAPAAALIGMPPVANCMPPLADKKNKODELIVLVNSGRRFQWRTTLIER 60  
 DB 1 MAAGVAAALPPAPAAALIGMPPVANCMPPLADKKNKODELIVLVNSGRRFQWRTTLIER 60  
 QY 61 YPDTLLGSTEKEKFFNEDTKYFFDRDPEVRCVINFRTGKLHPRYECISAYDDELAF 120  
 DB 61 YPDTLLGSTEKEKFFNEDTKYFFDRDPEVRCVINFRTGKLHPRYECISAYDDELAF 120  
 QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 QY 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 DB 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 QY 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 DB 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 QY 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300  
 DB 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300  
 QY 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300  
 DB 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300  
 QY 301 SRHSGRLIILGYLLKSCASELGFLLSLTMAIIPATMFAEKSSASKFTSIPASPMY 360  
 DB 301 SRHSGRLIILGYLLKSCASELGFLLSLTMAIIPATMFAEKSSASKFTSIPASPMY 360  
 QY 301 SRHSGRLIILGYLLKSCASELGFLLSLTMAIIPATMFAEKSSASKFTSIPASPMY 360  
 DB 301 SRHSGRLIILGYLLKSCASELGFLLSLTMAIIPATMFAEKSSASKFTSIPASPMY 360  
 QY 361 TIIVMTTLYGYDMPVKTIAGKIFGSIQSLGVLVIALPVPVIVSNFSRIYHONQADXR 420  
 DB 361 TIIVMTTLYGYDMPVKTIAGKIFGSIQSLGVLVIALPVPVIVSNFSRIYHONQADXR 420  
 QY 361 TIIVMTTLYGYDMPVKTIAGKIFGSIQSLGVLVIALPVPVIVSNFSRIYHONQADXR 420  
 DB 361 TIIVMTTLYGYDMPVKTIAGKIFGSIQSLGVLVIALPVPVIVSNFSRIYHONQADXR 420  
 QY 421 AOKKARLARIRIVATKSSNAVYHRSKRNGLNLEALVLTPTPEEHMGKTSILESHHLL 480  
 DB 421 AOKKARLARIRIVATKSSNAVYHRSKRNGLNLEALVLTPTPEEHMGKTSILESHHLL 480  
 QY 421 AOKKARLARIRIVATKSSNAVYHRSKRNGLNLEALVLTPTPEEHMGKTSILESHHLL 480  
 DB 421 AOKKARLARIRIVATKSSNAVYHRSKRNGLNLEALVLTPTPEEHMGKTSILESHHLL 480  
 QY 481 HCLEKTGTLSTLVDPDLSTVSTTIKNEHFIIDQWFEQNCMESSMONTPTSTSPSLSSHP 540  
 DB 481 HCLEKTGTLSTLVDPDLSTVSTTIKNEHFIIDQWFEQNCMESSMONTPTSTSPSLSSHP 540  
 QY 481 HCLEKTGTLSTLVDPDLSTVSTTIKNEHFIIDQWFEQNCMESSMONTPTSTSPSLSSHP 540  
 DB 481 HCLEKTGTLSTLVDPDLSTVSTTIKNEHFIIDQWFEQNCMESSMONTPTSTSPSLSSHP 540  
 QY 541 GLTTTCCRSRKTTHLNSUNLPATRLASMOELSTIHIQSEFQPSLTSRSLSLNKADG 600  
 DB 541 GLTTTCCRSRKTTHLNSUNLPATRLASMOELSTIHIQSEFQPSLTSRSLSLNKADG 600  
 QY 541 GLTTTCCRSRKTTHLNSUNLPATRLASMOELSTIHIQSEFQPSLTSRSLSLNKADG 600  
 DB 541 GLTTTCCRSRKTTHLNSUNLPATRLASMOELSTIHIQSEFQPSLTSRSLSLNKADG 600  
 QY 601 LRPNCKQTITTAIISIPTPALTPEGSRPPAPGNTNIPSTSNVVKSVL 655  
 DB 601 LRPNCKQTITTAIISIPTPALTPEGSRPPAPGNTNIPSTSNVVKSVL 655

DB 601 LRPNCKQTITTAIISIPTPALTPEGSRPPAPGNTNIPSTSNVVKSVL 655  
 RESULT 6  
 AAB6321  
 ID AAB6321 standard; protein; 655 AA.  
 AC AAB6321;  
 XX 13-SEP-2001 (first entry)  
 DT 13-SEP-2001 (first entry)  
 DE Human Kv4.3 protein.  
 XX Human, Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;  
 KM neurodegenerative disease; ischemia; stroke; Alzheimer's disease;  
 KM Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;  
 KM learning capacity; protein kinase activator; anti-arrhythmic.  
 OS Homo sapiens.  
 XX DE19963612-A1.  
 FN DE19963612-A1.  
 XX 12-JUL-2001.  
 PD 12-JUL-2001.  
 XX 29-DEC-1999; 99DE-01063612.  
 PF 29-DEC-1999; 99DE-01063612.  
 XX 29-DEC-1999; 99DE-01063612.  
 PR 29-DEC-1999; 99DE-01063612.  
 XX (GENI-) FORSCHUNGSEBELSCHAFT GENTON MBH.  
 DR WPI; 2001-426637/46.  
 PT New potassium channel subunit proteins, useful for identifying and  
 PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological  
 PT agents.  
 XX Claim 4; Page 32-33; 50pp; German.  
 PS This invention describes a novel potassium channel protein (I) that is  
 CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium  
 CC channels containing (I) are used to identify and test: (i) compounds for  
 CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
 CC stroke, Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
 CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
 CC activators of protein kinases. Host cells that express (I) can identify  
 CC agents that do not interact significantly with channels and control I-t-o  
 CC (a quickly activated transient current), so lack the side effects of  
 CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
 CC for testing on organ cultures  
 XX  
 SO Sequence 655 AA;  
 Query Match 99.4%; Score 3391; DB 4; Length 655;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 652; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAAGVAAALPPAPAAALIGMPPVANCMPPLADKKNKODELIVLVNSGRRFQWRTTLIER 60  
 DB 1 MAAGVAAALPPAPAAALIGMPPVANCMPPLADKKNKODELIVLVNSGRRFQWRTTLIER 60  
 QY 61 YPDTLLGSTEKEKFFNEDTKYFFDRDPEVRCVINFRTGKLHPRYECISAYDDELAF 120  
 DB 61 YPDTLLGSTEKEKFFNEDTKYFFDRDPEVRCVINFRTGKLHPRYECISAYDDELAF 120  
 QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAFENPHST 180  
 QY 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 DB 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 QY 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 DB 181 LALVFFYYTGFPIAVSVITNVEIVPCGTVGSKELPCGERYSVAFFCLDTACWMIFFVE 240  
 QY 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300  
 DB 241 YLLRFLFAPSRRYRFRSVMGSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRFRVRIKPF 300

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Db      |||
241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYIGLVMTNNEDVGAFTVLRVFRVRIKFX 300
QY      301 SRHSQGLRILGYTLKSCASELGFLLFTLMAIIIFATVMPVAEKGSASAKFTSIPASFWY 360
Db      301 SRHSQGLRILGYTLKSCASELGFLLFTLMAIIIFATVMPVAEKGSASAKFTSIPASFWY 360
QY      361 TIVMTTLGGVDMVPTIAGKIFGSIKSGVLVIALPVIVSNFRIYHONQADKRR 420
Db      361 TIVMTTLGGVDMVPTIAGKIFGSIKSGVLVIALPVIVSNFRIYHONQADKRR 420
QY      421 AOKKALARIKRVAKTSSNAVYLSKNGNLNEALBELTGPBEEMKTTSLIESQHHL 480
Db      421 AOKKALARIKRVAKTSSNAVYLSKNGNLNEALBELTGPBEEMKTTSLIESQHHL 480
QY      481 HCLEKTTGSLYVDDPLLSVRTSTIKNHEFIDQMEQNCMESSMONTSTRSPSLSSHP 540
Db      481 HCLEKTTGSLYVDDPLLSVRTSTIKNHEFIDQMEQNCMESSMONTSTRSPSLSSHP 540
QY      541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTHIOGSEQPSLTSSINLKADG 600
Db      541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTHIOGSEQPSLTSSINLKADG 600
QY      601 LRPNCKTSQITTAIISIPTPPALTPGSESRPPASPGPNTNIPSTSNVVKVSVL 655
Db      601 LRPNCKTSQITTAIISIPTPPALTPGSESRPPASPGPNTNIPSTSNVVKVSVL 655

RESULT 7
ABB79585
ID ABB79585 standard; protein; 636 AA.
XX AC ABB79585;
XX
DT 01-OCT-2002 (first entry)
DE Human Kv4.3 potassium channel (short form).
XX
XX Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
XX neurotropic; neuroprotective; cardiac; gene therapy.
XX
XX Homo sapiens.
XX
XX US6395477-B1.
XX
XX 28-MAY-2002.
XX
XX 23-OCT-1998; 98US-00178109.
XX
XX 23-OCT-1998; 98US-00178109.
XX
XX (AMHP) AMERICAN HOME PROD CORP.
XX
XX Cockett MI, Dilks DW, Ling HC, Sokol PT;
XX
XX WPI; 2002-556093/59.
XX
XX N-PSDB; ABN84401.
XX
XX
PT New isolated polynucleotide encoding human Kv4.3 potassium channel
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT diseases.
XX
XX
PS Claim 1; Col 23-26; 19pp; English.
XX
XX The present sequence is the protein sequence of the short isoform of
XX novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been
XX identified: a full-length form (hKv4.3 long) (see ABB79584); and the
XX short form, which has a deletion of 19 amino acids in the carboxy domain
XX after the predicted sixth transmembrane domain (hKv4.3 short). Human
XX heart primarily expresses hKv4.3 long, whereas human brain contains both
XX forms. The invention provides Kv4.3 polypeptides, polynucleotides, and
XX methods for producing these polynucleotides. The Kv4.3 polypeptides and

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CC polynucleotides are useful in the diagnosis, treatment and screening of
CC human diseases relating to an excess or deficiency of hKv4.3 activity,
CC including Alzheimer's disease and heart disease
XX
XX
SQ Sequence 636 AA:
Query Match 96.7%; Score 3300.5; DB 5; Length 636;
Best Local Similarity 97.1%; Pred. No. 1.4e-309;
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
1 MAGVAAWLPFAAAAIGMPVANCMPPLAPADKKNROELIVANSGRRPQTWTLRR 60
1 MAGVAAWLPFAAAAIGMPVANCMPPLAPADKKNROELIVANSGRRPQTWTLRR 60
QY 61 YPDTLLGSTEKEFFEDTKEYFFDRDPVFCVINFYTGKLYHRYECISAYDDELAF 120
Db 61 YPDTLLGSTEKEFFEDTKEYFFDRDPVFCVINFYTGKLYHRYECISAYDDELAF 120
QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQSEMPSLSPFQTWMPRAEPDHTST 180
Db 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQSEMPSLSPFQTWMPRAEPDHTST 180
QY 181 LALVFYVYGFPAVAVITNVVETVPCGTVPGSKELPCGERYSVAFFCDTACVMIFTE 240
Db 181 LALVFYVYGFPAVAVITNVVETVPCGTVPGSKELPCGERYSVAFFCDTACVMIFTE 240
QY 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYIGLVMTNNEDVGAFTVLRVFRVRIKFX 300
Db 241 YLLRLFAAPSRVRFIRSVMSIIDVVAIMPYIGLVMTNNEDVGAFTVLRVFRVRIKFX 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFTLMAIIIFATVMPVAEKGSASAKFTSIPASFWY 360
Db 301 SRHSQGLRILGYTLKSCASELGFLLFTLMAIIIFATVMPVAEKGSASAKFTSIPASFWY 360
QY 361 TIVMTTLGGVDMVPTIAGKIFGSIKSGVLVIALPVIVSNFRIYHONQADKRR 420
Db 361 TIVMTTLGGVDMVPTIAGKIFGSIKSGVLVIALPVIVSNFRIYHONQADKRR 420
QY 421 AOKKALARIKRVAKTSSNAVYLSKNGNLNEALBELTGPBEEMKTTSLIESQHHL 480
Db 421 AOKKALARIKRVAKTSSNAVYLSKNGNLNEALBELTGPBEEMKTTSLIESQHHL 480
QY 481 HCLEKTTGSLYVDDPLLSVRTSTIKNHEFIDQMEQNCMESSMONTSTRSPSLSSHP 540
Db 481 HCLEKTTGSLYVDDPLLSVRTSTIKNHEFIDQMEQNCMESSMONTSTRSPSLSSHP 540
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTHIOGSEQPSLTSSINLKADG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTHIOGSEQPSLTSSINLKADG 600
QY 601 LRPNCKTSQITTAIISIPTPPALTPGSESRPPASPGPNTNIPSTSNVVKVSVL 655
Db 601 LRPNCKTSQITTAIISIPTPPALTPGSESRPPASPGPNTNIPSTSNVVKVSVL 655

RESULT 8
AAW79589
ID AAW79589 standard; protein; 636 AA.
XX AC AAW79589;
XX
DT 11-JAN-1999 (first entry)
DE Human Kv potassium channel hKv4.3 (shorter isoform).
XX
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
XX therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX W09842833-A2.
XX
XX 01-OCT-1998.

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XX 23-MAR-1998; 98WO-EP001901.  
 XX 27-MAR-1997; 97GB-00006377.  
 PR 09-DEC-1997; 97EP-00402971.  
 PR 11-DEC-1997; 97EP-00403007.  
 XX (SMK ) SMITHKLINE BEECHAM LAB PHARM.  
 PI Brill AMA, Calmels TPG, Faivre USP, Javre J, Rouanet S;  
 DR WPI; 1998-542277/46.  
 DR N-PSDB; AAV61573.  
 XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
 PT poly:nucleotide(s) useful in the treatment of disorders including cardiac  
 PT arrhythmias and Alzheimer's disease.  
 XX Claim 2; Page 25; 47pp; English.  
 PS  
 XX This is the amino acid sequence for an isoform of human Kv potassium  
 CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3  
 CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3.  
 CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all  
 CC Kv family related proteins. A longer isoform (see AAW79590) has been  
 CC identified, which has an additional 19 amino acids inserted between amino  
 CC acids 487 and 488. The invention relates to hKv4.3 polypeptides and  
 CC polynucleotides, and to methods for producing such polypeptides by  
 CC recombinant techniques. hKv4.3 polypeptides can be used to identify  
 CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also  
 CC claimed are methods for utilizing such agonists and antagonists for the  
 CC treatment of subjects in need of enhanced or reduced activity or  
 CC expression of hKv4.3 polypeptide. These include the treatment of cardiac  
 CC arrhythmias and Alzheimer's disease. The invention can also be used to to  
 CC detect disease associated with inappropriate hKv4.3 expression or  
 CC activity  
 CC  
 XX Sequence 636 AA;  
 SQ  
 Query Match 96.5%; Score 3291.5; DB 2; Length 636;  
 Best Local Similarity 96.8%; Pred. No. 1e-308;  
 Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

DB 421 AOKKARLARIRVAKTGSSNAYLHSCRNGLNLEALLETGPREEHNGKTTSLIESQHHLL 480  
 QY 481 HLEKTTGLSLVDDPLSVRTSTIKNEFFIDEQMFQONCHSSQONTPTSRSPSLSSHP 540  
 DB 481 HLEKTT-----NHEFFIDEQMFQONCHSSQONTPTSRSPSLSSHP 521  
 QY 541 GLTTCCGRRSRKKTTHLPNSNLPATRLSMOELSTIHQGSROPSELTSRSSLNKADG 600  
 DB 522 GLTTCCGRRSRKKTTHLPNSNLPATRLSMOELSTIHQGSROPSELTSRSSLNKADG 581  
 QY 601 LRPNCKTSQITTAIISIPTPALTPGCSRRPPAPSGPNTNIPSTISNVVAVSVL 655  
 DB 582 LRPNCKTSQITTAIISIPTPALTPGCSRRPPAPSGPNTNIPSTISNVVAVSVL 636  
 RESULT 9  
 AAW79591  
 ID AAW79591 standard; protein; 636 AA.  
 XX  
 AC AAW79591;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human Kv potassium channel hKv4.3.  
 XX  
 KM Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
 KM therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 PN WO9842833-A2.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 23-MAR-1998; 98WO-EP001901.  
 PR 27-MAR-1997; 97GB-00006377.  
 PR 09-DEC-1997; 97EP-00402971.  
 PR 11-DEC-1997; 97EP-00403007.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM LAB PHARM.  
 PI Brill AMA, Calmels TPG, Faivre USP, Javre J, Rouanet S;  
 DR WPI; 1998-542277/46.  
 DR N-PSDB; AAV61573.  
 XX  
 PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
 PT poly:nucleotide(s) useful in the treatment of disorders including cardiac  
 PT arrhythmias and Alzheimer's disease.  
 XX  
 PS Claim 19; Page 28; 47pp; English.  
 XX  
 CC This is the amino acid sequence for an isoform of human Kv potassium  
 CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3  
 CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3.  
 CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all  
 CC Kv family related proteins. hKv4.3 isoforms (see AAW79589 and AAW79590)  
 CC are also claimed. The invention relates to hKv4.3 polypeptides and  
 CC polynucleotides, and to methods for producing such polypeptides by  
 CC recombinant techniques. hKv4.3 polypeptides can be used to identify  
 CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also  
 CC claimed are methods for utilizing such agonists and antagonists for the  
 CC treatment of subjects in need of enhanced or reduced activity or  
 CC expression of hKv4.3 polypeptide. These include the treatment of cardiac  
 CC arrhythmias and Alzheimer's disease. The invention can also be used to to  
 CC detect disease associated with inappropriate hKv4.3 expression or  
 CC activity  
 CC  
 XX Sequence 636 AA;  
 SQ  
 Query Match 95.7%; Score 3265.5; DB 2; Length 636;  
 Best Local Similarity 96.2%; Pred. No. 3.4e-306;

Matches 630; Conservative 1; Mismatches 5; Indels 19; Gaps 1;

QY 1 MAAGVAAAMLPPFAAAAGMMPVANCMPPLAPADKDKRODELYLVANSGRRFQWRTTLER 60  
XX :|||||  
PI 1 MAAGVAAAMLPPFAAAAGMMPVANCMPPLAPADKDKRODELYLVANSGRRFQWRTTLER 60  
XX :|||||

QY 61 YPDTLLGSTEKEFFNFEDTKEYFFDRDPEVFRVCVLFNRYTGKLYHYREYCISAYDEDLAF 120  
Db YPDTLLGSTEKEFFNFEDTKEYFFDRDPEVFRVCVLFNRYTGKLYHYREYCISAYDEDLAF 120

QY 121 YGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQESMPSLSFRQTMRAEENPHSTST 180  
Db YGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQESMPSLSFRQTMRAEENPHSTST 180

QY 181 LALVFYVVGFFIAVSITNVETVPCGTVPSCKELCGGRYSVAFFCLDTACVMTFTVE 240  
Db LALVFYVVGFFIAVSITNVETVPCGTVPSCKELCGGRYSVAFFCLDTACVMTFTVE 240

QY 241 YLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVRFLFKF 300  
Db YLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVRFLFKF 300

QY 301 SRHSGRLIGYTLKSCASELGLFLSLTMAIIIFATVMEYAEKGSASAKFTSIPASFMY 360  
Db SRHSGRLIGYTLKSCASELGLFLSLTMAIIIFATVMEYAEKGSASAKFTSIPASFMY 360

QY 361 TIYMTTLGVDWVPKTIAGKIFGSLGSLGVIALPVVIVSNFSRIYHONQADKRR 420  
Db TIYMTTLGVDWVPKTIAGKIFGSLGSLGVIALPVVIVSNFSRIYHONQADKRR 420

QY 421 AOKKARLARIRVAKTGSNNAYLHNSKNGLINEALELTGTPBEEMHGKTSLLIESOHHL 480  
Db AOKKARLARIRVAKTGSNNAYLHNSKNGLINEALELTGTPBEEMHGKTSLLIESOHHL 480

QY 481 HCEKKTGSLYVDDPLSVRTSTIKMHEPIDEOMFONCMESMOMVPSRSPSSSHR 540  
Db HCEKKT-----NHEPIDEOMFONCMESMOMVPSRSPSSSHR 521

QY 541 GLTTCCSRRSKKTTHLPNSNLPRTRLSMOELSTHIQSEOPSLTSSSLNLKADG 600  
Db GLTTCCSRRSKKTTHLPNSNLPRTRLSMOELSTHIQSEOPSLTSSSLNLKADG 581

QY 601 LRPNCKTSQITTAIISIPPPALTPBEGSRPPSPGPNNTNIPSTNSVVKSVL 655  
Db LRPNCKTSQITTAIISIPPPALTPBEGSRPPSPGPNNTNIPSTNSVVKSVL 636

RESULT 10  
ADE61252  
ID ADE61252 standard; protein; 611 AA.  
XX  
AC ADE61252;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein AAA80459, SEQ ID NO 7170.  
XX  
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI, spared nerve injury; SNI; Chung.  
OS Rattus norvegicus.  
XX  
PN W02003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002W0-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
XX 01-NOV-2001; 2001US-0346382P.  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI, 2003-268312/26.  
DR GENBANK; AAA80459.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
PS Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 611 Ab;  
Query Match 89.0%; Score 3035.5; DB 7; Length 611;  
Best Local Similarity 96.2%; Pred. No. 5.8e-284;  
Matches 584; Conservative 2; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGVAAAMLPPFAAAAGMMPVANCMPPLAPADKDKRODELYLVANSGRRFQWRTTLER 60  
Db 1 MAAGVAAAMLPPFAAAAGMMPVANCMPPLAPADKDKRODELYLVANSGRRFQWRTTLER 60

QY 61 YPDTLLGSTEKEFFNFEDTKEYFFDRDPEVFRVCVLFNRYTGKLYHYREYCISAYDEDLAF 120  
Db YPDTLLGSTEKEFFNFEDTKEYFFDRDPEVFRVCVLFNRYTGKLYHYREYCISAYDEDLAF 120

QY 121 YGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQESMPSLSFRQTMRAEENPHSTST 180  
Db YGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQESMPSLSFRQTMRAEENPHSTST 180

QY 181 LALVFYVVGFFIAVSITNVETVPCGTVPSCKELCGGRYSVAFFCLDTACVMTFTVE 240  
Db LALVFYVVGFFIAVSITNVETVPCGTVPSCKELCGGRYSVAFFCLDTACVMTFTVE 240

QY 241 YLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVRFLFKF 300  
Db YLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVRFLFKF 300

QY 301 SRHSGRLIGYTLKSCASELGLFLSLTMAIIIFATVMEYAEKGSASAKFTSIPASFMY 360  
Db SRHSGRLIGYTLKSCASELGLFLSLTMAIIIFATVMEYAEKGSASAKFTSIPASFMY 360

QY 361 TIYMTTLGVDWVPKTIAGKIFGSLGSLGVIALPVVIVSNFSRIYHONQADKRR 420  
Db TIYMTTLGVDWVPKTIAGKIFGSLGSLGVIALPVVIVSNFSRIYHONQADKRR 420

QY 421 AOKKARLARIRAKTGGSSNAVYLSKRNGLNEALTLGPEEHNGKTTSLIESQHLL 480  
 DB 421 AOKKARLARIRAKTGGSSNAVYLSKRNGLNEALTLGPEEHNGKTTSLIESQHLL 480  
 QY 481 HCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSMONTPTSTRSPSLSSHP 540  
 DB 481 HCLEKTT-----NHEFIDQMFQONCMSSMONTPTSTRSPSLSSHS 521  
 QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLSPMOELSTIHIQSEOPSLTTRSSSLNKADGG 600  
 DB 522 GLTTCCSRRSKKTTHLPNSNLPATRLTMOELSTIHIQSEOPSLTTRSSSLNKADGG 581  
 QY 601 LRPNCKT 607  
 DB 582 LRPNCKT 588

## RESULT 11

ADM10929  
 ID ADM10929 standard; protein, 630 AA.  
 AC ADM10929;  
 DT 20-MAY-2004 (first entry)  
 DE Human O647SgenomicContig3 homologue protein #4.  
 KM ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
 KM cytosol; gene therapy; human; ds.  
 OS Homo sapiens.  
 XX US2003206918-A1.  
 PD 06-NOV-2003.  
 PF 05-FEB-2003; 2003US-00361811.  
 XX 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00970966.  
 PR 02-AUG-2002; 2002US-00212677.  
 PA (CORI-) CORIXA CORP.  
 XX Fanger GR, Fling SP;  
 PI WPI; 2003-901037/82.  
 DR N-PSDB; ADM10923.  
 XX New polynucleotides encoding tumor proteins, treating or inhibiting the  
 PT development of cancer, particularly ovarian cancer, and for stimulating  
 PT and/or expanding T cells specific for a tumor protein.  
 XX Example 12; SEQ ID NO 260; 221bp; English.  
 PS This invention describes a novel ovarian tumour protein which can be used  
 CC to detecting the presence of an ovarian cancer in a patient by  
 CC stimulating and/or expanding T cells specific for the tumour protein. The  
 CC products of the invention can also be used in a method to inhibit the  
 CC development of a cancer in a patient comprising (a) incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian  
 CC tumour protein, such that T cell proliferate and (b) administering to the  
 CC patient the proliferated T cells. The cytosol polynucleotides or  
 CC polypeptides described in the invention are useful for treating or  
 CC inhibiting the development of cancer, particularly ovarian cancer and for  
 CC stimulating and/or expanding T cells specific for a tumour protein or for  
 CC gene therapy.

XX SQ Sequence 630 AA;

Query Match 73.2%; Score 2498.5; DB 7; Length 630;  
 Best local similarity 73.6%; Pred. No. 5.5e-232;  
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

QY 1 MAAGVAAALPAPRAAAGMVFANCPMLAADNKR--ODELIYVNVSGRRPQRTTLE 59  
 DB 1 MAAGVAAALPAPRAAAGMVFANCPMLAADNKR--ODELIYVNVSGRRPQRTTLE 60  
 QY RYPTLIGSTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDT 119  
 DB RYPTLIGSTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDTKEFFEDNEDT 120  
 QY 120 FYGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQES--MPSLSFRQTMARAFENPT 178  
 DB 121 FFGILPEIIGDCCYEEYKDRRENAERLMDNDSENNQES--MPSLSFRQTMARAFENPT 180  
 QY 129 STLALVFYVYTGFIANSVITNVVETVPCGIVPQS--KELPGERYSAVFCCLDTACWMI 237  
 DB 181 STMALVFYVYTGFIANSVITNVVETVPCGIVPQS--KELPGERYSAVFCCLDTACWMI 240  
 QY 238 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYIYIGLMTNNEDEVSGAFVTLRFRVPR 297  
 DB 241 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYIYIGLMTNNEDEVSGAFVTLRFRVPR 300  
 QY 298 FKFSRHSQGLRIILGYTLKSCASELGFLLFTMAIIFATVMPYAEKGSASAKETSIPAS 357  
 DB 301 FKFSRHSQGLRIILGYTLKSCASELGFLLFTMAIIFATVMPYAEKGSASAKETSIPAS 360  
 QY 358 FWYTIIVMTTIGYDMPKTIAGKIFGSGICSLGVLVIALPVPYIVSNFSKIYHONQPAD 417  
 DB 361 FWYTIIVMTTIGYDMPKTIAGKIFGSGICSLGVLVIALPVPYIVSNFSKIYHONQPAD 420  
 QY 418 KRAOKKARLARIRAKTGGSSNAVYLSKRNGLNEALTLGPEEHNGKTTSLIESQH 477  
 DB 421 KRAOKKARLARIRAKTGGSSNAVYLSKRNGLNEALTLGPEEHNGKTTSLIESQH 479  
 QY 478 HLHLCLEKTTGLSYLVDDPLLSVSTSTIKNHEFIDQMFQONCMSSMONTPTSTRSPSL 537  
 DB 480 HLHLCLEKTT-----NHEFIDQMFQONCMSSMONTPTSTRSPSL 520  
 QY 538 SHPGITTTCCSRRSKKTTHLPNSNLPATRLSPMOELSTIHIQSEOPSLTTRSSSLNK 597  
 DB 521 SQQGVSTSCSRRRKKTFRIPANAVSGSHQSIQELSTIQRCVERPPLSNSSSLNKKM 580  
 QY 598 DDGLRPNCKTSQITTAIISIPTPALTPGESRP--PPASGPTNTIPSTSNVYKVSVL 655  
 DB 581 EECVKLNCEOPYVTITAIISIPTPVTTPBGDDRPESPEYSGG-----NIVRSAL 630

## RESULT 12

ADM10928  
 ID ADM10928 standard; protein, 630 AA.  
 AC ADM10928;  
 DT 20-MAY-2004 (first entry)  
 DE Human O647SgenomicContig3 homologue protein #3.  
 KM ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
 KM cytosol; gene therapy; human; ds.  
 OS Homo sapiens.  
 XX US2003206918-A1.  
 PD 06-NOV-2003.  
 PF 05-FEB-2003; 2003US-00361811.  
 XX

10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00970966.  
 PR 02-AUG-2002; 2002US-00212677.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Fanger GR, Fling SP;  
 XX  
 DR WPI; 2003-901037/82.  
 XX N-PSDB; ADM10922.  
 PT New polynucleotides encoding tumor proteins, treating or inhibiting the  
 PT development of cancer, particularly ovarian cancer, and for stimulating  
 PT and/or expanding T cells specific for a tumor protein.

XX  
 PS Example 12; SEQ ID NO 259; 221bp; English.

XX  
 CC This invention describes a novel ovarian tumour protein which can be used  
 CC to detecting the presence of an ovarian cancer in a patient by  
 CC stimulating and/or expanding T cells specific for the tumour protein. The  
 CC products of the invention can also be used in a method to inhibit the  
 CC development of a cancer in a patient comprising (a) incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian  
 CC tumour protein, such that T cell proliferate and (b) administering to the  
 CC patient the proliferated T cells. The cytostatic polynucleotides or  
 CC polypeptides described in the invention are useful for treating or  
 CC inhibiting the development of cancer, particularly ovarian cancer and for  
 CC stimulating and/or expanding T cells specific for a tumour protein or for  
 CC gene therapy.

XX  
 SQ Sequence 630 AA;

Query Match 73.2%; Score 2498.5; DB 7; Length 630;  
 Best Local Similarity 73.6%; Pred. No. 5.5e-232;  
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

QY 1 MAAGVAAALPPARAAALGMPVANCMPPLAPADNKR-QDELIVANSGRRPQTMTTLE 59  
 DB 1 MAAGVAAALPPARAAALGMPVANCMPPLAPADNKR-QDELIVANSGRRPQTMTTLE 60  
 QY 60 RYDDTLTGSEKEFEFEDTKEVEFEDDPEVFCVNFYTGKLYRVCISAYDELA 119  
 DB 61 RYDDTLTGSEKEFEFEDTKEVEFEDDPEVFCVNFYTGKLYRVCISAYDELA 120  
 QY 120 FYGLPEIIGDCCEYEYKDKRENAERLMDNDSENNQES-MPSLSFRQTMRAFERPHT 178  
 DB 121 FYGLPEIIGDCCEYEYKDKRENAERLMDNDSENNQES-MPSLSFRQTMRAFERPHT 180  
 QY 179 STIALVYVYTGFFIAVSIVITNVETVPCGTVPS-KELPGERYVAFFCLDTACVIF 237  
 DB 181 STIALVYVYTGFFIAVSIVITNVETVPCGTVPS-KELPGERYVAFFCLDTACVIF 240  
 QY 238 TVEYLRLFAAPSRVIRIRISVMSIIDVVALMPYITGVMTNNNEVSGAPFTLRFRRFRI 297  
 DB 241 TVEYLRLFAAPSRVIRIRISVMSIIDVVALMPYITGVMTNNNEVSGAPFTLRFRRFRI 300  
 QY 298 FKFSRHSOGLRIIGYTKSCASELGFLLFSLTMAIIFATVMFAEKSSASKRTSIPAS 357  
 DB 301 FKFSRHSOGLRIIGYTKSCASELGFLLFSLTMAIIFATVMFAEKSSASKRTSIPAS 360  
 QY 358 FWYITVMTTLGVDWVPKTIAGKIFGSSICSLSGVAVIALPVPIVSNFSRIYHONRAD 417  
 DB 361 FWYITVMTTLGVDWVPKTIAGKIFGSSICSLSGVAVIALPVPIVSNFSRIYHONRAD 420  
 QY 418 KRBAOKKARLARIRVATGSSNATLHKKRGLNLEALGTPEEHMGKTTSLIESQHH 477  
 DB 421 KRBAOKKARLARIRVATGSSNATLHKKRGLNLEALGTPEEHMGKTTSLIESQHH 479

QY 478 HLHLCLEKTTGSLYVDPLLSVRSITIKNHEFIDEQMEFQNCMESSMONTPESTRSPSS 537  
 DB 480 HLHLCLEKTT-----NHFEVDQVEESCEVEAYATNRRPSHSPSS 520  
 QY 538 SHPGLTTTCCSRRSKKTTHLPNSNLBATRLRSMQELSTHIGSEPPSLTTRSSNLUA 597  
 DB 521 SOQGVSTCCSRHKKTFRIIPANVSGSHQSGISQIELSTQICVETTPLSNSSSINAAKM 580  
 QY 598 DQGLRPNCKTSQITTAIISIPPPALTPEGESRP--PPASPGPNTNIPSTSNVAVSVYL 655  
 DB 581 EECVKLNCQOPYVTIAIISIPPTPTTBGDDRPESPEYSGC-----NIYVNSAL 630

RESULT 13

ADM10930  
 ID ADM10930 standard; protein; 630 AA.  
 XX  
 AC ADM10930;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human O648SgenomicContig\_ORF protein.  
 XX  
 KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
 KW cytostatic; gene therapy; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003206918-A1.  
 XX  
 PD 06-NOV-2003.  
 XX  
 PF 05-FEB-2003; 2003US-00361811.  
 XX

PR 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00970966.  
 PR 02-AUG-2002; 2002US-00212677.  
 XX

PA (CORI-) CORIXA CORP.

PI Fanger GR, Fling SP;

XX  
 DR WPI; 2003-901037/82.  
 XX N-PSDB; ADM10931.

PT New polynucleotides encoding tumor proteins, treating or inhibiting the  
 PT development of cancer, particularly ovarian cancer, and for stimulating  
 PT and/or expanding T cells specific for a tumor protein.

XX  
 PS Example 12; SEQ ID NO 261; 221bp; English.

XX  
 CC This invention describes a novel ovarian tumour protein which can be used  
 CC to detecting the presence of an ovarian cancer in a patient by  
 CC stimulating and/or expanding T cells specific for the tumour protein. The  
 CC products of the invention can also be used in a method to inhibit the  
 CC development of a cancer in a patient comprising (a) incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian  
 CC tumour protein, such that T cell proliferate and (b) administering to the  
 CC patient the proliferated T cells. The cytostatic polynucleotides or  
 CC polypeptides described in the invention are useful for treating or  
 CC inhibiting the development of cancer, particularly ovarian cancer and for  
 CC stimulating and/or expanding T cells specific for a tumour protein or for  
 CC gene therapy.

SQ Sequence 630 AA;

Query Match 73.2%; Score 2498.5; DB 7; Length 630;  
 Best Local Similarity 73.6%; Pred. No. 5.5e-232;





```

Db      521 SOQGVSTCCSRHKKTFRIIPNANVSGSHQGSIOELSTIQIRCVERTPLSNRSLSINAKM 580
QY      598 DDGLRPNCKTSOITTAIIISIPTPALTPEGESRP--PPASPGPNTNIPSTSNVAVSVYL 655
      581 BECVKLNCEQPYVTTAIIISIPTPVTTPEGDDRPESPEYSGG-----NIVAVSAL 630

RESULT 15
ADJ11257
ID      ADJ11257 standard; protein; 630 AA.
AC      ADJ11257;
DT      15-APR-2004 (first entry)
XX      Human ovarian tumour antigen polypeptide SeqID 258.
XX      human; ovarian cancer; immunogenic; antibody; antigen presenting cell;
XX      APC; immune system cell; T cell; tumourigenic; cytostatic.
XX      Homo sapiens.
PN      US2003232056-A1.
XX      18-DEC-2003.
XX      14-FEB-2003; 2003US-00369186.
XX      10-SEP-1999; 99US-00394374.
XX      01-MAY-2000; 2000US-00561778.
XX      15-AUG-2000; 2000US-00640173.
XX      07-SEP-2000; 2000US-00656668.
XX      14-NOV-2000; 2000US-00713550.
XX      03-APR-2001; 2001US-00825294.
XX      02-OCT-2001; 2001US-00970966.
XX      02-AUG-2002; 2002US-00212677.
XX      05-FEB-2003; 2003US-00361811.
PA      (CORI-) CORIXA CORP.
XX      Fanger GR, Fling SP;
XX      WPI; 2004-178717/17.
XX      N-PSDB; ADJ11251.
PT      Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT      polypeptide, useful as probes of primers for detecting presence of cancer
PT      in a patient.
XX      Example 12; SEQ ID NO 258; 222pp; English.
PS      This invention relates to novel isolated polynucleotides and methods for
XX      the therapy and diagnosis of cancer, particularly ovarian cancer.
XX      Specifically, it refers to these polynucleotides and the encoded
XX      polypeptides thereof, as well as immunogenic peptides, antibodies,
XX      antigen presenting cells (APCs) and immune system cells (e.g. T cells)
XX      that are targeted to those cells expressing the proteins of interest. The
XX      present invention describes methods that are useful for stimulating and/or
XX      expanding T cells specific for a tumourigenic protein (i.e. T cell
XX      therapy). Furthermore, compositions can be used for the diagnosis,
XX      treatment and/or prevention of ovarian cancer by stimulating an immune
XX      response in a patient. Accordingly, these compositions exhibit cytostatic
XX      activity. This polypeptide is a human ovarian tumour antigen protein
XX      sequence given in an exemplification of the invention.
SQ      Sequence 630 AA;

```

Query Match 73.2%; Score 2498.5; DB 8; Length 630;  
 Best Local Similarity 73.6%; Pred. No. 5.5e-232;  
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

QY 1 MAAGVAAWLPFARAAAIIGMPVANCMPMLAPADKNKR-QDELIVLVNSGRRFQTRTTTLE 59

```

Db      1 MAAGVAAWLPFARAAAIIGMPVASCMPAPPPROERKRTDAILVNVSGTRFQTMQDTTLE 60
QY      60 RYPDTLTGSTEKEFFENEDTKEVFPDRDEVEVRCVLANFRTGKLHYPRFECISAYDELA 119
      61 RYPDTLGSSERDFFPHPTQGYFPDRDPIFRHILNFRITGKLHYPRFECISAYDELA 120
QY      120 FYGILPEIIGDCCYEYKDKRKENMERLMDNDSENNOES-MPSLSFQGTMMRAFENPHT 178
Db      121 FGLIPEIIGDCCYEYKDKRRRENAERLQDDADTDAGSALPTMTARQVRMARFENPHT 180
QY      179 STLALVYVYVVGFFLAIVSIVTNVETVPCGYVGS-KELPCGERVYAFPCLDTAQMTF 237
Db      181 STMALVFYVYVVGFFLAIVSIVANVETVPCGSSPGHITKELPCGERVYAFPCLDTAQMTF 240
QY      238 TVEYLRLFAAPSRYVFISVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFVFR1 297
Db      241 TVEYLRLFAAPSRRIRFVSVMSIIDVVAIMPYYIGLVMTNEDVSGAVTLRVFVFR1 300
QY      298 FKFSRHSGRLRILGYTLKSCASELGLFSLTMAIIIFATVWFYAEKGSASAKFTSIPAS 357
Db      301 FKFSRHSGRLRILGYTLKSCASELGLFSLTMAIIIFATVWFYAEKGSASAKFTSIPAS 360
QY      358 FWYTIYMTTIGYGVMPPTTIAGTFGSTCSLGVVIALPVVIVYSNFSRIYHONORD 417
Db      361 FWYTIYMTTIGYGVMPPTTIAGTFGSTCSLGVVIALPVVIVYSNFSRIYHONORD 420
QY      418 KRAQKARLARIRVAKTSSNAYLHRSKNGLINEALELTGPDEEHMKTSLISQHH 477
Db      421 KRAQKARLARIRAKSSANAYHMQSKNGLSNLO-QSSEEQAFVSKSGSFFTOHH 479
QY      478 HLHLCLEKTTGSLYVDDPLLVSRTSIKNHEFIDQMEFQNCMESSMONTPESTRPSLS 537
Db      480 HLHLCLEKTT-----NHEFVDQVEESCMETVAIVNRPSSHPSSLS 520
QY      538 SHPGLTTTCCSRRSKTTTHLPNSNLPATRLRSMQELSTHIGSBEPSLITRSLSINLKA 597
Db      521 SOQGVSTCCSRHKKTFRIIPNANVSGSHQGSIOELSTIQIRCVERTPLSNRSLSINAKM 580
QY      598 DDGLRPNCKTSOITTAIIISIPTPALTPEGESRP--PPASPGPNTNIPSTSNVAVSVYL 655
Db      581 BECVKLNCEQPYVTTAIIISIPTPVTTPEGDDRPESPEYSGG-----NIVAVSAL 630

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Search completed: April 6, 2005, 06:53:18  
 Job time : 501.211 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 07:13:52 ; Search time 455.608 Seconds  
(without alignments)  
477.292 Million cell updates/sec

Title: US-10-062-879-2

Perfect score: 3412  
Sequence: 1 MAAGVAAWLPFARAATGWM.....PGPNTNPSITSNVVKSVL 655

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3412	100.0	655	US-10-062-879-2	Sequence 2, Appl1
2	3395	99.5	655	US-10-377-139-6	Sequence 6, Appl1
3	3300.5	96.7	636	US-10-062-879-4	Sequence 4, Appl1
4	2498.5	73.2	630	US-10-212-677-258	Sequence 258, App
5	2498.5	73.2	630	US-10-212-677-259	Sequence 259, App
6	2498.5	73.2	630	US-10-212-677-260	Sequence 260, App
7	2498.5	73.2	630	US-10-212-677-261	Sequence 261, App
8	2498.5	73.2	630	US-10-361-811-258	Sequence 258, App
9	2498.5	73.2	630	US-10-361-811-259	Sequence 259, App
10	2498.5	73.2	630	US-10-361-811-260	Sequence 260, App
11	2498.5	73.2	630	US-10-361-811-261	Sequence 261, App
12	2498.5	73.2	630	US-10-369-186-258	Sequence 258, App
13	2498.5	73.2	630	US-10-369-186-259	Sequence 259, App

14	2498.5	73.2	630	US-10-369-186-260	Sequence 260, App
15	2498.5	73.2	630	US-10-369-186-261	Sequence 261, App
16	2113	61.9	647	US-10-286-115-1112	Sequence 1112, App
17	2102	61.6	646	US-10-121-746-10	Sequence 10, Appl
18	825	24.2	255	US-10-212-677-257	Sequence 257, App
19	825	24.2	255	US-10-361-811-257	Sequence 257, App
20	825	24.2	255	US-10-369-186-257	Sequence 257, App
21	767	22.5	806	US-09-833-466-13	Sequence 13, Appl
22	767	22.5	806	US-10-199-869-6	Sequence 6, Appl
23	767	22.5	811	US-10-815-297-13	Sequence 13, Appl
24	755.5	22.1	916	US-10-408-765A-1482	Sequence 1482, App
25	748.5	21.9	985	US-10-154-486-20	Sequence 20, Appl
26	742.5	21.8	854	US-09-833-466-12	Sequence 12, Appl
27	742.5	21.8	854	US-10-199-869-5	Sequence 5, Appl
28	742.5	21.8	854	US-10-815-297-12	Sequence 12, Appl
29	741	21.7	857	US-10-377-139-4	Sequence 4, Appl
30	726.5	21.3	656	US-10-377-139-4	Sequence 4, Appl
31	724	21.2	539	US-10-325-891-13	Sequence 13, Appl
32	721.5	21.1	456	US-09-993-811-2	Sequence 2, Appl
33	721.5	21.1	456	US-09-974-712-2	Sequence 2, Appl
34	721.5	21.1	456	US-09-989-920-175	Sequence 175, App
35	721.5	21.1	456	US-10-254-010-4	Sequence 4, Appl
36	721	21.1	539	US-09-804-014A-27	Sequence 27, Appl
37	721	21.1	559	US-09-804-014A-8	Sequence 8, Appl
38	720.5	21.1	601	US-10-121-746-4	Sequence 4, Appl
39	718	21.0	599	US-10-403-161-18	Sequence 18, Appl
40	715	21.0	499	US-10-322-281-766	Sequence 766, App
41	714.5	20.9	425	US-09-804-014A-29	Sequence 29, Appl
42	714.5	20.9	425	US-09-804-014A-75	Sequence 75, Appl
43	714	20.9	525	US-09-804-014A-33	Sequence 33, Appl
44	713.5	20.9	523	US-09-804-014A-32	Sequence 32, Appl
45	713.5	20.9	523	US-10-408-765A-2015	Sequence 2015, App

# ALIGNMENTS

RESULT 1  
US-10-062-879-2  
; Sequence 2, Application US/10062879  
; Publication No. US20020127649A1  
; GENERAL INFORMATION:  
; APPLICANT: Cockett, Mark I.  
; APPLICANT: Dilks, Daniel W.  
; APPLICANT: Chang Ling, Hwai-Ping  
; APPLICANT: Sokol, Patricia T.  
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
; TITLE OF INVENTION: Polypeptides and Uses Therefor  
; FILE REFERENCE: ahp-98083  
; CURRENT APPLICATION NUMBER: US/10/062,879  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US/09/178,109  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 655  
; TYPE: PRT  
; ORGANISM: human  
US-10-062-879-2

Query Match 100.0%; Score 3412; DB 13; Length 655;  
Best Local Similarity 100.0%; Pred. No. 1.3e-283;  
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFARAATGMPVANCMPPLAPADGNKODELIYVNSGRRPQRTTLIER 60  
DB 1 MAAGVAAWLPFARAATGMPVANCMPPLAPADGNKODELIYVNSGRRPQRTTLIER 60  
QY YPDTLLGSTEKEFFFNEDTKEYFFFDPRDEVEFRCVLYNFRGKLAHYPRYCISAYDDEIAF 120  
DB YPDTLLGSTEKEFFFNEDTKEYFFFDPRDEVEFRCVLYNFRGKLAHYPRYCISAYDDEIAF 120

QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180  
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180  
QY 181 LALVFYVYTGFFLAIVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTV 240  
DB 181 LALVFYVYTGFFLAIVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTV 240  
QY 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNNEVDGAFVTLRVFRVRIKFK 300  
DB 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNNEVDGAFVTLRVFRVRIKFK 300  
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFVAEKGSASAKFTSIPASFV 360  
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFVAEKGSASAKFTSIPASFV 360  
QY 361 TIYMTTLGVDWPKTIAGKIFGSLCSLGVVLALPVPVIVSNRSRIYHONQADKRR 420  
DB 361 TIYMTTLGVDWPKTIAGKIFGSLCSLGVVLALPVPVIVSNRSRIYHONQADKRR 420  
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALBLTGPPEEHMGKTTSLIESQHHL 480  
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALBLTGPPEEHMGKTTSLIESQHHL 480  
QY 481 HCLEKTTGLSYLVDPLLSVSTSTIKNHEFIDQMFQONCMSSMONYPSRSPSLSSHP 540  
DB 481 HCLEKTTGLSYLVDPLLSVSTSTIKNHEFIDQMFQONCMSSMONYPSRSPSLSSHP 540  
QY 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIOGSEOPSLTSSRSINLAKADG 600  
DB 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIOGSEOPSLTSSRSINLAKADG 600  
QY 601 LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655  
DB 601 LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655

## RESULT 2

US-10-377-139-6  
; Sequence 6, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackinnon, Roderick  
; APPLICANT: Jjiang, Youxing  
; APPLICANT: Lee Mackinnon, Alice  
; APPLICANT: Rura, Vanessa  
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
; CURRENT APPLICATION NUMBER: US/10/377,139  
; CURRENT FILING DATE: 2003-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 655  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-377-139-6

Query Match 99.5%; Score 3395; DB 16; Length 655;  
Best Local Similarity 99.7%; Pred. No. 3,76-282;  
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIVLVNNGRRFQWRRTLLER 60  
DB 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIVLVNNGRRFQWRRTLLER 60  
QY 61 YPDTLGSSTKEKFFFNEDTKEVFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELAIF 120  
DB 61 YPDTLGSSTKEKFFFNEDTKEVFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELAIF 120  
QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180  
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180

DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180  
QY 181 LALVFYVYTGFFLAIVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTV 240  
DB 181 LALVFYVYTGFFLAIVSVITNVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTV 240  
QY 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNNEVDGAFVTLRVFRVRIKFK 300  
DB 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNNEVDGAFVTLRVFRVRIKFK 300  
QY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFVAEKGSASAKFTSIPASFV 360  
DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFVAEKGSASAKFTSIPASFV 360  
QY 361 TIYMTTLGVDWPKTIAGKIFGSLCSLGVVLALPVPVIVSNRSRIYHONQADKRR 420  
DB 361 TIYMTTLGVDWPKTIAGKIFGSLCSLGVVLALPVPVIVSNRSRIYHONQADKRR 420  
QY 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALBLTGPPEEHMGKTTSLIESQHHL 480  
DB 421 AOKKARLARIRVAKTGSSNAYLHRSKNGLLNEALBLTGPPEEHMGKTTSLIESQHHL 480  
QY 481 HCLEKTTGLSYLVDPLLSVSTSTIKNHEFIDQMFQONCMSSMONYPSRSPSLSSHP 540  
DB 481 HCLEKTTGLSYLVDPLLSVSTSTIKNHEFIDQMFQONCMSSMONYPSRSPSLSSHP 540  
QY 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIOGSEOPSLTSSRSINLAKADG 600  
DB 541 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMOELSTHIOGSEOPSLTSSRSINLAKADG 600  
QY 601 LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655  
DB 601 LRPNCKTSQITTAIISIPPPALTPEGESRPPASPGPNTNIPSTSNVAVSVL 655

## RESULT 3

US-10-062-879-4  
; Sequence 4, Application US/10062879  
; Publication No. US20020127649A1  
; GENERAL INFORMATION:  
; APPLICANT: Cockett, Mark I.  
; APPLICANT: Dilks, Daniel W.  
; APPLICANT: Chang Ling, Huiat-Ping  
; APPLICANT: Sokol, Patricia T.  
; TITLE OF INVENTION: Human Potassium Channel Polypeptides and Uses Therefor  
; FILE REFERENCE: ahp-98089  
; CURRENT APPLICATION NUMBER: US/10/062,879  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US/09/178,109  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 636  
; TYPE: PRT  
; ORGANISM: human  
US-10-062-879-4

Query Match 96.7%; Score 3300.5; DB 13; Length 636;  
Best Local Similarity 97.1%; Pred. No. 4,6e-274;  
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIVLVNNGRRFQWRRTLLER 60  
DB 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLAPADKNKRODELIVLVNNGRRFQWRRTLLER 60  
QY 61 YPDTLGSSTKEKFFFNEDTKEVFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELAIF 120  
DB 61 YPDTLGSSTKEKFFFNEDTKEVFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDELAIF 120  
QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180  
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNPTST 180

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Db      121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSPFQTMRAFENPHST 180
Qy      181 LALVYVYTGFFIAVSVINNVETVPCGVPSKELPCGERISVAFPCLDPAQWIFVE 240
Db      181 LALVYVYTGFFIAVSVINNVETVPCGVPSKELPCGERISVAFPCLDPAQWIFVE 240
Qy      241 YLRLFAAPSRIRFIRSVMSIIDVAIMPYYIGLWMTNNEVDGAFVTLRVRVRIKFE 300
Db      241 YLRLFAAPSRIRFIRSVMSIIDVAIMPYYIGLWMTNNEVDGAFVTLRVRVRIKFE 300
Qy      301 SRHSGQRLILGYTLKSCASEIGFLFSLTMAIIFATWVFAEKSSASKFTSIDASFWY 360
Db      301 SRHSGQRLILGYTLKSCASEIGFLFSLTMAIIFATWVFAEKSSASKFTSIDASFWY 360
Qy      361 TIVMTTIGYGDMPKTIAGKIFGSI CSLSGVLVIALPVIVSNFSRIYHONQADXR 420
Db      361 TIVMTTIGYGDMPKTIAGKIFGSI CSLSGVLVIALPVIVSNFSRIYHONQADXR 420
Qy      421 AOKKARLARIRAVAKTGSNAIYLSKRNGLNEALGTGPREEHMGKTTSLIESQHHLL 480
Db      421 AOKKARLARIRAVAKTGSNAIYLSKRNGLNEALGTGPREEHMGKTTSLIESQHHLL 480
Qy      481 HCLEKTTGLSYLVDDPLLVRSTIKNHEFIDQMFQEQNCMESSMONTPTSTRPSLSHP 540
Db      481 HCLEKTT-----NHEFIDQMFQEQNCMESSMONTPTSTRPSLSHP 521
Qy      541 GLTTCCSRRSKKTTHLPNSULPATRLRSQMOELSTIHIQSEOPSLTTSRSSLNKADG 600
Db      522 GLTTCCSRRSKKTTHLPNSULPATRLRSQMOELSTIHIQSEOPSLTTSRSSLNKADG 581
Qy      601 LRPNCKTSQITTAIISIPTPALPPEGSRPPASPGNTNIPSTSNVVKVSVL 655
Db      582 LRPNCKTSQITTAIISIPTPALPPEGSRPPASPGNTNIPSTSNVVKVSVL 636

```

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RESULT 4
US-10-212-677-258
; Sequence 258, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-258

```

```

Query Match      73.2%; Score 2498.5; DB 14; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

```

Qy      179 STIALVYVYTGFFIAVSVINNVETVPCGVPSKELPCGERISVAFPCLDPAQWIF 237
Db      181 STIALVYVYTGFFIAVSVINNVETVPCGVPSKELPCGERISVAFPCLDPAQWIF 240
Qy      238 TVEYLRLFAAPSRIRFIRSVMSIIDVAIMPYYIGLWMTNNEVDGAFVTLRVRVRI 297
Db      241 TVEYLRLFAAPSRIRFIRSVMSIIDVAIMPYYIGLWMTNNEVDGAFVTLRVRVRI 300
Qy      298 FKPSRHSQRLILGYTLKSCASEIGFLFSLTMAIIFATWVFAEKSSASKFTSIDAS 357
Db      301 FKPSRHSQRLILGYTLKSCASEIGFLFSLTMAIIFATWVFAEKSSASKFTSIDAS 360
Qy      358 FWTITVMTTIGYGDMPKTIAGKIFGSI CSLSGVLVIALPVIVSNFSRIYHONQAD 417
Db      361 FWTITVMTTIGYGDMPKTIAGKIFGSI CSLSGVLVIALPVIVSNFSRIYHONQAD 420
Qy      418 KRAOKKARLARIRAVAKTGSNAIYLSKRNGLNEALGTGPREEHMGKTTSLIESQHH 477
Db      421 KRAOKKARLARIRAVAKTGSNAIYLSKRNGLNEALGTGPREEHMGKTTSLIESQHH 479
Qy      478 HILHCLKETTTGLSYLVDDPLLVRSTIKNHEFIDQMFQEQNCMESSMONTPTSTRPSLS 537
Db      480 HILHCLKETTT-----NHEFIDQMFQEQNCMESSMONTPTSTRPSLS 520
Qy      538 SHPGITTTCCSRRSKKTTHLPNSULPATRLRSQMOELSTIHIQSEOPSLTTSRSSLNK 597
Db      521 SQQGVSTCCSRRSKKTTHLPNSULPATRLRSQMOELSTIHIQSEOPSLTTSRSSLNK 580
Qy      598 DDGLRPNCKTSQITTAIISIPTPALPPEGSRPPASPGNTNIPSTSNVVKVSVL 655
Db      581 DDGLRPNCKTSQITTAIISIPTPALPPEGSRPPASPGNTNIPSTSNVVKVSVL 630

```

```

RESULT 5
US-10-212-677-259
; Sequence 259, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-259

```

```

Query Match      73.2%; Score 2498.5; DB 14; Length 630;
Best Local Similarity 73.6%; Pred. No. 3.1e-205;
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy	179	TLTLLVFFYVYMGFFLPAVSIVITNVSEVPCGATPGS-KEI,PCGERSVAFFCLDPAVMFE	237
Db	181	STMLAVFYVYMGFFLPAVSIVANVETVPCGSPBGHKEI,PCGERIAVAFFCLDPAVMFE	240
Qy	238	TVEYLLRLPAAPSRFRYFTRSVMSIIDVAIMEBYIYGLVMTNEDVSGAFVTLRVFEVFR	297
Db	241	TVEYLLRLTAAPSRFRYFTRSVMSIIDVVAII,RYIYGLVMTNEDVSGAFVTLRVFEVFR	300
Qy	298	EKFSHSGGLRLTGLTILKSCASELGFLLPSLTMATIIIFPTNVFV,EEKSSASKTSIPAS	357
Db	301	EKFSHSGGLRLTGLTILKSCASELGFLLPSLTMATIIIFATVFAKGSASAKTSIPAS	360
Qy	358	FWYITVMTTTLGDMVPRTKIINGKIFGSGICSLSGVLVIALPVPVIVNSFSRIYHQNORAD	417
Db	361	FWYITVMTTTLGDMVPRTKIINGKIFGSGICSLSGVLVIALPVPVIVNSFSRIYHQNORAD	420
Qy	418	KRRPAKKARLARIRAVATGSSNAAYLHRSKNGNLINELTGTPRPEEHMGKTSILISQNH	477
Db	421	KRRPAKKARLARIRAKSGSANAYMQSKNGLLSNLQ--SSDEQAFVSKSGSFFETQIH	479
Qy	478	HLHLCKEKTGSLYVDDPELTSVSTIINGHEFIDEQMEONCESSMONYPSTRSPSIS	537
Db	480	HLHLCKEKT-----NHFEVDEQVFEESGEMEAVALYNNRPSHSPSIS	520
Qy	538	SHPGLTITTCSSRSKKTTHLPNSNL,PAYRLKSMOELSTIHIOGSEOPSLTTSRSSLNKA	597
Db	521	SOQGVTSITCCSRHKKTFEIRIPANVYSGSHQGSIOELSTIOICVETPTPLSNSRSSLNAM	580
Qy	598	DDGARLNCKTISQITTAIISIPTRPALTPREGSR--PRA,SPGNTNIPSTNSVYVAVSVL	655
Db	581	EECVVLANCEQPYVATTAIISIPTRPPTTPGGDPRSFEYSGG-----NIVAVSAL	630

## RESULT 6

```

US-10-212-677-260
: Sequence 260, Application US/10212677
: Publication No. US20030129192A1
: GENERAL INFORMATION:
: APPLICANT: Chenault, Ruth A.
: APPLICANT: Xu, Jiaqichun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48ac7
: CURRENT APPLICATION NUMBER: US/10/212,677
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 260
: LENGTH: 630
: TYPE: prt
: ORGANISM: Homo sapiens
US-10-212-677-260

```

Query Match	73.2%	Score 2498.5;	DB 14;	Length 630;
Best Local Similarity	73.6%	Pred. No. 3.1e-205;		
Matches 486; Conservative	69;	Mismatches 70;	Indels 35;	Gaps 7;

[illegible]

Db	181	STMALVYYTGTGFIASVINAVETYPCCSSPGHIKELPCGERANAFAFLCDTACWIF	240
Qy	238	TVEYLLRLFAAPSRYPRLSRVMSIIDVAALMPYIIGLVMTNNEDEVSAFVTLRVRVRI	297
Db	241	TVEYLLRLAAPSRYPRLSRVMSIIDVAALMPYIIGLVMTNNEDEVSAFVTLRVRVRI	300
Qy	298	PKFERHSGGLRLIGYTLTKSCASELGFLLFSLTMAIIPATWMPFAEKSSASAKFTSPIS	357
Db	301	PKFERHSGGLRLIGYTLTKSCASELGFLLFSLTMAIIPATWMPFAEKSSASAKFTSPIS	360
Qy	358	FWYIIVMTTLGYGDMVPKTIAGKIFGSGISGLGVLTALPVYIVSNFSRYYHONORAD	417
Db	361	FWYIIVMTTLGYGDMVPKTIAGKIFGSGISGLGVLTALPVYIVSNFSRYYHONORAD	420
Qy	418	KRAOKTARLARIRIVAKTSSNAALYSKRNGLNEALELTGTPEEBHNGKTTSLIESQH	477
Db	421	KRRQOKARLARIRIAKSGSANAAMQSRNGLNSLOQ-SSEDEQAFQSKSSSFEQOH	479
Qy	478	HLHCHLEKTTGLSYLVDDPLLSVTRSTIKNHEFLIDEOMFEONCMESSMONYPTSPIS	537
Db	480	HLHCHLEKTT-----NHEFVDEQVFEESCMEVATNRPSSSPIS	520
Qy	538	SHPLGJTTCGRBCKTTHLPLNSULPATRLASMOELSTPHIOGSOPLTTSRRSLNKA	597
Db	521	SQOGVSTSCCRHKKFTFRIPANAVSGHOSIOELSTPHIQRCVBRPTLSNRRSSINAAQM	580
Qy	598	DDGLRPNCKTQITTAISIPTPPALPREGESRP--PASPGPNINIPISITSNVAVSYL	655
Db	581	EECVKNCQEPYVTAIISIPTPPPTTPEGDRPESPEYSG-----NIRAVSYL	630

## RESULT 7

```

US-10-212-677-261
; Sequence 261, Application US/10212677
; Publication No. US20030129192A1
GENERAL INFORMATION:
; APPLICANT: Chenaule, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.46AC7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-261

```

Query Match	73.2%	Score	2498.5	DB	14	Length	630
Best Local Similarity	73.6%	Pred.	No. 3.1e-205				
Best Match 486; Conservative	69	Mismatches	70	Indels	35	Gaps	7

```

QY 1 MAAGYAAALPBARAAALICMMPVANCPMLAPADKKR--ODELIVLVNSGRRTQWMTTLE 59
Db 1 MAAGYAAALPBARAAALICMMPVASGPMWAPRQERKKQTODALIVLVNSTRTQWTDLIE 60
QY 60 RYPDTLIGSTEKEPFENEDTKEYFFDRDPBEVRCULNFRCTKLYHPRYECISAYDELA 119
Db 61 RYPDTLLGSSSRDPFYHPDETQOYFFDRDPDIPRHILNFRCTKLYHPRHRCISAYDELA 120
QY 120 FYGLIPETIGCCVEEYKDKRKNRNLMDNDSDNNQES-MPSLSFRQTMARAPENPHT 178
Db 121 FFGILPEIIGCCVEEYKDRRKNRNLQDDADDTTAGSALPLTMARQVRMARFENPHT 180
QY 179 STLAIVFYVYVGFIAVSVITNVVTVTCGTVPGS-KELPGCGRYSVAFFCIDLACVMIF 237

```

Db 181 STMALVFYVVTGFTIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACWMI 240  
 Qy 238 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 297  
 Db 241 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 300  
 Qy 298 FKFSSHSGGLRILGLTLLKSCASELGFLLFSLTMAIIIFATVWFAEKSSASKFTSIPAS 357  
 Db 301 FKFSSHSGGLRILGLTLLKSCASELGFLLFSLTMAIIIFATVWFAEKSSASKFTSIPAS 360  
 Qy 358 FMYITVMTTIGYGMVPEKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHONORAD 417  
 Db 361 FMYITVMTTIGYGMVPEKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHONORAD 420  
 Qy 418 KRRACKARLARIRAKTGSSNAYLHRSKNGILNEALBLTGTPEEHNGKTTSLIESQHH 477  
 Db 421 KRRACKARLARIRAKTGSSNAYLHRSKNGILNEALBLTGTPEEHNGKTTSLIESQHH 479  
 Qy 478 HLHLEKTTGSLYVLDPLSVRTSTIKNHEFIDQVFEONCMSSMONTPTSTSPSL 537  
 Db 480 HLHLEKTTGSLYVLDPLSVRTSTIKNHEFIDQVFEONCMSSMONTPTSTSPSL 520  
 Qy 538 SHPGITTCGSRRSKKTTHLPNSNLPATRLSMOELSTIHIQSGEOPSLTSSSLNKA 597  
 Db 521 SOQGVSTCCSRHKKTRIRIPNAVSGSHQSIQELSTIQRICVETPLSNRSSLNAM 580  
 Qy 598 DDGLRPNCKTQITTAIIISITPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 655  
 Db 581 EECVLANCEQPYVTTAIIISITPPALTPEGEDDRPESPESVSG-----NIVRSAL 630

RESULT 8

US-10-361-811-258  
 ; Sequence 258, Application US/10361811  
 ; Publication No. US20030206918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C8  
 ; CURRENT APPLICATION NUMBER: US/10/361,811  
 ; CURRENT FILING DATE: 2003-02-05  
 ; NUMBER OF SEQ ID NOS: 293  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 258  
 ; LENGTH: 630  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-361-811-258

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;  
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

Qy 1 MAAGVAAWLPPARAAAIIGMPVANCMPMLAPADKRR--ODELIVINSGRRFQWRTTLE 59  
 Db 1 MAAGVAAWLPPARAAAIIGMPVANCMPMLAPADKRR--ODELIVINSGRRFQWRTTLE 60  
 Qy 60 RYPTLLGSTEKEPFENEDTKEYFFDRDPEVRCVLANFRTGKLHYPRYECISAYDEBLA 119  
 Db 61 RYPTLLGSSERDPEFYHETQOYFFDRDPEIFRHLINLFRYFGKLHYPRHECISAYDEBLA 120  
 Qy 120 FYGLPEIIGCCYEEYKDRRENAERLQDDADDTJAGESALPTMTAQWRARAFENHT 178  
 Db 121 FYGLPEIIGCCYEEYKDRRENAERLQDDADDTJAGESALPTMTAQWRARAFENHT 180  
 Qy 179 STMALVFYVVTGFTIAVSIVIANVETVPCGTPGS--KELPCGERYSVAFCLDTACWMI 237  
 Db 181 STMALVFYVVTGFTIAVSIVIANVETVPCGTPGS--KELPCGERYSVAFCLDTACWMI 240  
 Qy 238 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 297

Db 241 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 300  
 Qy 298 FKFSSHSGGLRILGLTLLKSCASELGFLLFSLTMAIIIFATVWFAEKSSASKFTSIPAS 357  
 Db 301 FKFSSHSGGLRILGLTLLKSCASELGFLLFSLTMAIIIFATVWFAEKSSASKFTSIPAS 360  
 Qy 358 FMYITVMTTIGYGMVPEKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHONORAD 417  
 Db 361 FMYITVMTTIGYGMVPEKTIAGKIFGSIICSLGVLVIALPVPIVSNFSRIYHONORAD 420  
 Qy 418 KRRACKARLARIRAKTGSSNAYLHRSKNGILNEALBLTGTPEEHNGKTTSLIESQHH 477  
 Db 421 KRRACKARLARIRAKTGSSNAYLHRSKNGILNEALBLTGTPEEHNGKTTSLIESQHH 479  
 Qy 478 HLHLEKTTGSLYVLDPLSVRTSTIKNHEFIDQVFEONCMSSMONTPTSTSPSL 537  
 Db 480 HLHLEKTTGSLYVLDPLSVRTSTIKNHEFIDQVFEONCMSSMONTPTSTSPSL 520  
 Qy 538 SHPGITTCGSRRSKKTTHLPNSNLPATRLSMOELSTIHIQSGEOPSLTSSSLNKA 597  
 Db 521 SOQGVSTCCSRHKKTRIRIPNAVSGSHQSIQELSTIQRICVETPLSNRSSLNAM 580  
 Qy 598 DDGLRPNCKTQITTAIIISITPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 655  
 Db 581 EECVLANCEQPYVTTAIIISITPPALTPEGEDDRPESPESVSG-----NIVRSAL 630

RESULT 9

US-10-361-811-259  
 ; Sequence 259, Application US/10361811  
 ; Publication No. US20030206918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C8  
 ; CURRENT APPLICATION NUMBER: US/10/361,811  
 ; CURRENT FILING DATE: 2003-02-05  
 ; NUMBER OF SEQ ID NOS: 293  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 259  
 ; LENGTH: 630  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-361-811-259

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
 Best Local Similarity 73.6%; Pred. No. 3.1e-205;  
 Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

Qy 1 MAAGVAAWLPPARAAAIIGMPVANCMPMLAPADKRR--ODELIVINSGRRFQWRTTLE 59  
 Db 1 MAAGVAAWLPPARAAAIIGMPVANCMPMLAPADKRR--ODELIVINSGRRFQWRTTLE 60  
 Qy 60 RYPTLLGSTEKEPFENEDTKEYFFDRDPEVRCVLANFRTGKLHYPRYECISAYDEBLA 119  
 Db 61 RYPTLLGSSERDPEFYHETQOYFFDRDPEIFRHLINLFRYFGKLHYPRHECISAYDEBLA 120  
 Qy 120 FYGLPEIIGCCYEEYKDRRENAERLQDDADDTJAGESALPTMTAQWRARAFENHT 178  
 Db 121 FYGLPEIIGCCYEEYKDRRENAERLQDDADDTJAGESALPTMTAQWRARAFENHT 180  
 Qy 179 STMALVFYVVTGFTIAVSIVIANVETVPCGTPGS--KELPCGERYSVAFCLDTACWMI 237  
 Db 181 STMALVFYVVTGFTIAVSIVIANVETVPCGTPGS--KELPCGERYSVAFCLDTACWMI 240  
 Qy 238 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 297  
 Db 241 TVEYLLRLFAAPSRPRFIRSVMSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVERPRI 300  
 Qy 298 FKFSSHSGGLRILGLTLLKSCASELGFLLFSLTMAIIIFATVWFAEKSSASKFTSIPAS 357

```

Db      301 FKSRHSQGLRIIGYTLKSCASELGLFSLTMAIIIPATVMEYAEKSSASKFTSIPAA 360
Qy      358 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 417
Db      361 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 420
Qy      418 KRAQKAKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMKTSLIESQHH 477
Db      421 KRAQKAKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMKTSLIESQHH 479
Qy      478 HLHCKEKTGLSYLVDDPLSVRTSTIKNHEFIDQMEONCESMOMYPTSTRPSLS 537
Db      480 HLHCKEKT-----NHEFVDEQVFEESCEVAATVNRPSHSLS 520
Qy      538 SHPGLTTCSSRRSKKTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTSSSLNLKA 597
Db      521 SQGVSTSCSSRRHKTKFRIPNANVSGSHQSIQELSTIQICRVERPLSNSSSLNAKM 580
Qy      598 DDLGRPNCKTSQTTTAIISIPTPALTPGESRP--PPASPGPNTNIPSTSNVAVSVL 655
Db      581 BECVKLNCEQPYVTTAIISIPTPVTPBGGDRPESPEVSGG-----NIVRVSL 630

```

## RESULT 10

```

US-10-361-811-260
; Sequence 260, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361.811
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-361-811-260

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
Best Local Similarity 73.6%; Pred. No. 3.1e-205;

Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy      1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNR-ODELIVLVNSGRRFQWRTTLE 59
Db      1 MAAGVAAWLPFARAALIGMMPVASCMPAPAPROERKKTODALIVLVNSGTRFQWQDTLE 60
Qy      60 RYDPTLLGSTEKEFFNEDETKYEFPRDPEVRCVNFRTGKLHYPRYCISAYDELA 119
Db      61 RYDPTLLGSSERDFPHPTQOYFFRDPDPIFRHIIINFRTGKLHYRHCISAYDELA 120
Qy      120 FYGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQES--MPSLSFRQTMRAFENPHT 178
Db      121 FFGILPEIIGDCCYEYKDKRRENAERLQDDADTDGASALPTMTARQVWRAFENPHT 180
Qy      179 STALVFFVYVYTGFFIAVSITNVVETVPCGVPGS--KELPCGERYSVAFCCLDTACMIF 237
Db      181 STMALVFFVYVYTGFFIAVSIVIANVETVPCGSSPGHIELPCGERYVAVAFCLDTACMIF 240
Qy      238 TVEYLRLPAAPSRRYRFSVMSIIDVVAIMPYIIGLVNTNEDVSGAFVTLRVERFERI 297
Db      241 TVEYLRLPAAPSRRYRFSVMSIIDVVAIMPYIIGLVNTNEDVSGAFVTLRVERFERI 300
Qy      298 FKFSRHSQGLRIIGYTLKSCASELGLFSLTMAIIIPATVMEYAEKSSASKFTSIPAS 357
Db      301 FKFSRHSQGLRIIGYTLKSCASELGLFSLTMAIIIPATVMEYAEKSSASKFTSIPAA 360
Qy      358 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 417

```

```

Db      361 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 420
Qy      418 KRAQKAKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMKTSLIESQHH 477
Db      421 KRAQKAKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMKTSLIESQHH 479
Qy      478 HLHCKEKTGLSYLVDDPLSVRTSTIKNHEFIDQMEONCESMOMYPTSTRPSLS 537
Db      480 HLHCKEKT-----NHEFVDEQVFEESCEVAATVNRPSHSLS 520
Qy      538 SHPGLTTCSSRRSKKTHLPNSNLPATRLRSMOELSTIHIOGSEOPSLTSSSLNLKA 597
Db      521 SQGVSTSCSSRRHKTKFRIPNANVSGSHQSIQELSTIQICRVERPLSNSSSLNAKM 580
Qy      598 DDLGRPNCKTSQTTTAIISIPTPALTPGESRP--PPASPGPNTNIPSTSNVAVSVL 655
Db      581 BECVKLNCEQPYVTTAIISIPTPVTPBGGDRPESPEVSGG-----NIVRVSL 630

```

## RESULT 11

```

US-10-361-811-261
; Sequence 261, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361.811
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 630
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-361-811-261

```

Query Match 73.2%; Score 2498.5; DB 15; Length 630;

Best Local Similarity 73.6%; Pred. No. 3.1e-205;

Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

```

Qy      1 MAAGVAAWLPFARAALIGMMPVANCMPPLAPADKNR-ODELIVLVNSGRRFQWRTTLE 59
Db      1 MAAGVAAWLPFARAALIGMMPVASCMPAPAPROERKKTODALIVLVNSGTRFQWQDTLE 60
Qy      60 RYDPTLLGSTEKEFFNEDETKYEFPRDPEVRCVNFRTGKLHYPRYCISAYDELA 119
Db      61 RYDPTLLGSSERDFPHPTQOYFFRDPDPIFRHIIINFRTGKLHYRHCISAYDELA 120
Qy      120 FYGILPEIIGDCCYEYKDKRRENAERLMDNDSENNQES--MPSLSFRQTMRAFENPHT 178
Db      121 FFGILPEIIGDCCYEYKDKRRENAERLQDDADTDGASALPTMTARQVWRAFENPHT 180
Qy      179 STALVFFVYVYTGFFIAVSITNVVETVPCGVPGS--KELPCGERYSVAFCCLDTACMIF 237
Db      181 STMALVFFVYVYTGFFIAVSIVIANVETVPCGSSPGHIELPCGERYVAVAFCLDTACMIF 240
Qy      238 TVEYLRLPAAPSRRYRFSVMSIIDVVAIMPYIIGLVNTNEDVSGAFVTLRVERFERI 297
Db      241 TVEYLRLPAAPSRRYRFSVMSIIDVVAIMPYIIGLVNTNEDVSGAFVTLRVERFERI 300
Qy      298 FKFSRHSQGLRIIGYTLKSCASELGLFSLTMAIIIPATVMEYAEKSSASKFTSIPAS 357
Db      301 FKFSRHSQGLRIIGYTLKSCASELGLFSLTMAIIIPATVMEYAEKSSASKFTSIPAA 360
Qy      358 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 417
Db      361 FWTTIVMTTLGYDGMVPTKIAGKIFGSIKSGVLVIALPVPIVSNFSRIYHONQRAD 420
Qy      418 KRAQKAKARLARIRVAKTSSNAYLHSKRNGLLNEALELTGTPEEHMKTSLIESQHH 477

```



Db 421 KRAQKARLARIRAKSGANAYMOSKRNGLNSNOLQ-SSDEQAFAVSKSGSPETQHH 479  
Qy 478 HLHCLKLEKTTGSLYVDDPLSVRTSTIKNEHFIDEQNEQNCMESSMONTSTSPSL 537  
Db 480 HLHCLKLEKTT-----NHEFVDEQVEESCEVATVNRPSHSPSL 520  
Qy 538 SHPGITTCSSRRSKKTHLPNSNLPATRLSMOELSTIHIOGSEOPSLTSSRLNKA 597  
Db 521 SOQGVSTCCSRHKKTRIPANAVSGSHQSIQELSTIQIRCVERTPLSNSRSLNKM 580  
Qy 598 DDGLRPNCKTSQITTAIISIPTPALTPEGESRP--PASPGPNNTNIPSTSNVAVYL 655  
Db 581 BECVLNCQEPYVTTAIIISIPTPYTPBGDRPESPESG-----NIVRSAL 630

RESULT 12  
US-10-369-186-258  
; Sequence 258, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Flang, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 258  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-258

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
Best Local Similarity 73.6%; Pred. No. 3.1e-205;  
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;  
Qy 1 MAAGAAALPPARAALGMPVANCMPMLAPADKNKR-ODELIYLVNSGRFPQRTTLE 59  
Db 1 MAAGAAALPPARAALGMPVANCMPMLAPADKNKR-ODELIYLVNSGRFPQRTTLE 60  
Qy 60 RYPTLLGSTEKEFFENEDTKEYFFDRDPEVRCVLFNRYRGKLYHPRECIISAYDELA 119  
Db 61 RYPTLLGSSSRDFFHYHETQYFFDRDPDIFRHILNFYRGKLYHPRECIISAYDELA 120  
Qy 120 FYGLIPEIIGDCYCEYKDRRENAERLMDNDSENNOES-MPSLSFQTMWRAFENPHT 178  
Db 121 FFGIPEIIGDCYCEYKDRRENAERLMDNDSENNOES-MPSLSFQTMWRAFENPHT 180  
Qy 179 STLALVFYVYVGFIAVSVINNVVETVPCGTVPGS-KELPCGERYSVAFCLDTACWIF 237  
Db 181 STMALVFYVYVGFIAVSVINNVVETVPCGSSPGHILKELPCGERYAVAFCLDTACWIF 240  
Qy 238 TVEYILRLFAAPSRRYFRYSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLRVERVRI 297  
Db 241 TVEYILRLFAAPSRRYFRYSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLRVERVRI 300  
Qy 298 FKFSRHSGRLILGYTLKSCASELGFILFSLTMAIIIPATYMFYAEKSSASKFTSIPAS 357  
Db 301 FKFSRHSGRLILGYTLKSCASELGFILFSLTMAIIIPATYMFYAEKSSASKFTSIPAA 360  
Qy 358 FMYITVMTTLYGDMVPKTIAGKIFGSIQSLGVLVIALPVPIVSNFSRIYHONQAD 417  
Db 361 FMYITVMTTLYGDMVPKTIAGKIFGSIQSLGVLVIALPVPIVSNFSRIYHONQAD 420  
Qy 418 KRAQKARLARIRAKTGSANAYHSGRNGLNLEALSLTGPPEEHMKTSLIESQHH 477  
Db 421 KRAQKARLARIRAKTGSANAYHSGRNGLNLEALSLTGPPEEHMKTSLIESQHH 479  
Qy 478 HLHCLKLEKTTGSLYVDDPLSVRTSTIKNEHFIDEQNEQNCMESSMONTSTSPSL 537

Db 480 HLHCLKLEKTT-----NHEFVDEQVEESCEVATVNRPSHSPSL 520  
Qy 538 SHPGITTCSSRRSKKTHLPNSNLPATRLSMOELSTIHIOGSEOPSLTSSRLNKA 597  
Db 521 SOQGVSTCCSRHKKTRIPANAVSGSHQSIQELSTIQIRCVERTPLSNSRSLNKM 580  
Qy 598 DDGLRPNCKTSQITTAIISIPTPALTPEGESRP--PASPGPNNTNIPSTSNVAVYL 655  
Db 581 BECVLNCQEPYVTTAIIISIPTPYTPBGDRPESPESG-----NIVRSAL 630

RESULT 13  
US-10-369-186-259  
; Sequence 259, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Flang, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 259  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-259

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
Best Local Similarity 73.6%; Pred. No. 3.1e-205;  
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;  
Qy 1 MAAGAAALPPARAALGMPVANCMPMLAPADKNKR-ODELIYLVNSGRFPQRTTLE 59  
Db 1 MAAGAAALPPARAALGMPVANCMPMLAPADKNKR-ODELIYLVNSGRFPQRTTLE 60  
Qy 60 RYPTLLGSTEKEFFENEDTKEYFFDRDPEVRCVLFNRYRGKLYHPRECIISAYDELA 119  
Db 61 RYPTLLGSSSRDFFHYHETQYFFDRDPDIFRHILNFYRGKLYHPRECIISAYDELA 120  
Qy 120 FYGLIPEIIGDCYCEYKDRRENAERLMDNDSENNOES-MPSLSFQTMWRAFENPHT 178  
Db 121 FFGIPEIIGDCYCEYKDRRENAERLMDNDSENNOES-MPSLSFQTMWRAFENPHT 180  
Qy 179 STLALVFYVYVGFIAVSVINNVVETVPCGTVPGS-KELPCGERYSVAFCLDTACWIF 237  
Db 181 STMALVFYVYVGFIAVSVINNVVETVPCGSSPGHILKELPCGERYAVAFCLDTACWIF 240  
Qy 238 TVEYILRLFAAPSRRYFRYSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLRVERVRI 297  
Db 241 TVEYILRLFAAPSRRYFRYSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLRVERVRI 300  
Qy 298 FKFSRHSGRLILGYTLKSCASELGFILFSLTMAIIIPATYMFYAEKSSASKFTSIPAS 357  
Db 301 FKFSRHSGRLILGYTLKSCASELGFILFSLTMAIIIPATYMFYAEKSSASKFTSIPAA 360  
Qy 358 FMYITVMTTLYGDMVPKTIAGKIFGSIQSLGVLVIALPVPIVSNFSRIYHONQAD 417  
Db 361 FMYITVMTTLYGDMVPKTIAGKIFGSIQSLGVLVIALPVPIVSNFSRIYHONQAD 420  
Qy 418 KRAQKARLARIRAKTGSANAYHSGRNGLNLEALSLTGPPEEHMKTSLIESQHH 477  
Db 421 KRAQKARLARIRAKTGSANAYHSGRNGLNLEALSLTGPPEEHMKTSLIESQHH 479  
Qy 478 HLHCLKLEKTTGSLYVDDPLSVRTSTIKNEHFIDEQNEQNCMESSMONTSTSPSL 537  
Db 480 HLHCLKLEKTT-----NHEFVDEQVEESCEVATVNRPSHSPSL 520  
Qy 538 SHPGITTCSSRRSKKTHLPNSNLPATRLSMOELSTIHIOGSEOPSLTSSRLNKA 597

Db 521 SQQGVSTCCSRHKKTFRIIPNANVSGSHGSIQELSTIOICRVERTPLSNSSSLNAKM 580  
Qy 598 DDGLRPCKTSQITTAIISIPTPALPPEGESRP--PPASGPGNTNIPSTSNVVKSVL 655  
Db 581 BECVKLNCEOPYTTTAIISIPPTVTTPGDDRPESPEYSGG-----NIVRSAL 630

RESULT 14  
US-10-369-186-260  
; Sequence 260, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 260  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-260

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
Best Local Similarity 73.6%; Pred. No. 3.1e-205; Indels 35; Gaps 7;  
Matches 486; Conservative 69; Mismatches 70;

Qy 1 MAAGVAAMLPFARAAAIIGMPVANCMPPLAPADKNKR--ODELIVANVSGRRFQMTTLE 59  
Db 1 MAAGVAAMLPFARAAAIIGMPVANGMPAPRQGRKGTQDALIVANVSGRRFQMTTLE 60  
Qy 60 RYPTDLLGSTEKEFFNEDTKEYFFDRDPEVRCVINFRTGKLAHYRPECISAYDELA 119  
Db 61 RYPTDLLGSSERDFPHETQYFFDRDPIFRHILNFRTGKLAHYRHECISAYDELA 120  
Qy 120 FYGLIBELIIGDCCYEERKDRRENAERLMDNDSENNOES--MPSLFRQTMRAFFENPHT 178  
Db 121 FPGILBELIIGDCCYEERKDRRENAERLQDDADTDITGESALPMTARQRMARAFENPHT 180  
Qy 179 STALVFYVYTGFFIVASVITNVETVPCGTVPGS--KELPCGERYSVAFFCLDTACMIF 237  
Db 181 STALVFYVYTGFFIVASVIANVETVPCGSSPGHIELPCGERYVAFFCLDTACMIF 240  
Qy 238 TVEYLRLFAAPSRFYRIRSVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVFVRFR 297  
Db 241 TVEYLRLFAAPSRFYRIRSVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVFVRFR 300  
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 357  
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 360  
Qy 358 FWYTIYMTTLGVDWPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 417  
Db 361 FWYTIYMTTLGVDWPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420  
Qy 418 KRAQOKKARLARIRVAKTGSNAYLHSGKNGLEALBELTGPBEEMGKTTSLIESQHH 477  
Db 421 KRAQOKKARLARIRVAKTGSNAYLHSGKNGLEALBELTGPBEEMGKTTSLIESQHH 479  
Qy 478 HLHLCLEKTTGLSYLVDDPLLSVTRSTIKNHEFIDEOMFEONCMESMOMYBSTRSPSL 537  
Db 480 HLHLCLEKTT-----NHEFVDEOVFEESCMEEVATVNRPSHSPSL 520  
Qy 538 SHPGLTTCSSRRSKKTTLHNSNLPAIRLSMOELSTIHIOGSEOPSLTTSRSNLKA 597  
Db 521 SQQGVSTCCSRHKKTFRIIPNANVSGSHGSIQELSTIOICRVERTPLSNSSSLNAKM 580  
Qy 598 DDGLRPCKTSQITTAIISIPTPALPPEGESRP--PPASGPGNTNIPSTSNVVKSVL 655

Db 581 BECVKLNCEOPYTTTAIISIPPTVTTPGDDRPESPEYSGG-----NIVRSAL 630

RESULT 15  
US-10-369-186-261  
; Sequence 261, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 261  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-261

Query Match 73.2%; Score 2498.5; DB 15; Length 630;  
Best Local Similarity 73.6%; Pred. No. 3.1e-205; Indels 35; Gaps 7;  
Matches 486; Conservative 69; Mismatches 70;

Qy 1 MAAGVAAMLPFARAAAIIGMPVANCMPPLAPADKNKR--ODELIVANVSGRRFQMTTLE 59  
Db 1 MAAGVAAMLPFARAAAIIGMPVANGMPAPRQGRKGTQDALIVANVSGRRFQMTTLE 60  
Qy 60 RYPTDLLGSTEKEFFNEDTKEYFFDRDPEVRCVINFRTGKLAHYRPECISAYDELA 119  
Db 61 RYPTDLLGSSERDFPHETQYFFDRDPIFRHILNFRTGKLAHYRHECISAYDELA 120  
Qy 120 FYGLIBELIIGDCCYEERKDRRENAERLMDNDSENNOES--MPSLFRQTMRAFFENPHT 178  
Db 121 FPGILBELIIGDCCYEERKDRRENAERLQDDADTDITGESALPMTARQRMARAFENPHT 180  
Qy 179 STALVFYVYTGFFIVASVITNVETVPCGTVPGS--KELPCGERYSVAFFCLDTACMIF 237  
Db 181 STALVFYVYTGFFIVASVIANVETVPCGSSPGHIELPCGERYVAFFCLDTACMIF 240  
Qy 238 TVEYLRLFAAPSRFYRIRSVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVFVRFR 297  
Db 241 TVEYLRLFAAPSRFYRIRSVMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRVFVRFR 300  
Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 357  
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLPSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 360  
Qy 358 FWYTIYMTTLGVDWPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 417  
Db 361 FWYTIYMTTLGVDWPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420  
Qy 418 KRAQOKKARLARIRVAKTGSNAYLHSGKNGLEALBELTGPBEEMGKTTSLIESQHH 477  
Db 421 KRAQOKKARLARIRVAKTGSNAYLHSGKNGLEALBELTGPBEEMGKTTSLIESQHH 479  
Qy 478 HLHLCLEKTTGLSYLVDDPLLSVTRSTIKNHEFIDEOMFEONCMESMOMYBSTRSPSL 537  
Db 480 HLHLCLEKTT-----NHEFVDEOVFEESCMEEVATVNRPSHSPSL 520  
Qy 538 SHPGLTTCSSRRSKKTTLHNSNLPAIRLSMOELSTIHIOGSEOPSLTTSRSNLKA 597  
Db 521 SQQGVSTCCSRHKKTFRIIPNANVSGSHGSIQELSTIOICRVERTPLSNSSSLNAKM 580  
Qy 598 DDGLRPCKTSQITTAIISIPTPALPPEGESRP--PPASGPGNTNIPSTSNVVKSVL 655  
Db 581 BECVKLNCEOPYTTTAIISIPPTVTTPGDDRPESPEYSGG-----NIVRSAL 630

Search completed: April 6, 2005, 08:33:59

Thu Apr 7 08:08:04 2005

us-10-062-879-2.apr5.rapb

Page 9

Job time : 457.608 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:45:50 ; Search time 118.215 Seconds  
(without alignments)  
533.115 Million cell updates/sec

Title: US-10-062-879-2

Sequence: 1 MAGVAAWLPFARAAAGMW.....PGPNTNIPSITSNVKSVL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*  
5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2499.5	73.3	630	2 J00271	voltage-sensitive
2	2122	62.2	651	2 A39372	potassium channel
3	1915.5	56.1	490	2 A35312	potassium channel
4	1103	32.3	236	2 I57681	potassium channel
5	766.5	22.5	802	2 JH0595	potassium channel
6	742.5	21.8	858	2 S31761	potassium channel
7	741	21.7	853	1 CHR1D1	potassium channel
8	736	21.6	602	2 JH0166	potassium channel
9	735	21.5	857	2 I56529	potassium voltage-
10	728	21.3	643	2 S00480	potassium channel
11	727.5	21.3	656	2 JH0193	potassium channel
12	726	21.3	924	2 S12746	potassium channel
13	719	21.1	598	2 S66659	potassium channel
14	719	21.1	602	2 A49507	potassium channel
15	715	21.0	499	2 I77466	potassium channel
16	714	20.9	525	2 A43531	potassium channel
17	713	20.9	499	2 I84204	potassium channel
18	713	20.9	499	2 A33814	potassium channel
19	712.5	20.9	523	2 A38101	potassium channel
20	712	20.9	585	2 A39395	delayed rectifier
21	709.5	20.8	489	2 I51532	potassium channel
22	709	20.8	528	2 I84205	potassium channel
23	709	20.8	924	2 B41359	potassium channel
24	708	20.8	613	2 A39402	potassium channel
25	707.5	20.7	511	2 A46020	potassium channel
26	707	20.7	460	2 T27759	hypothetical prote
27	706.5	20.7	511	2 S07095	potassium channel
28	706.5	20.7	769	2 I56546	Shaw type potassi
29	706	20.7	495	2 A40090	potassium channel

30	706	20.7	495	2 B39113	potassium channel
31	705	20.7	476	2 S21144	potassium channel
32	705	20.7	597	2 S51212	BAKs protein - bov
33	704	20.6	495	2 I57680	potassium channel
34	701.5	20.6	498	2 A41359	potassium channel
35	700	20.5	679	2 A42073	potassium channel
36	699.5	20.5	489	2 J04787	shaw protein - Cal
37	699	20.5	499	2 JH0313	potassium channel
38	699	20.5	624	2 S22703	voltage-gated pota
39	697.5	20.4	625	2 S13919	potassium channel
40	697	20.4	499	2 A48672	delayed rectifier
41	694.5	20.4	660	2 S24125	potassium channel
42	692.5	20.3	581	2 S17150	potassium channel
43	692.5	20.3	653	2 A39922	potassium channel
44	692.5	20.3	654	2 S11049	potassium channel
45	690	20.2	558	2 T23991	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

J00271 voltage-sensitive potassium channel protein [validated] - rat

N:Alternate names: rat sha/1

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C:Accession: J00271; A39113

R:Baldwin, T.J.; Teaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.

Neuron 7, 471-483, 1991

A:Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K+ c

A:Reference number: J00271; MUID:92000693; PMID:1840649

A:Accession: J00271

A:Molecule type: mRNA

A:Residues: 1-630 <BAL>

A:Cross-references: UNIPROT:Q63881; GB:S64320; NID:G236196; PIDN:AB19939.1; PID:G236197

A:Experimental source: hippocampus

R:Roberts, S.L.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel

A:Reference number: A39113; MUID:91156694; PMID:1705709

A:Accession: A39113

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>

A:Cross-references: GB:M59980; NID:G203467; PIDN:AAA40929.1; PID:G203468

C:Function:

A:Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [valida

C:Superfamily: potassium channel protein drkl

C:Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel

F:38/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #sta

F:54/280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status

F:70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta

F:101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status

F:113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase

F:592/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 73.3%; Score 2499.5; DB 2; Length 630;

Best Local Similarity 73.6%; Pred. No. 1.1e-182;

Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;

Oy	1	MAGVAAWLPFARAAAGMWVANCMPPLAPADKNKR-ODELYLTVNSGRRFQWRITLLE 59
Db	1	MAGVAAWLPFARAAAGMWVASCMPAPPRORRKTODALIVNSGTRFQWRITLLE 60
Oy	60	RYPTLLGSTEKEFFNEDTKREYFPDRDPPEVFRVCLNFTYTGKLVRYRECSAYDEBLA 119
Db	61	RYPTLLGSSSRDFFHYPERQOYFFDDPDPIFRHILNFTYTGKLVRRHETSAYDEBLA 120
Oy	120	FYGLPFIIGDCCEEYKDRRENAERLMDNDSENNQES-MPSLRSQTMWRAFENPHT 178
Db	121	FFGILPFIIGDCCEEYKDRRENAERLMDNDSENNQES-MPSLRSQTMWRAFENPHT 180

Qy	179	STLALVFYVMGFFLAASVINNVETVCGVTPGS-KELPGGERSVAFPCLDTRCWMIF	237
Db	181	STMLALVFYVTGFFLAASVINANVETVPCSSPGHKKELPGGERXAAVAFCLDTRCWMIF	240
Qy	238	TVEYLRLFLAAPSRFRFIRSVMSIIDVAIMPPYIGLVTMTNNEEDVSGAFVTLRVFRVRI	297
Db	241	TVEYLRLFLAAPSRFRFIRSVMSIIDVAIIPYYIGLVTMTNNEEDVSGAFVTLRVFRVRI	300
Qy	298	FKFSRHSQGLILIGTLTKSCASELGFLFSLTMALIIIPATWVFVYKSSASKPTISPA	357
Db	301	FKFSRHSQGLILIGTLTKSCASELGFLFSLTMALIIIPATWVFVYKSSASKPTISPA	360
Qy	358	FWYIVTMTTLYGQDMPKTIAGKIFGSIICSLGVLVIALPVPYIVSNFSRIYHONQAD	417
Db	361	FWYIVTMTTLYGQDMPKTIAGKIFGSIICSLGVLVIALPVPYIVSNFSRIYHONQAD	420
Qy	418	KRRQOKKARLARIRVAKTGGSNAYIHSKRNGLINALELTGTPEEHEHNGKTTSLIESQHH	477
Db	421	KRRQOKKARLARIRVAKTGGSNAYIHSKRNGLINAMQLO-SSEDEPAFPAKSSGSETEYQH	479
Qy	478	HLHLCLEKTTGSLYDPPLLSVRTSTIKNEHFIQEQMFQEQCMSSMOMONYSTRSPISL	537
Db	480	HLHLCLEKTT-----NHEFVDEQVFEESCMEVATVYNNRSSHSPISL	520
Qy	538	SHPGJLTTCSSNRASKKTHLPNSNLPATRLRSMOELSTIHHQSSBOPLSTTSSRSSLINKA	597
Db	521	SOQGVTSCTCSRHHKSKFRIPANVANGSHRGVQDELSTIQICVETRTPLSNRSSSLINAKM	580
Qy	598	DDGLRPNCKTSGQITAIISIPRPLATREGESR--PASPECPNINISITSNNVYKAVL	655
Db	581	EECVANLCEQRPVYTAIIISIPRPLATTEBQDNRPSPEYSG-----NIVKVASL	630

## RESULT 2

Potassium channel protein Shall - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
 C:Accession: A59372  
 R:Pa, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salkoff, L.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991  
 A:Title: msnal, a subfamily of A-type K(+) channel cloned from mammalian brain.  
 A:Reference number: A59372; MUID:91239573; PMID:2034678  
 A:Accession: A59372  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-651 <PAK>  
 A:Cross-references: UNIPROT:003719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813

Query Match	62.2%	Score 2122	DB 2	Length 651
Best Local Similarity	63.8%	Pred. No. 7,3e-154		
Matches 434	Conservative 76	Mismatches 116	Indels 54	Gaps 14
Qy	1	MAAGAAALMPFARAALIGMMPVANCMPPLAPADKNNKROBELIVLVNVSGRGFOTWRTTLER	60	
Dd	1	MAAGATATLPPFARAALVGMPLAQOPLPAPEYKASRGDEVULVNVSGRRFETWKNITLDR	60	
Qy	61	YPTLLGSTEKEFPFNEDETKFEYFPRDPEVEFRVCVINFYRTGKLHYPRYECISAYDELALF	120	
Dd	61	YPTLLGSSSEKKEFFYDASGEYFFPRDPDMFPHVINFYRTGRLHCRQGCIGAPBELALF	120	
Qy	121	YGLPEITIGDCCYEYKORKRENAERLMDNDSENNOQSBUL---SFRQMTMAFENE	176	
Dd	121	YGLVELVGDCCLEERDRCKENARLEADEBAEQAGS-PALPAGSSILROELMRAFENP	179	
Qy	177	HTSTLALVFYVTTGFRFIAVSVTINVTENYPCGTVP--GSKELPCGERYSVARFCIDTACV	234	
Dd	180	HTSTALVFYVTTGFRFIAVSIVANVEITPCGRTPMPSEKSCGGRFEPFATFCMDTACV	239	
Qy	235	MIFTVEYLRLPFAASRYAFIRSVMSIIDVVAIMPYYIIGLWNTNDEVGAFYTLRLVFRV	294	
Dd	240	LIFTEYELRLPFAASRCRFLASVMSLIDVAAILPIYIIGLFPKDDVSGAFYTLRLVFRV	299	

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QY 295 RIRPFSSHSGOLRILGTLTKSCAELEFLPSLTMALIIIPATWVEAKSGSASKEFTSI 354
Db 300 RIRPFSSHSGOLRILGTLTKSCAELEFLPSLTMALIIIPATWVEAKSGSKINFTSI 359
QY 355 PASFWYITVIMTTGGYGDMPVPTIAGKI FGSICSLGVLVIALPVVIVISNFSRIYHONO 414
Db 360 PAAFYITVIMTTGGYGDMPVPTIAGKIFGSGICSLGVLVIALPVVIVISNFSRIYHONO 419
QY 415 RADRRACKKARLAIIRVAKTGSSNAYLHKSXNGNLNMLTELATGPREEBH- GKTLSLE 473
Db 420 RADRRACKKARLAIIRAKSGTNALFYQXNG- GLEBSGSDGMLCVRSASRE 475
QY 474 SOHHHLHCELEKTTGLSYLVDDPLLVSRTIKNEHFIDEOMPEQNCMESSQONYPSTRS 533
Db 476 QOHHHLHCELEKTT-----CHEFTDELTFSEMLGAVSLGRTS- RS 515
QY 534 PLSLSHP---GLTTTCCSR- SKYTHLPNSNLPATRLRSNOELSTIHIQSGEOPSLTT 588
Db 516 TSVSQPMGPQSLFSSCCSRVNRPAIRLANSTASVSR- GSWQELDT--LAGLRSPAPQ 572
QY 589 SRSSSLNAKADGCLRNCKTSQITLAIISIPTPPALTPBESRPPPASPG-----PNTNI 642
Db 573 TRSSSLNAPRHSILDINCDSRDFVAAIISIPTPPANTPD- ESQPPSSPSGGSGSGGTENTTL 631
QY 643 -----PSITSNVYKSVL 655
Db 632 RNSSLGTCPLCLPEYVIXISL 651

```

### RESULT 3

C:Species: Drosophila melanogaster  
 C:Date: 14-Sep-1990 #sequence\_revision 06-Nov-1992 #text\_change 09-Jul-2004  
 C:Accession: A35312; S12747  
 R:Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salikoff, L.  
 A:Title: K+ current diversity is produced by an extended gene family conserved in Drosophila  
 A:Reference number: A35312; MUID:50239553; PMID:2333511  
 A:Accession: A35312  
 A:Molecule type: mRNA  
 A:Residues: 1-490 <WEI>  
 A:Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457  
 R:Butler, A.; Wei, A.; Salikoff, L.  
 Nucleic Acids Res. 18, 2173-2174, 1990  
 A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.  
 A:Reference number: S12746; MUID:90245668; PMID:2336335  
 A:Accession: S12747  
 A:Molecule type: mRNA  
 A:Residues: 1-490 <BU>  
 A:Cross-references: EMBL:M32660; NID:g158456; PID:g158457  
 C:Genetics:  
 A:Gene: shal2  
 A:Cross-references: FlyBase:FBgn0005564  
 C:Superfamily: potassium channel drk1  
 C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

[illegible]





C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #ext\_change 09-Jul-2004  
 C/Accession: S31761  
 R:Albrecht, B.; Llorca, C.; Stocker, K.; Pongs, O.  
 Submitted to the EMBL Data Library, September 1992  
 A>Description: Cloning, expression and chromosomal localization of the delayed rectifier  
 A/Reference number: S31761  
 A/Accession: S31761  
 A/Molecule type: DNA  
 A/Residues: 1-858 <ALB>  
 A/Cross-references: UNIPROT:Q14721; EMBL:X68302; NID:G30892; PIDN:CAA48374.1; PID:G30893  
 C/Genetic:  
 A:Gene: GDB:KCNB1; KV2.1; DRK1  
 A/Cross-references: GDB:128081; OMIM:600397  
 A/Map position: 20q13.2-20q13.3  
 C/Superfamily: potassium channel protein drk1

Query Match 21.8%; Score 742.5; DB 2; Length 858;  
 Best Local Similarity 29.1%; Pred. No. 2.1e-48; Indels 143; Gaps 20;  
 Matches 194; Conservative 116; Mismatches 213;

27 MFLAPAD--KNKRQDELIVLVNNGRRFQT-WRTTLERYPTLLG-----STEKEFF-----74  
 16 LPEPEMEIYRSKACSRVRLNVLGGLAHEVLMR-TLDRLPRTTRGKRGKRDCTHDSLLQVCD 74  
 QY -FNEDEKTEFFPRDPEVFCVNFYRTGKLHYPRYECISAYDDELAIFYGLPEIIGDCCY 133  
 DB DYSLDNEVEFFDHPAPAFISILNFYRTGRLHMEEMCALSFQSELDYWGIDEIYLESSCCQ 134  
 QY 134 EEYKDKRENAERLMDNDSENNOE-----SMPSLFRQTMRAFNPHSTIALVIFYV 188  
 DB 135 ARYHCKEQMNEBELKREAEFLREREGEFPNCTCAEKRRKLMULEKPNSSVAAKTILAI 194  
 QY 189 TGEFFIVSVITNVETVPCGTVPKSGELPCGERYSVA-----FPCDLTACWMLFTVEYLL 243  
 DB 195 SIMFIVLSTIALSLNLTLP-----ELQSLDFEGSTDPQALHAENAVCIAMFTMEYLL 246  
 QY 244 RLFAAPSRRFRFISVMSIIDVVAIMPYIGLVNTN-----EDVSGAFVTLVFRVFR 296  
 DB 247 RLFSSEPKMKFFGCPNALDILAILPYVYIIFLTESNKSVALQFQVNRVAVQIFRIMRIIR 306  
 QY 297 IFKFSHSGRLILGTYLKSACSELGFLPSLTMAIIFATWMEVYAEKSSASKFTSIPA 356  
 DB 307 ILKLARHSTGLQSLGFTLRSTVNEGLLILFLAMGIMIFSLVFAEKDEDDTKFSIPA 366  
 QY 357 SFWYITVMTTGLGYGMVPEKTIAGKIFGSIQSLGVLVIALPVVIVNSFSRIYHONORA 416  
 DB 367 SFWMATITMTVGYGDIYPTLTKIVGGLCCAGVLVIALPIPIIVNNSEFYKQKQK 426  
 QY 417 DKRAQKARLARIYAKTGSSNAVYHSGKNGLL-----NEALELTGTPEEHH 464  
 DB 427 EKAIKREALELTER-----AKNGSIVSNMMDAPARSIEEMDIVVEKNGEN 471  
 QY 465 MGKTTSLIESQHHLHLCLEKTTGLSLVDDPLLSVTRSTIKNHEFIDEQMFQNCSS 524  
 DB 472 MGKKDYV---QDNHLSBNKKMKTKRT-----LS-ETSSSKS-----PEIK 507  
 QY 525 MONYPTSPSLSSHPGLTTCCSRSSKKTTHLPNSNLPAIRLSMOELSTIHIOGSECP 584  
 DB 508 EQGSPEK-----ARSSSSRPHL-----NQGLEDMNMKAKQOSOP 543  
 QY 585 SLTTSRSSSLMKADDGLRPNCSTQITTAIISITPPALPTEGESRPPAPSPGPNNTIPS 644  
 DB 544 ILNTKESAAQSKPEEL-----EMESIPSPVAP-----LPT 574  
 QY 645 ITSNVY 650  
 DB 575 RTEGVI 580

RESULT 7  
 CHRTD1  
 potassium channel protein drk1 - rat  
 C/Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #ext\_change 09-Jul-2004  
 C/Accession: S05448; A44838  
 R:Frech, G.C.; Vandongen, A.M.J.; Schueter, G.; Brown, A.M.; Joho, R.H.  
 Nature 340, 642-645, 1989  
 A>Title: A novel potassium channel with delayed rectifier properties isolated from rat b1  
 A/Reference number: S05448; MUID:89365157; PMID:2770868  
 A/Accession: S05448  
 A/Molecule type: mRNA  
 A/Residues: 1-853 <FRE>  
 A/Cross-references: UNIPROT:P15387; EMBL:X16476; NID:G57785; PIDN:CAA34497.1; PID:G57786  
 A/Title: it is uncertain whether Met-1 or Met-17 is the initiator  
 R:Drewe, J.A.; Verna, S.; Frech, G.; Joho, R.H.  
 J. Neurosci. 12, 538-548, 1992  
 A/Reference number: A44838; MUID:92156897; PMID:1740690  
 A/Accession: A44838  
 A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA  
 A/Residues: 'MPAG', 1-571 <DRE>  
 A/Cross-references: GB:M81783; NID:G205038  
 A/Experimental source: brain  
 A/Note: sequence extracted from NCBI backbone (NCBIP:81768)  
 C/Genetics:  
 A:Gene: drk1  
 C/Superfamily: potassium channel protein drk1  
 C/Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane  
 F:1-182/Domain: intracellular #status predicted <INT1>  
 F:183-204/Domain: transmembrane #status predicted <TM1>  
 F:225-245/Domain: transmembrane #status predicted <TM2>  
 F:256-276/Domain: transmembrane #status predicted <TM3>  
 F:291-312/Domain: transmembrane #status predicted <TM4>  
 F:327-348/Domain: transmembrane #status predicted <TM5>  
 F:389-410/Domain: transmembrane #status predicted <TM6>  
 F:411-853/Domain: intracellular #status predicted <INT2>  
 F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.7%; Score 741; DB 1; Length 853;  
 Best Local Similarity 27.8%; Pred. No. 2.8e-48;  
 Matches 207; Conservative 126; Mismatches 266; Indels 146; Gaps 22;

27 MFLAPAD--KNKRQDELIVLVNNGRRFQT-WRTTLERYPTLLG-----STEKEFF-----74  
 12 LPEPEMEIYRSKACSRVRLNVLGGLAHEVLMR-TLDRLPRTTRGKRGKRDCTHDSLLQVCD 70  
 QY -FNEDEKTEFFPRDPEVFCVNFYRTGKLHYPRYECISAYDDELAIFYGLPEIIGDCCY 133  
 DB DYSLDNEVEFFDHPAPAFISILNFYRTGRLHMEEMCALSFQSELDYWGIDEIYLESSCCQ 130  
 QY 75 ARYHCKEQMNEBELKREAEFLREREGEFPNCTCAEKRRKLMULEKPNSSVAAKTILAI 188  
 DB 131 ARYHCKEQMNEBELKREAEFLREREGEFPNCTCAEKRRKLMULEKPNSSVAAKTILAI 190  
 QY 134 EEYKDKRENAERLMDNDSENNOE-----SMPSLFRQTMRAFNPHSTIALVIFYV 188  
 DB 135 ARYHCKEQMNEBELKREAEFLREREGEFPNCTCAEKRRKLMULEKPNSSVAAKTILAI 190  
 QY 189 TGEFFIVSVITNVETVPCGTVPKSGELPCGERYSVA-----FPCDLTACWMLFTVEYLL 243  
 DB 191 SIMFIVLSTIALSLNLTLP-----ELQSLDFEGSTDPQALHAENAVCIAMFTMEYLL 242  
 QY 244 RLFAAPSRRFRFISVMSIIDVVAIMPYIGLVNTN-----EDVSGAFVTLVFRVFR 296  
 DB 247 RLFSSEPKMKFFGCPNALDILAILPYVYIIFLTESNKSVALQFQVNRVAVQIFRIMRIIR 302  
 QY 297 IFKFSHSGRLILGTYLKSACSELGFLPSLTMAIIFATWMEVYAEKSSASKFTSIPA 356  
 DB 307 ILKLARHSTGLQSLGFTLRSTVNEGLLILFLAMGIMIFSLVFAEKDEDDTKFSIPA 362  
 QY 357 SFWYITVMTTGLGYGMVPEKTIAGKIFGSIQSLGVLVIALPVVIVNSFSRIYHONORA 416  
 DB 367 SFWMATITMTVGYGDIYPTLTKIVGGLCCAGVLVIALPIPIIVNNSEFYKQKQK 422  
 QY 417 DKRAQKARLARIYAKTGSSNAVYHSGKNGLL-----LARIYAKTGSSNAVYHSGKNGLL 445  
 DB 427 EKAIKREALELTER-----TPEEHNGKTTSLIESQHHLHLCLEKTTGLSLVDDPLLS 499  
 QY 446 RGLNLEALELTG-----TPEEHNGKTTSLIESQHHLHLCLEKTTGLSLVDDPLLS 499

Db	483	KWKTQKALSTSSSKSPETKEQSPKARSSSPQHNLNVQQLIEDPMYSKMAKTOQSOPILN	542
Qy	500	VRITIKKHEITIDQMFPONCMESMONYPS-----	530
Db	543	TKENAPQSK--PPEBLEMSMSPBVADLPARTBGVIDMRSMSSIDFISCATDPPEATR	599
Qy	531	-TRSP--SLASHPGILTYT-----CCSRSKKTHL-----PNSNLPAT	565
Db	600	FSHPLPLASLSKASSTPAEYGMWKGALGASGRLETETPIETPSRSGFVESPSSMKTN	659
Qy	566	RLRSMOELSTHIIGSEOPSLTTSRSSLNLKADQLRNCKTSQITTAI--ISLPTPAL	623
Db	660	NPLKLRALKNVFVGDDPTPLL-----PSLGL-YHPIPLRRGGAAAVAGLECASLIDKPYL	714
Qy	624	TPE-----GSRPPSPASGPNPNI	642
Db	715	SPSSSIYTTASAKTPPSPREKHTAI	739

## RESULT 8

potassium voltage-gated channel - rat  
N1:Alternate names: potassium channel KV1; potassium channel RK4; shaker-related potassium channel  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: J01016; D39113; I53392  
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunn  
Neuron 4, 929-939, 1990  
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectifying  
A:Reference number: J01016; MUID:90297965; PMID:2361015  
A:Accession: J01016

A:Cross-references: UNIPROT:P19024; GB:M27158; NID:g205100; PIDN:AAA41498.1; PID:g205101  
A:molecule type: mRNA  
A:Residues: 1-602 <SWA>

A: Experimental source: Dr. R. Roberts, S.L.; Tamkun, M.M. Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel  
A:Reference number: A39113; MUID:91156694; PMID:1705709  
A:Accession: D39113

A:Status: preliminary/ nucleic acid sequence not shown; not compared with conceptual trs  
A:Molecule type: mRNA  
A:Residues: 1-552, 'S', 554-602 <ROB>

R;Mori, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.  
J. Biol. Chem. 268, 26482-26493, 1993

A:Reference number: I55392; MUID:94075338; PMID:8253777  
A:Accession: I55392  
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-15 <RES>  
;Cross-references: GB:123434, NID:9443766, PIDN:AAA42337.1, PID:9443767

A:Experimental source: Sprague-Dawley  
C:Genetics:  
A:Gene: Kv1.5

C:Superfamily potassium channel protein drk1  
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; voltage-gated potassium channel  
F:242-260:Domain: transmembrane #status predicted <TM>

F_3316-336/Domain:	transmembrane	#status	predicted	<TM2>
F_3347-368/Domain:	transmembrane	#status	predicted	<TM3>
F_3387-408/Domain:	transmembrane	#status	predicted	<TM4>

F	#status predicted	<TM5>
F_423-444/Domain	#status predicted	<TM6>
F_484-505/Domain	#status predicted	<TM6>
F_10_44,116,181,290/Binding site: carbohydrate (asn)	#status predicted	

Query Match 21.6%; Score 736; DB 2; length 602; F,81,535,546,569/Banding site: phosphate (Ser) (covalent) #status predicted

Best Local Similarity 34.0%; Pred. No. 4.1e-48;  
Matches 177; Conservative 90; Mismatches 162; Indels 92; Gaps 11;

```

0y      30  APADKNROBELIVLVNSGRRFQWTWTLTERYPDTLLSGTEKEF-FNEEDTKEYFPDRP 88
      |||      : ::::: ||| : ::::: ||| : ::::: ||| : ::::: ||| :

```

```

Db 101 APODGSJLHQBVLINIISGLRPEFQJGLTACPPNTLLGPBARLHNFDELRNRYEFPDDR 160
QY 89 EYFRCVLNFYR-GLUHYPRYCISAYDEDLAFYGLPEBITDDCCBEYKDKRREAE 147
Db 161 PSFDJLYYYGSGGLRRRVNLSLVFADEIRFYQ-----LDDEAMERERE----- 206
QY 148 MDNDSENNQOESMPSLSFROTMMRAPENDHSTLALVFYYVNGFFIYAVVITNVETVP- 206
Db 207 -DEGRIKBEKRLPNNEFQOWWLLFEYDESSGARAIAIVSLVLISITFCLETPLE 265
QY 207 -----CGYPSGE-----LPGGRYSVAPFCIDTACY 234
Db 266 FRDERELLRHPRVDPQPARAPAGINGSVSGALSSGPTVALPLP--RTIADPFEIVETCV 323
QY 235 MIFUYELLYRLAASRYRFRISVMSIIDVVAIMPEYIIGLVMTNNEVSGA----- 285
Db 324 IMFTBELLVRFACSGSKAFSFINMNIIDVVAIFPFIITLGHLEMAEQQGGGQNGQAM 383
QY 286 ---FVTLRVFRVRFIFKFSRHSQGLRIIGYLLKCSASLGLSLTMAIIIFATVMFY 341
Db 384 SLALIRVLRILVRFVFIPIKLSRSHKQIOLIKTLOASMRLGILIFELFGLVILFSSAVP 443
QY 342 AEKGSASAKFTSIPRASFYTIIVMTTLGXYGDWVPKTIACKIFGSIISLGSVIALRPVY 401
Db 444 AEADNGHGFSSIRPAIFMAVYMTTIVGDXMRPIITVGKILVGSILCAIGVLTALRPV 503
QY 402 IVSNFSRIYH-----ONORADRR-----AOKKARLARIVAKTSSNAUYH 443
Db 504 IVSNFNYFYRHETDHEOQALKEFGONORRESGLDTGCGRKVSCSKAFCKTGSLESSD 563
QY 444 SKRNLMLAEALLETGTREEMHGKTTSLIEQHNHLLHLE 484
Db 564 SIRRQ-----SCPLEKCHLKAKSNVDRKSLYALCLD 595

```

## RESULT 5

156529 potassium channel protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 156529  
J:Park, M.D.; Covarrubias, M.; Ratcliffe, A.; Salikoff, L.  
J:Neurosci. 11, 869-880, 1991  
A:Title: A mouse brain homolog of the Drosophila Shab K<sup>+</sup> channel with conserved delayed-  
A:Reference number: 156529; MUID:91162315; PMID:2002364  
A:Accession: 156529  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residuals: 1-857 <RES>  
A:Cross-references: UNIPROT:Q03717; GB:M64228; NID:g200975; PID:g200976  
C:Name: Prc

C1:Gene: Shab  
C1:Superfamily: potassium channel protein drkl

Query Match	21.5%	Score 735,	DB 2,	Length 857;
Best Local Similarity	27.3%	Pred. No. 8e-48;		
Matches	205	Consecutive	11	Mismatches 358. Totals 563.
				Gaps 23.

27	MEAPAD--KXKRODELIYANSGRRFQT--WRTTLERYPTDILG-----STEKEFF----	74
QY		
MACHES	203 COMBVALVE 121, MACHES 220, INCHES 120, Q&P 22,	

Db 16 LPPEPMIEIVRSKACSHRRVRLNVGSLAEHVLNR -TLDRLPTRLKLRDCNTHDSLIIQVCD 74

DB 75 DYSLEEDNEKFFPRHGAFTSLNFYRTGRLLHMMHEMCALSPSQGLDYGWIGIDIEYLSCCQ 134

QY 134 EBYKORKRENAERLMDNDSENNO-----SMPSLSFROTMRAFENPHSTLALVFFVV 188  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DS ANHVTAVTAMMTI VRAAFET DEEDDEPPNNMTCCEAEFPKYI WNI FYNCSUMATIT AT I 104

DU            103 ARIKIVLQWVIBUNLEAL LIRKROGBFNI CRRNNNMMULLENFSOY WPAVL DML I      1 27  
QY         189 TGFPIAVSYITNVETVPQGVTVGSKELPCGERISVA -----FFCLDPACMIIFVEYL          243

Db 195 SIMFIVLSIALSLNTLP-----ELQSLDFGSGSTNDNPQLAHVEAVCIAMFTMEYL 246





```

Db      550 ILKVLARSTLQSGFTLRNSYKELGLMLFLMGVLIFPSLAVFAEKEDKTFVS 609
Qy      354 IPASFVYTYVTMTLGGDMVPKTIAGKIPGSCISGVLVIALPVPVIVNSFRSLYHQN 413
        610 IPAFWMAGITMTTGTGIRDCPTTALGKIVGICCCIGVAVMLPFIIVNNAEYKQ 669
Qy      414 QRADKRAOKKARLARIRAKTSSNAYLSKNGELNEALBELTGPBEHMKKTSLIE 473
        670 MRREK---ALKRREALDRAKREGSIVSFHHINLKAFAKSMIDLIVLD--TGKQTNVH 724
Db      474 SQHHHLHLEKTKTGLSYVDLVSRTIK-NHEFIDQMFQONCESSNQNTPSR 532
        725 PK-----GKQSTPNIGRQTLDVQSGPHNLQTDGN--STE 759
Qy      533 SPFLSS-HPGLTTCCSRKSKTTTHLPSNVLPAITRLRSMOE 572
        760 GESTSGRNPAITGTGCTKAYDHAANLNSMLNHRGSSSEQ 800

```

## RESULT 13

S66669

potassium channel (Kv1.5) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S66669

R/Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.

FEBS Lett. 372, 20-24, 1995

A/Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit

A/Reference number: S66669; MUID:96032538; PMID:7556635

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-598 &lt;SAS&gt;

C/References: UNIPROT:P50638; EMBL:D45025; NID:g1060972; PIDN:BA08082.1; PID:d100

C/Superfamily: potassium channel protein drkl

Query Match 21.1%; Score 719; DB 2; Length 598;

Best Local Similarity 35.0%; Pred. No. 8e-47;

Matches 166; Conservative 85; Mismatches 141; Indels 82; Gaps 9;

```

Qy      42 IVANSGRRFQMTTLERKYPDTLLGSTEKEF-FENEDTEYFPDRDDEYFRCVLAIFYRT 100
        106 VLNISGLRRETQGLTADPNNLLGPAKRLRYFPLRNEFFDRRPSFDGLLYYQS 165
Qy      101 -GKLHYPRYCISAYDEDLAFYGLPEIIGDCCEBEYKDKRKAERLMDNSENNOES 159
        166 GGRLRPVNSLDVFADEIRFYQ-----LDDEMERRE-----DEGFIKDEKP 210
Db      160 MPDLFRQTMRAFENPHSTLTALVFYVYTGFIASVITNVETVP----- 206
        211 LPNEFQROQWMLFEYESSGSARALIVSVILISITFCLETLPEFDERELNHRP 270
Qy      207 -----CGT--PQSKELPCGER-YSAFPCLDTACMITVEYLRLFA 247
        271 VPHQPPAPALGANGSAGVAPASGSTVAPLLPRLTADPFIVETTCVIMTFELLYRFA 330
Db      248 APSRYPRIRSVMSIIDVVAIMPYIGLWMTNNEVSGA-----FVTLRVF 292
        331 CPKAEFSRIKIMIIDVVAIPFYLGTLEAEQPGGGGQGOQAMSLAIRVRLV 390
Qy      293 RVERIRFNRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWFAVEKSSASKPT 352
        391 RVFRIFLSSHSGILQILGKTQLASMRLEGILIFLFIIGVILPSSAAYFPEADNQTGHS 450
Qy      353 SIPASFTYTYVTMTLGYGDMVPKTIAGKIPGSCISGVLVIALPVPVIVNSFRSLYHQ 412
        451 SIDAFAWVAVYVTWGYGDMRPITVGAKIVGSLCAIAGVLTIALPVPVIVNSFNYFYHR 510
Qy      413 NQADAKRA-----OKKARLARIRVATGSSNAYLSKRNK 448
        511 ETDHEOALAKBEGSGSGSTSLDAGGQRIASWSKASLCKAGGSLFTADSVRRG 564

```

## RESULT 14

A49507

potassium channel Kv1.5 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: A49507; B49507

R/Attali, B.; Lesage, F.; Zilianti, P.; Gulliemare, E.; Honore, E.; Waldmann, R.; Hugnot, J. Biol. Chem. 268, 24283-24289, 1993

A/Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+) c

A/Reference number: A49507; MUID:94043264; PMID:8226576

A/Accession: A49507

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-602 &lt;ATT&gt;

A/Cross-references: UNIPROT:Q61762; GB:I22218; NID:g435603; PIDN:AAA9365.1; PID:g435604

A/Accession: B49507

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 201-602 &lt;AT2&gt;

A/Cross-references: GB:I22218

C/Superfamily: potassium channel protein drkl

C/Keywords: alternative splicing

Query Match 21.1%; Score 719; DB 2; Length 602;

Best Local Similarity 34.3%; Pred. No. 8.1e-47;

Matches 176; Conservative 93; Mismatches 168; Indels 76; Gaps 12;

```

Qy      30 APADKKKQDELIVANSGRRFQMTTLERKYPDTLLGSTEKEF-FENEDTEYFPDRD 88
        101 APQDSGLHQRVLNLSIRFETQDITLVPNNLLGPAKRLRYFPLRNEFFDRR 160
Qy      89 EYFRCVLAIFYRT-GKLHYPRYCISAYDEDLAFYGLPEIIGDCCEBEYKDKRKAERL 147
        161 PEGDGLIYVYGGGRLRRVNVNSLDVFADEIRFYQ-----LDDEMERRE----- 206
Db      148 MDDNSENNOESNPISLFRQTMRAFENPHSTLTALVFYVYTGFIASVITNVETVP- 206
        207 -DEGFIKEEKPLRNEFQROWMLFEYESSGSARALIVSVILISITFCLETLPE 265
Qy      207 -----CGT--VPQSKELPCGERVSA-----PFCIDTACV 234
        266 FRYDRRLHPPVPPQPPAPAPETNAGSGVSSGT--TVAPLLPRLTADPFIVETTCV 323
Db      235 MIFTVEYLRLFAAPRYRFRSVMSIIDVVAIMPYIGLWMTNNEVSGA----- 285
        324 IMTFELLYRFAFCPSKAEFSRIKIMIIDVVAIPFYLGTLEAEQPGGGGQGOQAM 383
Qy      286 ---FVTLRVFRVFRIRFESRHSQGLRILGYTLKSCASELGFLLFSLTMAIIFATWMEY 341
        384 SLAIVRLVIRLVFRIRFSLSRHSKGLQILGKTQLASMRLEGILIFLFIIGVILFSSAVYF 443
Qy      342 AEKGSASAKFTSPASFVYTYVTMTLGYGDMVPKTIAGKIPGSCISGVLVIALPVPV 401
        444 AEAADNGSGLSSIPDAFWVAVYVTWGYGDMRPITVGAKIVGSLCAIAGVLTIALPVPV 503
Qy      402 IVNSFRIRHONRAKRAOKKARLARIRVA-----KTGSSNAYLSKRNK--N 451
        504 IVSNFNYFTHRETDHEOALAKBEGSILQRRBSGLDGGQKIVSCASRSH-KTGGPLEST 562
Db      452 EALELTGTPDEEHMGKTTSLIESQHHHLHLE 484
        563 DSIIRGSCPLKCKHLAKASNVDLRSLVYALCLD 595

```

## RESULT 15

I77466

potassium channel - human

C/Species: Homo sapiens (man)

C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C/Accession: I77466

R/Ramshaw, M.; Gautam, M.; Kam, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.

Mol. Cell. Neurosci. 1, 214-223, 1990

A/Title: Human potassium channel genes: molecular cloning and functional expression.

A/Reference number: 157680

A/Accession: 177466

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-499 <RES>

A/Cross-references: UNIPROT:P16389; GB:L02752; NID:9186668; PID:AAA6141.1; PID:9186669

C/Superfamily: potassium channel protein drk1

Query Match 21.0%; Score 715; DB 2; Length 499;

Best Local Similarity 35.7%; Pred. No. 1.3e-46;

Matches 158; Conservative 94; Mismatches 136; Indels 54; Gaps 10;

```

QY 40 ELIYLTNSGRREFQRTWRTTLERYPTLLGSTKEF-FENEDTKKEYFEDRDPEVFRCLNFY 98
Db 33 ERVINISGLRFEQULKTQAFPELTLDGDPKRMRYFPDPLRNEYFFDRNRPSPDAILYY 92
QY 99 RT-GKLAHYPRECTSAVDDELAIFYGILPEIIGDCCYEYKDKRKRENAERLMDNDSENQ 157
Db 93 QSGGRLRRPVNVPLDIPSEIRIYE-----LGEEMEMFRE-----DEGIKEE 137
QY 158 ESMPSLSFRQTMRAFENPHTSTLALVYYTGFFIAVSITNVETVPC-----GIVPG 212
Db 138 RPLPENEFQOVWLLFEYESSGPARIYAIVSMVILISVSFCLETLPIRDEREDMHG 197
QY 213 S-----KELPCGERYSVA----FPCLDTCWMIFTVEYLLRLFAAPSRYPFRSVMSI 261
Db 198 SGVTFHTYSNSTIGYQOSTFTDPFFIVETLCIIFSFPEFLVRFPACPSKAGFFTNIMI 257
QY 262 IDVVAIMPEYYIGL-----VMTNEDVSGAFV-TLRVFRVERIRKFSRHSQGLRIL 310
Db 258 IDIVAIITPFTLTGTELAKEPEDAQGGQAMSLAIRVIRLVVRIRIKLSRHSKGLQIL 317
QY 311 GYTLKSCASBELGFLFLFSLTMAIIIFATVMFYAEKSSASKPTSIPASFYTIVTMTLGY 370
Db 318 GQTLKASMRBELGLIFLFLIGVILFSSAVYFAADERESQPSIPDAFMMAVMSWITVGY 377
QY 371 GDMVPKTIAGKIFSGISGLSVLVIALPVPYIVSNFSRIYHQNQRADK-----R 420
Db 378 GDMVPPTIGIKIVGSLCAIAGVLTIALPVPYIVSNFNFYHRETEGEBOAQYLOVTSQPK 437
QY 421 AOKKARLARIIRVAKTGSNAYL 442
Db 438 IPSSPDLKKSRSASTISKSDYM 459

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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:33:59 ; Search time 612.889 Seconds  
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547.263 Million cell updates/sec

Title: US-10-062-879-2

Perfect score: 3412

Sequence: 1 MAAVAAWLPFARAAATGWM.....PGPNTNIPSINSVVKSVL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3407	99.9	655	1 KCD3_HUMAN	Q9UK17 homo sapien
2	3400	99.6	655	1 KCD3_RAT	Q62897 rattus norv
3	3390	99.4	655	1 KCD3_MOUSE	Q920V1 mus musculu
4	3381	99.1	655	1 KCD3_RABIT	Q921T5 oryctolagus
5	3378	99.0	655	2 KCD3_MOUSE	Q8NM02 mustela put
6	3237.5	94.9	658	2 O9PTD3	Q9PTD3 gallus galli
7	2925	85.7	659	2 O57662	Q57662 xenopus lae
8	2570.5	75.3	638	2 Q7ZM36	Q7ZM36 brachydanto
9	2510.5	73.6	630	2 Q8HY21	Q8HY21 mustela put
10	2504.5	73.4	630	1 KCD2_RABIT	P55995 oryctolagus
11	2503.5	73.4	630	1 KCD2_MOUSE	Q920V2 mus musculu
12	2499.5	73.3	630	1 KCD2_RAT	Q63881 rattus norv
13	2498.5	73.2	630	1 KCD2_HUMAN	Q9NZV8 homo sapien
14	2497.5	73.2	632	2 Q8UW33	Q8UW33 gallus galli
15	2122	62.2	651	1 KCD1_MOUSE	Q03719 mus musculu
16	2113	61.9	647	1 KCD1_HUMAN	Q9NA82 homo sapien
17	2013	59.0	660	2 O95PC8	Q95PC8 panulirus i
18	2007	58.8	660	2 O95PC7	Q95PC7 panulirus i
19	2004	58.7	680	2 O95PC6	Q95PC6 panulirus i
20	1967	57.6	579	2 O95PC5	Q95PC5 panulirus i
21	1965	57.6	546	2 O95PC4	Q95PC4 panulirus i
22	1961.5	57.5	585	2 Q26040	Q26040 panulirus i
23	1961.5	57.0	551	2 O95PC0	Q95PC0 panulirus i
24	1946.5	57.0	561	2 O95PC9	Q95PC9 panulirus i
25	1944	57.0	608	2 O95PC3	Q95PC3 panulirus i
26	1915.5	56.1	490	1 CTKL_DROME	P17971 drosophila
27	1908.5	55.9	490	2 Q7Q1S7	Q7Q1S7 atropheles g
28	1885.5	55.3	800	2 Q6R4N6	Q6R4N6 clona intes
29	1842	54.0	633	2 Q8IAD3	Q8IAD3 halocynthia
30	1786	52.3	471	2 Q8IAD2	Q8IAD2 halocynthia
31	1750.5	51.3	609	2 Q95XD1	Q95XD1 caenorhabdi

32	1654.5	48.5	372	2 Q75LS7	Q75LS7 homo sapien
33	1328.5	38.9	478	2 P91784	P91784 polyorchis
34	1103	32.3	236	2 Q61986	Q61986 rattus norv
35	837	24.5	409	2 P91783	P91783 polyorchis
36	767	22.5	908	2 O18476	O18476 loligo peal
37	766.5	22.5	907	1 KCB2_RAT	Q63099 rattus norv
38	761	22.3	911	2 Q7Z7D0	Q7Z7D0 homo sapien
39	756	22.2	815	2 Q98SV4	Q98SV4 ictalurus p
40	755.5	22.1	911	1 KCB2_HUMAN	Q92953 homo sapien
41	754.5	22.1	898	2 Q91592	Q91592 xenopus lae
42	750	22.0	911	1 KCB2_RABIT	Q95111 oryctolagus
43	748.5	21.9	985	1 CTKB_DROME	P17970 drosophila
44	746	21.9	858	1 KCB1_RABIT	Q9M219 oryctolagus
45	745	21.8	494	2 Q91830	Q91830 oncorhynch

#### ALIGNMENTS

RESULT 1  
KCD3\_HUMAN STANDARD; PRT; 655 AA.  
AC Q9UK17; O60576; O60577; Q9UH85; Q9UH86; Q9UK16;  
ID 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE potassium voltage-gated channel subfamily D member 3 (Voltage-gated  
DE potassium channel subunit Kv4.3).  
GN Name=KCNQ3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND  
RP FUNCTION.  
RC TISSUE=Heart;  
RX MEDLINE=99061682; PubMed=9843794;  
RA Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.,  
RT "Isolation and characterization of the human gene encoding Ito:  
RT further diversity by alternative mRNA splicing.";  
RL Am. J. Physiol. 275:H1963-H1970(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain, and Heart;  
RX MEDLINE=99218223; PubMed=10200233;  
RA Dilks D., Ling H.-P., Cockett M., Sokol P., Nunnann R.,  
RT "Cloning and expression of the human Kv4.3 potassium channel.";  
RL J. Neurophysiol. 81:1974-1977(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX Calmele T.P.G., Faivre J.-F., Javre J.-L., Cheval B., Rouanet S.,  
RA Brill A.,  
RT "Long and short human isoforms of the Kv4.3 channel: cloning,  
RT expression, electrophysiology, pharmacology and phosphorylation by  
RT protein kinase C.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
RC TISSUE=Brain cortex;  
RX MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;  
RA Isbrandt D., Leichter T., Waldschuetz R., Zhu X.-R., Luhnann U.,  
RA Michel U., Sauter K., Pongs O.,  
RT "Gene structures and expression profiles of three human KCND (Kv4)  
RT potassium channels mediating A-type currents I(TO) and I(SA).";  
RL Genomics 64:144-154(2000).  
RN [5]  
RP INTERACTION WITH KCNIP2; KCNE1; KCNE2; SCN1B AND KCNAB1.  
RX MEDLINE=2223757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9;  
RA Deschenes I., Tomaselli G.F.,  
RT "Modulation of Kv4.3 current by accessory subunits.";

RL FEBS Lett. 528:183-188(2002).

CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(to) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.

CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4 (By similarity). Interacts with KCNE1, KCNE2, SCN1B and KCNB1.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=KCNB1L, long;

CC IsoId=Q9UK17-1; Sequence=Displayed;

CC Name=2; Synonyms=KCNB3S, short;

CC IsoId=Q9UK17-2; Sequence=VSP\_008826;

CC -1- TISSUE SPECIFICITY: Highly expressed in heart and brain, in particular in cortex, cerebellum, amygdala and caudate nucleus. Detected at lower levels in liver, skeletal muscle, kidney and pancreas. Isoform 1 predominates in most tissues. Isoform 1 and isoform 2 are detected at similar levels in brain, skeletal muscle and pancreas.

CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.

CC -----

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CC -----

DR EMBL: AF048712; AAC05121.1; -

DR EMBL: AF048713; AAC05122.1; -

DR EMBL: AF187963; AAF01044.1; -

DR EMBL: AF187964; AAF01045.1; -

DR EMBL: AF205856; AAF20924.1; -

DR EMBL: AF205857; AAF20925.1; -

DR EMBL: AF120491; AAD38898.1; -

DR EMBL: AF166011; AAF68177.1; -

DR EMBL: AF166009; AAF68177.1; JOINED.

DR EMBL: AF166010; AAF68177.1; JOINED.

DR EMBL: AF166011; AAF68178.1; -

DR EMBL: AF166009; AAF68178.1; JOINED.

DR EMBL: AF166010; AAF68178.1; JOINED.

DR HSSP: Q16968; 1A68.

DR Genew: HGNC:6239; KCND3.

DR MIM: 605411; -

DR InterPro: IPR005821; Ion\_trans.

DR InterPro: IPR001622; K+channel\_pore.

DR InterPro: IPR003091; K\_channel.

DR InterPro: IPR003131; K\_tetra.

DR InterPro: IPR004056; KV43channel.

DR InterPro: IPR003966; Kv\_channel.

DR InterPro: IPR005820; W+channel\_nlg.

DR InterPro: IPR003975; Shal\_channel.

DR Pfam: PF00520; Ion\_trans\_1.

DR Pfam: PF02214; K\_tetra\_1.

DR PRINTS: PR00169; KCHANNEL.

DR PRINTS: PR01518; KV43CHANNEL.

DR PRINTS: PR01491; KVCHANNEL.

DR PRINTS: PR01497; SHALCHANNEL.

KM Alternative splicing; Ion transport; Ionic channel; Multigene family; K+ Potassium; Potassium channel; Potassium transport; Transmembrane; KM Transport; Voltage-gated channel.

FT DOMAIN 1 181 Cytoplasmic (potential).

FT TRANSMEM 182 202 Segment S1 (potential).

FT TRANSMEM 222 242 Segment S2 (potential).

FT DOMAIN 243 256 Cytoplasmic (potential).

FT TRANSMEM 257 277 Segment S3 (potential).

FT TRANSMEM 287 307 Segment S4 (potential).

FT DOMAIN 308 320 Cytoplasmic (potential).

FT TRANSMEM 321 341 Segment S5 (potential).

FT TRANSMEM 360 380 Segment H5 (pore-forming) (potential).

FT TRANSMEM 382 402 Segment S6 (potential).

FT DOMAIN 403 655 Cytoplasmic (potential).

FT SITE 367 372 Selectivity filter (By similarity).

FT VARSPLIC 488 506 Missing (in isoform 2).

FT FTID=VSP\_008826.

FT CONFLICT 239 239 V -> G (in Ref. 1).

FT CONFLICT 375 375 P -> L (in Ref. 1).

FT CONFLICT 408 408 R -> G (in Ref. 2).

FT CONFLICT 452 452 B -> G (in Ref. 2).

FT CONFLICT 531 531 T -> Q (in Ref. 2).

FT CONFLICT 564 564 A -> D (in Ref. 2).

FT CONFLICT 646 646 A -> T (in Ref. 1).

FT CONFLICT 654 654 V -> A (in Ref. 3 and 4).

FT SEQUENCE 655 AA; 73479 MW; ADCE502A97204764 CRC64;

Query Match 99.9%; Score 3407; DB 1; Length 655;

Best Local Similarity 99.8%; Pred. No. 3.6e-205;

Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGVAAWLPFAFAAAIGMPPVANCMPPLAPADKNRQDELIVLVNYSGRFPQWRTTLER 60

1 MAAGVAAWLPFAFAAAIGMPPVANCMPPLAPADKNRQDELIVLVNYSGRFPQWRTTLER 60

QY 61 YPDTLLGSTRKEFPFEDTKEYPFDNDPEVFCVNLFFRTGKLIHYRYSICAYDEDLAF 120

61 YPDTLLGSTRKEFPFEDTKEYPFDNDPEVFCVNLFFRTGKLIHYRYSICAYDEDLAF 120

QY 121 YGILPEIIGDCCCEEXKDKRRENAERLMDNDSENNQESMPSLSPQTMRAENPHST 180

121 YGILPEIIGDCCCEEXKDKRRENAERLMDNDSENNQESMPSLSPQTMRAENPHST 180

QY 121 YGILPEIIGDCCCEEXKDKRRENAERLMDNDSENNQESMPSLSPQTMRAENPHST 180

121 YGILPEIIGDCCCEEXKDKRRENAERLMDNDSENNQESMPSLSPQTMRAENPHST 180

QY 181 LALVFYVYVGFPIAVSVITNVVETVPCGTVPQSKELPCGERYSVAFFCLDTACWMLFTVE 240

181 LALVFYVYVGFPIAVSVITNVVETVPCGTVPQSKELPCGERYSVAFFCLDTACWMLFTVE 240

QY 181 LALVFYVYVGFPIAVSVITNVVETVPCGTVPQSKELPCGERYSVAFFCLDTACWMLFTVE 240

181 LALVFYVYVGFPIAVSVITNVVETVPCGTVPQSKELPCGERYSVAFFCLDTACWMLFTVE 240

QY 241 YLRLFAASRRRFRFISVMSIIDVVAIMPYIGLVNTNEDVSGAVTLRVFVFRIFPK 300

241 YLRLFAASRRRFRFISVMSIIDVVAIMPYIGLVNTNEDVSGAVTLRVFVFRIFPK 300

QY 241 YLRLFAASRRRFRFISVMSIIDVVAIMPYIGLVNTNEDVSGAVTLRVFVFRIFPK 300

241 YLRLFAASRRRFRFISVMSIIDVVAIMPYIGLVNTNEDVSGAVTLRVFVFRIFPK 300

QY 301 SRHSQGLRILGYTLKSCASELGFSLFMAIIFATVNFYAEKSSASAKFTSIPASFV 360

301 SRHSQGLRILGYTLKSCASELGFSLFMAIIFATVNFYAEKSSASAKFTSIPASFV 360

QY 301 SRHSQGLRILGYTLKSCASELGFSLFMAIIFATVNFYAEKSSASAKFTSIPASFV 360

301 SRHSQGLRILGYTLKSCASELGFSLFMAIIFATVNFYAEKSSASAKFTSIPASFV 360

QY 361 TIYMTTLLGYDMVPTIAGKIFGSIQSLSGVLVIALPVVIVSNFSRIYHQNRADKR 420

361 TIYMTTLLGYDMVPTIAGKIFGSIQSLSGVLVIALPVVIVSNFSRIYHQNRADKR 420

QY 361 TIYMTTLLGYDMVPTIAGKIFGSIQSLSGVLVIALPVVIVSNFSRIYHQNRADKR 420

361 TIYMTTLLGYDMVPTIAGKIFGSIQSLSGVLVIALPVVIVSNFSRIYHQNRADKR 420

QY 421 AOKKARLARIYVAKTSSNVAYLHSKRNGLNEALBTGPPEEHMGKTSLISQHHLL 480

421 AOKKARLARIYVAKTSSNVAYLHSKRNGLNEALBTGPPEEHMGKTSLISQHHLL 480

QY 421 AOKKARLARIYVAKTSSNVAYLHSKRNGLNEALBTGPPEEHMGKTSLISQHHLL 480

421 AOKKARLARIYVAKTSSNVAYLHSKRNGLNEALBTGPPEEHMGKTSLISQHHLL 480

QY 481 HCLEKTTGSLYVDDPLSVRTSTIKNHEFIDQMEQNCMESSMNYSTRSPSSHP 540

481 HCLEKTTGSLYVDDPLSVRTSTIKNHEFIDQMEQNCMESSMNYSTRSPSSHP 540

QY 481 HCLEKTTGSLYVDDPLSVRTSTIKNHEFIDQMEQNCMESSMNYSTRSPSSHP 540

481 HCLEKTTGSLYVDDPLSVRTSTIKNHEFIDQMEQNCMESSMNYSTRSPSSHP 540

QY 541 GLTTTCCSRSSKKTTHLPNSNLPATRLRSQMOELSTHIOGSEOPSLTTSRSSLNLKADG 600

541 GLTTTCCSRSSKKTTHLPNSNLPATRLRSQMOELSTHIOGSEOPSLTTSRSSLNLKADG 600

QY 541 GLTTTCCSRSSKKTTHLPNSNLPATRLRSQMOELSTHIOGSEOPSLTTSRSSLNLKADG 600

541 GLTTTCCSRSSKKTTHLPNSNLPATRLRSQMOELSTHIOGSEOPSLTTSRSSLNLKADG 600

QY 601 LRPNCKTSQITTAIISIPTPALTPGESRPPASGPNNTNITSNVKVSVL 655

601 LRPNCKTSQITTAIISIPTPALTPGESRPPASGPNNTNITSNVKVSVL 655

QY 601 LRPNCKTSQITTAIISIPTPALTPGESRPPASGPNNTNITSNVKVSVL 655

601 LRPNCKTSQITTAIISIPTPALTPGESRPPASGPNNTNITSNVKVSVL 655

RESULT 2

KCD3\_KAT STANDARD; PRT; 655 AA.

ID KCD3\_RAT

AC 062897; 008723; P70622; 063286; 099P42;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated  
DE potassium channel subunit Kv4.3).  
GN Name=Kv4.3;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
RX MEDLINE=96428386; PubMed=8831489;  
RA Dixon J.E., Shi W., Wang H.-S., McDonald C., Yu H., Wymore R.S.,  
RA Cohen J.S., McKinnon D.;  
RT "Role of the Kv4.3 K+ channel in ventricular muscle. A molecular  
RT correlate for the transient outward current.";  
RL Circ. Res. 79:659-668(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=96317227; PubMed=8734615;  
RA Tesar M.-U., Chou C.-C., Shih Y.-H., Wang H.-L.;  
RT "Cloning, expression and CNS distribution of Kv4.3, an A-type K+  
RT channel alpha subunit.";  
RL FEBS Lett. 400:215-220(1997).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Smooth muscle, and Vas deferens;  
RX MEDLINE=96111009; PubMed=9450548; DOI=10.1016/S0014-5793(97)01483-X;  
RA Ohya S., Tanaka M., Oki T., Asai Y., Watanabe M., Giles W.R.,  
RA Imazumi Y.;  
RT "Molecular cloning and tissue distribution of an alternatively spliced  
RT variant of an A-type K+ channel alpha-subunit, Kv4.3 in the rat.";  
RL FEBS Lett. 420:47-53(1997).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=Sprague-Dawley; TISSUE=uterus;  
RX MEDLINE=21402960; PubMed=11427525; DOI=10.1074/jbc.M101058200;  
RA Song M., Helguera G., Eghbali M., Zhu N., Zarek M.M., Olcese R.,  
RA Toro L., Stefani E.;  
RT "Remodeling of Kv4.3 potassium channel gene expression under the  
RT control of sex hormones.";  
RL J. Biol. Chem. 276:31883-31890(2001).  
RN [6]  
RP SEQUENCE OF 455-606 FROM N.A. (ISOFORM 1).  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=97460452; PubMed=9314834;  
RA Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Levitan E.S.;  
RT "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel subunit  
RT mRNAs in ventricles of renovascular hypertensive rats.";  
RL Circ. Res. 81:533-539(1997).  
RN [7]  
RP INTERACTION WITH KCNIP1; KCNIP2 AND KCNIP3.  
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;  
RA An W.-P., Bowldy M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,  
RA Hinson J.W., Mattsson K.I., Strassle B.W., Trimmer J.S., Rhodes K.J.;  
RT "Modulation of A-type potassium channels by a family of calcium  
RT sensors.";  
RL Nature 403:553-556(2000).  
RN [8]  
RP SUBCELLULAR LOCATION.  
RX MEDLINE=22128857; PubMed=12006572; DOI=10.1074/jbc.M203651200;  
RA Takimoto K., Yang E.-K., Conforti L.;

RT "Palmitoylation of KChIP splicing variants is required for efficient  
RT cell surface expression of Kv4.3 channels.";  
RL J. Biol. Chem. 277:26904-26911(2002).  
RN [9]  
RP INTERACTION WITH KCNIP4.  
RX MEDLINE=21664433; PubMed=11805342; DOI=10.1073/pnas.022509299;  
RA Holmqvist M.H., Cao J., Hernandez-Pineda R., Jacobson M.D.,  
RA Carroll K.I., Sung M.A., Betty M., Ge P., Gilbride K.J., Brown M.E.,  
RA Urtman M.E., Lawson D., Sliob-Santiago I., Xie Y., Covarrubias M.,  
RA Rhodes K.J., Di Stefano P.S., An W.F.;  
RT "Elimination of fast inactivation in Kv4 A-type potassium channels by  
RT an auxiliary subunit domain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:1035-1040(2002).  
RN [10]  
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
RP inactivating A-type potassium channels. May contribute to I(TO)  
RP current in heart and I(Sa) current in neurons. Channel properties  
RP are modulated by interactions with other alpha subunits and with  
RP regulatory subunits.  
RN [11]  
RP SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.  
RP Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
RP KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNA1 (by  
RP similarity).  
RN [12]  
RP SUBCELLULAR LOCATION: Integral membrane protein. Interaction with  
RP palmitoylated KCNIP2 and KCNIP3 enhances cell surface expression.  
RN [13]  
RP ALTERNATIVE PRODUCTS:  
RP Event-Alternative splicing; Named isoforms=3;  
RP Name=1; Synonyms=Kv4.3 long form;  
RP IsoId=Q62897-1; Sequence=Displayed;  
RP Name=2;  
RP IsoId=Q62897-2; Sequence=VSP\_008831;  
RP Name=3;  
RP IsoId=Q62897-3; Sequence=VSP\_008832;  
RN [14]  
RP TISSUE SPECIFICITY: Highly expressed in brain, in particular in  
RP the retrosplenial cortex, medial habenula, anterior thalamus,  
RP hippocampus, cerebellum and lateral geniculate and superior  
RP colliculus. Highly expressed in heart atrium and throughout the  
RP ventricle wall, in lung and vas deferens.  
RN [15]  
RP DOMAIN: The segment S4 is probably the voltage-sensor and is  
RP characterized by a series of positively charged amino acids at  
RP every third position.  
RN [16]  
RP SIMILARITY: Belongs to the potassium channel family. D (Shal)  
RP subfamily.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
CC EMBL; U42975; AAC52695.1; -;  
CC EMBL; U75448; AAB18337.1; -;  
CC EMBL; L48619; AAB04459.1; -;  
CC EMBL; AF334791; AAK07651.1; -;  
CC EMBL; AB003587; BAA24525.1; -;  
CC EMBL; U92897; AAB53321.1; -;  
CC HSSP; Q16968; 1A68.  
CC InterPro; IPR005821; Ion trans.  
CC InterPro; IPR001622; K+channel\_pore.  
CC InterPro; IPR003091; K\_channel.  
CC InterPro; IPR003131; K\_tetra.  
CC InterPro; IPR004056; KV43channel.  
CC InterPro; IPR003968; Kv channel.  
CC InterPro; IPR005820; M-channel\_nlg.  
CC InterPro; IPR003975; Shal channel.  
CC Pfam; PF00520; Ion trans\_1.  
CC Pfam; PF02214; K\_tetra\_1.  
CC PRINTS; PR00169; KCHANNEL.  
CC PRINTS; PR01518; KV43CHANNEL.  
CC PRINTS; PR01491; KVCHANNEL.  
CC PRINTS; PR01497; SHALCHANNEL.  
CC Alternative splicing; Ion transport; Ionic channel; Multigene family;  
KW



CC	-1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC	inactivating A-type potassium channels. May contribute to I(To)
CC	current in heart and I(Sa) current in neurons. Channel properties
CC	are modulated by interactions with other alpha subunits and with
CC	regulatory subunits.
CC	-1- SUBUNIT: Homotrimer or heterotrimer with KCND1, KCNIP2 and
CC	KCNIP3. Associates with the regulatory subunits KCNIP1, KCNIP2 and
CC	KCNIP3. Interacts with KCNE1, KCNE2, SCN1B and KCNA1 (by
CC	similarity).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=3;
CC	Name=1; Synonyms=Kv4.3b;
CC	IsoId=Q9Z0V1-1; Sequence=Displayed;
CC	Name=2; Synonyms=Kv4.3M;
CC	IsoId=Q9Z0V1-2; Sequence=VSP_008827;
CC	Name=3;
CC	IsoId=Q9Z0V1-3; Sequence=VSP_008828, VSP_008829;
CC	Note=May be due to intron retention. No experimental
CC	confirmation available;
CC	-1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC	characterized by a series of positively charged amino acids at
CC	every third position.
CC	-1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC	subfamily.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF107781; AAD16973.1; -
DR	EMBL; AF107782; AAD16974.1; -
DR	EMBL; AK033962; BAC28529.1; -
DR	HSSP; Q16968; 1A68.
DR	MCD; MG1:1928743; Kcnd3.
DR	InterPro; IPR005821; Ion trans.
DR	InterPro; IPR001622; K-channel_pore.
DR	InterPro; IPR003091; K_channel.
DR	InterPro; IPR003131; K_tetra.
DR	InterPro; IPR004056; KV43channel.
DR	InterPro; IPR003968; Kv channel.
DR	InterPro; IPR005820; M-channel_nlg.
DR	InterPro; IPR003975; Shal_channel.
DR	Pfam; PF00520; Ion_trans_1.
DR	Pfam; PF02214; K_tetra_1.
DR	PRINTS; PRO0169; KCHANNEL.
DR	PRINTS; PRO1518; KV43CHANNEL.
DR	PRINTS; PRO1491; KYCHANNEL.
DR	PRINTS; PRO1497; SHALCHANNEL.
DR	Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW	Potassium; Potassium channel; Potassium transport; Transmembrane;
KW	Transport; Voltage-gated channel.
FT	DOMAIN 1 181
FT	TRANSMEM 182 202 Cytoplasmic (Potential).
FT	TRANSMEM 222 242 Segment S1 (Potential).
FT	DOMAIN 243 256 Segment S2 (Potential).
FT	TRANSMEM 257 277 Cytoplasmic (Potential).
FT	TRANSMEM 287 307 Segment S3 (Potential).
FT	DOMAIN 308 320 Segment S4 (Potential).
FT	TRANSMEM 321 341 Cytoplasmic (Potential).
FT	TRANSMEM 360 380 Segment S5 (Potential).
FT	TRANSMEM 382 402 Segment H5 (pore-forming) (Potential).
FT	TRANSMEM 403 422 Segment S6 (Potential).
FT	DOMAIN 403 655 Cytoplasmic (Potential).
FT	SITE 367 372 Selectivity filter (by similarity).
FT	FT GSTYVDPLSVRTSKNBFDEQFEONCESSWONY
FT	VARSPPLIC 488 531 PST -> VSSLPLPPASLSGCTHIIIRRESSSTPQP
FT	SKTVSLPLDG (in isoform 3).
FT	/FTID=VSP_008828.
FT	Missing (in isoform 2).
VARSPPLIC 488 506	

[illegible]

```

Rt Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 73-645 FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE
RP SPECIFICITY.
RX MEDLINE=22117972; PubMed=12121318;
RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G.,
RA Obeso A., Galfornia M.D., Gonzalez C.;
RT "Molecular identification of Kv alpha subunits that contribute to the
RT oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit
RT carotid body."
RL J. Physiol. (Lond.) 542:369-382(2002).
CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
CC inactivating A-type potassium channels. May contribute to I(To)
CC current in heart and I(Sa) current in neurons. Channel properties
CC are modulated by interactions with other alpha subunits and with
CC regulatory subunits.
CC -1- SUBUNIT: Homotrimer or heterotrimer with KCNP1 and/or KCNP2.
CC Associates with the regulatory subunits KCNP1, KCNP2, KCNP3 and
CC KCNP4. Interacts with KCNE1, KCNE2, SCN1B and KCNA1B (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=Q9JTT5-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=Q9JTT5-2; Sequence=VSP_008830;
CC -1- TISSUE SPECIFICITY: Detected in carotid body chemoreceptor cells
CC and in frontal cortex.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation --
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF198445; AAC6021.1; -
CC EMBL; AF493549; AAM46843.1; -
CC HSSP; Q16958; 1A68.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+-channel.pore.
CC InterPro; IPR003091; K_channel.
CC InterPro; IPR004316; K_tetra.
CC InterPro; IPR004056; KV43channel.
CC InterPro; IPR003968; Kv channel.
CC InterPro; IPR005820; M-channel.ng.
CC InterPro; IPR003975; Shal_channel.
CC Pfam; PF00520; Ion_trans_1.
CC Pfam; PF02214; K_tetra; 1.
CC PRINTS; PRO1518; KV4CHANNEL.
CC PRINTS; PRO1491; KVCHANNEL.
CC PRINTS; PRO1497; SHALCHANNEL.
KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT DOMAIN 1 181
FT TRANSMEM 182 202 Cytoplasmic (Potential).
FT TRANSMEM 222 242 Segment S1 (Potential).
FT DOMAIN 243 256 Segment S2 (Potential).
FT TRANSMEM 257 277 Cytoplasmic (Potential).
FT TRANSMEM 287 307 Segment S3 (Potential).
FT DOMAIN 308 320 Segment S4 (Potential).
FT TRANSMEM 321 341 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Segment S5 (Potential).
FT TRANSMEM 382 402 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 382 402 Segment S6 (Potential).

```

FT	DOMAIN	403	655	Cytoplasmic (potential).
FT	SITE	367	372	Selectivity filter (By similarity).
FT	VARSPLIC	488	506	Missing (in isoform 2).
FT	SEQUENCE	655 AA;	73380 MW;	/FTid=VSP_008830.
SO				
SC				
Query Match		99.1%;	Score 3381;	DB 1; Length 655;
Best Local Similarity		99.1%;	Pred. No. 1.5e-203;	
Matches	649;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0;
QY	1	MAAGVAAMLPEFARAAAIGMPVANCMPPLAPADKNKQDELIIVNVSGRRPQWRTTLER	60	
Db	1	MAAGVAAMLPEFARAAAIGMPVANCMPPLAPADKSKQDELIIVNVSGRRPQWRTTLER	60	
QY	61	YEDPTLLGSTEKEFFPNEDTKEYFFDRDDEVRVCYLNFPRTCKLHYPRECTISAIDDELAF	120	
Db	61	YEDPTLLGSTEKEFFPNEDTKEYFFDRDDEVRVCYLNFPRTCKLHYPRECTISAIDDELAF	120	
QY	121	YGLIPEIIGDCCVEEYDKRKENARLMDNDSDNNQSMPSLSPROTMHAFENPHST	180	
Db	121	YGLIPEIIGDCCVEEYDKRKENARLMDNDSDNNQSMPSLSRQTMMAFENPHST	180	
QY	181	LALVFYVYTGFFIIVSVYITNVVEVPCGVVSGSKELPCGERYSVAFFCLDTACWMIPTVE	240	
Db	181	LALVFYVYTGFFIIVSVYITNVVEVPCGVVSGSKELPCGERYSVAFFCLDTACWMIPTVE	240	
QY	241	YLRLFPAPSPRYRIRTSYMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRPRVPRITKF	300	
Db	241	YLRLFPAPSPRYRIRTSYMSIIDVVAIMPYIIGLVMTNNEVSGAFVTLRPRVPRITKF	300	
QY	301	SRHSGRIIGYTLKSCASELGFLLFSITLMAIIPATMFAAEKSSASKFTSIPASFMY	360	
Db	301	SRHSGRIIGYTLKSCASELGFLLFSITLMAIIPATMFAAEKSSASKFTSIPASFMY	360	
QY	361	TIYVMTTLGYDMPKTIAGKIPGSI CSLSGVLVIALPVPVIVSNFSRIYHQNQADRR	420	
Db	361	TIYVMTTLGYDMPKTIAGKIPGSI CSLSGVLVIALPVPVIVSNFSRIYHQNQADRR	420	
QY	421	AQKARLARIRVAKTGSNNAYLHSKRNLNLEALETGTPEEHNKGTSLIESQHHL	480	
Db	421	AQKARLARIRVAKTGSNNAYLHSKRNLNLEALETGTPEEHNKGTSLIESQHHL	480	
QY	481	HCEKRTGSLVUDPPLSVRTSTIKHHEFIDEQMFENCMSSQNPSTRSPSLSHP	540	
Db	481	HCEKRTGSLVUDPPLSVRTSTIKHHEFIDEQMFENCMSSQNPSTRSPSLSHA	540	
QY	541	GLTTTCCSRREKTKTHLPNSULPATRLRSMOELSTIHQSEOPSLTTRSRSLNKADDG	600	
Db	541	GLTTTCCSRREKTKTHLPNSULPATRLRSMOELSTIHQSEOPSLTTRSRSLNKADDG	600	
QY	601	LRPNCKTSQITTAIISIPTPPALPPEGSGRPPSPGENTNIPSTISNVKVSVL	655	
Db	601	LRPNCKTSQITTAIISIPAPALPPEGSTRPPSPGENTNIPSTISNVKVSVL	655	
RESULT 5				
Q8WN02				
AC	08WN02	PRELIMINARY;	PRT;	655 AA.
DT	01-MAR-2002	(TREMBLrel. 20, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE		Voltage-gated potassium channel Kv4.3 long form.		
OS		Mustela putorius furo (Ferret).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Mustelinae;		
OC		Mustela.		
OX	NCBI_TaxID=9669;			
RN	[1]			
RC		SEQUENCE FROM N.A.		
RC		TISSUE=Heart;		
RX		MEDLINE=21896086; PubMed=11897837;		
RA		Patel S.P., Campbell D.L., Morales M.J., Straus H.C.;		

RT "Heterogeneous expression of Kchir2 isoforms in the ferret heart."  
 RL J. Physiol. 539:649-656(2002).  
 DR EMBL; AF454388; AAL51038.1; --  
 DR HSSP; Q63881; 1S6C.  
 DR GO; GO:0016021; C:Integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PR02214; K\_tetra; 1.  
 DR PRINTS; PR00169; KCHANNEL.  
 DR PRINTS; PR01491; KCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 655 AA; 73375 MW; 3DD3E94819FE6C1 CRC64;

Query Match 99.0%; Score 3378; DB 2; Length 655;  
 Best Local Similarity 98.8%; Pred. No. 2.3e-203;  
 Matches 647; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAGVAAWLPFAPRAAAGMPPVANCMPMLAPADKKRQDELIVNVSGRRPQRTTLIER 60
DB 1 MAAGVAAWLPFAPRAAAGMPPVANCMPMLAPADKKRQDELIVNVSGRRPQRTTLIER 60
QY YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
DB YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
QY 61 YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
DB 61 YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
QY 181 LAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
DB 181 LAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
QY 181 LAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
DB 181 LAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
QY 241 YLRLFLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
DB 241 YLRLFLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
QY 241 YLRLFLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
DB 241 YLRLFLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
QY 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
DB 301 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 420
QY 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 420
DB 361 TIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 420
QY 421 AOKKARLARIVAKTGSNNAYLHSGKGLNLBALLELTGTPBEHNGKTTSLIESOHHL 480
DB 421 AOKKARLARIVAKTGSNNAYLHSGKGLNLBALLELTGTPBEHNGKTTSLIESOHHL 480
QY 421 AOKKARLARIVAKTGSNNAYLHSGKGLNLBALLELTGTPBEHNGKTTSLIESOHHL 480
DB 421 AOKKARLARIVAKTGSNNAYLHSGKGLNLBALLELTGTPBEHNGKTTSLIESOHHL 480
QY 481 HCLEKTGSLVLDPDLVSTRSTIKNHFIDEQMFEQNCMESSNQNPSTRSPSLSSHP 540
DB 481 HCLEKTGSLVLDPDLVSTRSTIKNHFIDEQMFEQNCMESSNQNPSTRSPSLSSHP 540
QY 481 HCLEKTGSLVLDPDLVSTRSTIKNHFIDEQMFEQNCMESSNQNPSTRSPSLSSHP 540
DB 481 HCLEKTGSLVLDPDLVSTRSTIKNHFIDEQMFEQNCMESSNQNPSTRSPSLSSHP 540
QY 541 GLTTTCCSRSKKTTTHLPNSULPATRLASMOELSTIHQSGSOPBLTTSRSLSLNKADG 600
DB 541 GLTTTCCSRSKKTTTHLPNSULPATRLASMOELSTIHQSGSOPBLTTSRSLSLNKADG 600
QY 541 GLTTTCCSRSKKTTTHLPNSULPATRLASMOELSTIHQSGSOPBLTTSRSLSLNKADG 600
DB 541 GLTTTCCSRSKKTTTHLPNSULPATRLASMOELSTIHQSGSOPBLTTSRSLSLNKADG 600
QY 601 LRPNCKTSQITTAIISITPPALTPEGESRPPAPSGPNTNIPSTISVWVYVYL 655
DB 601 LRPNCKTSQITTAIISITPPALTPEGESRPPAPSGPNTNIPSTISVWVYVYL 655
QY 601 LRPNCKTSQITTAIISITPPALTPEGESRPPAPSGPNTNIPSTISVWVYVYL 655
DB 601 LRPNCKTSQITTAIISITPPALTPEGESRPPAPSGPNTNIPSTISVWVYVYL 655

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RESULT 6  
 Q9PTD3 PRELIMINARY; PRT; 658 AA.  
 AC Q9PTD3;

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Potassium channel Kv4.3.  
 GN Name=KCND3;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=breed White Leghorn; TISSUE=Iens epithelium;  
 RA Rae J.L.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF209722; AAF2832.1; --  
 DR HSSP; Q63881; 1S6C.  
 DR GO; GO:0016021; C:Integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR004056; KV43channel.  
 DR InterPro; IPR003968; Kv channel.  
 DR InterPro; IPR003091; K\_channel.  
 DR InterPro; IPR003131; K\_tetra.  
 DR InterPro; IPR005820; M-channel\_nlg.  
 DR InterPro; IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PR00169; KCHANNEL.  
 DR PRINTS; PR01518; KV43CHANNEL.  
 DR PRINTS; PR01491; KCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 658 AA; 73896 MW; 0F8743DAFA8B12A8 CRC64;

Query Match 94.9%; Score 3237.5; DB 2; Length 658;  
 Best Local Similarity 94.8%; Pred. No. 1.5e-194;  
 Matches 624; Conservative 19; Mismatches 12; Indels 3; Gaps 3;

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QY 1 MAAGVAAWLPFAPRAAAGMPPVANCMPMLAPADKKRQDELIVNVSGRRPQRTTLIER 60
DB 1 MAAGVAAWLPFAPRAAAGMPPVANCMPMLAPADKKRQDELIVNVSGRRPQRTTLIER 60
QY YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
DB YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
QY 61 YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
DB 61 YPDTLLGSTEKEFFFNEDTKEFFFDRODEVEFCVNFRTGKLHPRECIASAYDELIAP 120
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
QY 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
DB 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAAFENPATST 180
QY 180 TLAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 239
DB 180 TLAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 239
QY 181 TLAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
DB 181 TLAIVFYVYVGFIAVSITNVETVPCGTVPKSGKELPCGERSVAFPCLDPAACWIFIVE 240
QY 240 EYLLRLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 299
DB 240 EYLLRLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 299
QY 241 EYLLRLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
DB 241 EYLLRLFAPSRVRFIRSVMSIIDVAIMPYYIGLVMTNNEDESGAFVTLRVFRVRIKPF 300
QY 300 FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 359
DB 300 FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 359
QY 301 FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
DB 301 FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVWFYAEKSSASKETSIPASFW 360
QY 360 YTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 419
DB 361 YTIIVMTTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVPVIVSNFSRIYHQNORADRR 420

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QY 420 RAQKARLARIRVAKTSSNAYLHRSKNGLLNEALBELTG-TPEEHMGKTTSLIESQHH 478  
 DB 421 RAQKARLARIRVAKTSSNAYLHRSKNGLLNEALBELTGSTDEBQHTTKGTSIJESQHH 480  
 QY 479 LHLCEKTTGLSYLVDDPLSVRTSTIKNHEFIDEQMFQONCESSQONTPTSRPSLS 538  
 DB 481 LHLCEKTTGLSYLVDDPLSVRTSTIKNHEFIDEQMFQONCESSQONTPTSRPSLS 540  
 QY 539 HPGITTCSSRSRKTTHLPNSNLPATRLSMOELSTHIOGSEQPSLTSTRSLSLNKAD 598  
 DB 541 HPGITTCSSRSRKTTHLPNSNLPATRLSMOELSTHIOGSEQPSLTSTRSLSLNKAD 600  
 QY 599 DGLRPNCSTQITTAIISIPTPALTPEGESRPPSPGPNNTN-PSITSNVAVSVL 655  
 DB 601 DGLRPNCSTQITTAIISIPTPALTPEGESRPPSPGPNNTN-PSITSNVAVSVL 658

## RESULT 7

057662 ID 057662 PRELIMINARY; PRT; 659 AA.  
 AC 057662;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Potassium channel xkv4.3.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lautermilch N.J., Spitzer N.C.;  
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, U89265; AAB94379.1; -.  
 DR HSSP, Q63881; 1S6C.  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0008076; C: voltage-gated potassium channel complex; IEA.  
 DR GO: GO:0005515; F: protein binding; IEA.  
 DR GO: GO:0005249; F: voltage-gated potassium channel activity; IEA.  
 DR GO: GO:0006812; P: cation transport; IEA.  
 DR GO: GO:0006813; P: potassium ion transport; IEA.  
 DR InterPro: IPR00210; BTB\_POZ.  
 DR InterPro: IPR005821; Ion trans.  
 DR InterPro: IPR001622; K-channel pore.  
 DR InterPro: IPR004056; K433channel.  
 DR InterPro: IPR003968; Kv\_channel.  
 DR InterPro: IPR003091; K\_channel.  
 DR InterPro: IPR003131; K\_tetra.  
 DR InterPro: IPR005820; Mcchannel nlg.  
 DR InterPro: IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans\_1.  
 DR Pfam; PF02214; K\_tetra\_1.  
 DR PRINTS; PRO0169; KCHANNEL.  
 DR PRINTS; PRO1518; KV43CHANNEL.  
 DR PRINTS; PRO1491; KVCHANNEL.  
 DR PRINTS; PRO1497; SHALCHANNEL.  
 DR SMART; SM00225; BTB\_1.  
 DR PROSITE; PS50097; BTB\_1.  
 KM Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 659 AA; 74515 MW; 73F5CF339C6A0F47 CRC64;

Query Match 85.7%; Score 2925; DB 2; Length 659;  
 Best Local Similarity 86.3%; Pred. No. 5.7e-175;  
 Matches 573; Conservative 37; Mismatches 40; Indels 14; Gaps 7;

QY 1 MAAGVAAWLPAPAAAGWMPVANCMPMLPADKNGKODELIVNVSGRRFQRTTLIER 60  
 DB 1 MASGVAAWLPAPAAAGWMPVANCMPMLPADKNGKODEVITILNVSGRRFQRTTLIER 60  
 QY 61 YPDTLLGSTEKEFFFNEDTKSEYFFDRDPEVRVCVNFYRTGKLYPRYECISAYDELAF 120

DB 61 YPDNLLGPEKEFFFNEDTKSEYFFDRDPEVRVSLNFYRTGKLYPRYISAYDELSLF 120  
 QY 121 YGILPEIIDDCCYEYKDKRRENAERLMDNDSENNQESMPSLSPFQTMRAPEPHST 180  
 DB 121 YGILPEIIDDCCYEYKDKRRENAERLMDNDSENNQESMPSLSPFQTMRAPEPHST 180  
 QY 181 LAIVFYVTGFPFIASVITNVVETVPDGVPGSKELPCGERYSVAFPCIDTACVMI 240  
 DB 181 LAIVFYVTGFPFIASVITNVVETVPDGVPGSKELPCGERYSVAFPCIDTACVMI 240  
 QY 241 YILRLFAASRYRFRISNM---SIIDVVAIMPYIGLVNTN-NEVSGAFVTLRVRVR 296  
 DB 241 YILRLFAASRYRFRISNM---SIIDVVAIMPYIGLVNTN-NEVSGAFVTLRVRVR 300  
 QY 297 IFKFSRHSGRLRIGLTKSCASELGFLLFSLTMAIIPATWFAEKSSASKFTSIPA 356  
 DB 301 IFKFSRHSGRLRIGLTKSCASELGFLLFSLTMAIIPATWFAEKSSASKFTSIPA 360  
 QY 357 SFWYTIIVMTTIGYGMVPEKTIAGKIFG-SICSLGVLVIALPVIVSNFSRIYQNR 415  
 DB 361 SFWYTIIVMTTIGYGMVPEKTIAGKIFG-SICSLGVLVIALPVIVSNFSRIYQNR 420  
 QY 416 ADRRAQKARLARIRVAKTSSNAYLHRSKNGLLNEALBELTGTPREEHMGKTTSLIESQ 475  
 DB 421 ADRRAQKARLARIRVAKTSSNAYLHRSKNGLLNEALBELTGSTDEBQHTTKGTSIJESQ 480  
 QY 476 HHLHLCEKTTGLSYLVDDPLSVRTSTIKNHEFIDEQMFQONCESSQONTPTSRPSLS 531  
 DB 481 HHLHLCEKTTGLSYLVDDPLSVRTSTIKNHEFIDEQMFQONCESSQONTPTSRPSLS 537  
 QY 532 RSPSLSHPGITTCSSRSRKTTHLPNSNLPATRLSMOELSTHIOGSEQPSLTSTRS 551  
 DB 538 RSPSLSHPGITTCSSRSRKTTHLPNSNLPATRLSMOELSTHIOGSEQPSLTSTRS 597  
 QY 592 SLNLKXDDGLRPNCSTQITTAIISIPTPALTPEGESRPPSPGPNNTN-PSITSNVAVSVL 651  
 DB 598 SLNLKXDDGLRPNCSTQITTAIISIPTPALTPEGESRPPSPGPNNTN-PSITSNVAVSVL 655  
 QY 652 VSVL 655  
 DB 656 VSVL 659

## RESULT 8

072W36 ID 072W36 PRELIMINARY; PRT; 638 AA.  
 AC 072W36;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Potassium voltage-gated channel, Shal-related family, member 3.  
 GN OHPNames=zgc:55306;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=AB; TISSUE=Whole body;  
 RC MDL=LINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Rana S.S., Loguellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,



RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
RA Krzywinski M.I., Skalski J., Smallos D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Mair M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB; TISSUE=Whole body;  
RL Straubeberg R.;  
DR EMBL; BC045304; AA045304.1; -.  
DR HSP; Q63881; 156C.  
DR ZFIN; ZDB-GENE-030131-5626; zgc:55306.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR000210; BTB POZ.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K\_channel\_pore.  
DR InterPro; IPR004056; KV43channel.  
DR InterPro; IPR003968; Kv\_channel.  
DR InterPro; IPR003091; K\_channel.  
DR InterPro; IPR003131; K\_tetra.  
DR InterPro; IPR005820; M\_channel\_nlg.  
DR InterPro; IPR003975; Shal\_channel.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR Pfam; PF02214; K\_tetra; 1.  
DR PRINTS; PRO0169; KCHANNEL.  
DR PRINTS; PRO1518; KV43CHANNEL.  
DR PRINTS; PRO1491; KVCHANNEL.  
DR PRINTS; PRO1497; SHALCHANNEL.  
DR SMART; SM00225; BTB; 1.  
DR Ion transport; Ionic channel; Transmembrane; Transport.  
DR KW SEQUENCE 638 AA; 72053 MW; 038645FB28947F47 CRC64;  
SQ

Query Match 75.3%; Score 2570.5; DB 2; Length 638;  
Best Local Similarity 75.6%; Pred. No. 8.8e-153;  
Matches 501; Conservative 71; Mismatches 56; Indels 33; Gaps 11;

QY 1 MAAGVAAWLPFPAAALIGMPFVANCMPPLADKKNKRODELIIVLVSGRRFQWRTTLER 60  
DB 1 MAAGVAAWLPFPAAALIGMPFVANCMPPLADKKNKRODELIIVLVSGRRFQWRTTLER 60  
QY 61 YPDTLLSGTEKEFFPNEDTKYFFPDRODEVRVCVINFRTGKLHPRYECISAYDEIAF 120  
DB 61 YPDTLLSGTEKEFFPNEDTKYFFPDRODEVRVCVINFRTGKLHPRYECISAYDEIAF 120  
QY 121 YGILPEITIGDCPEYKORRENERLMDNDSENNQSMPSLRQMMRAFEHPHST 180  
DB 121 YGILPEITIGDCPEYKORRENERLMDNDSENNQSMPSLRQMMRAFEHPHST 180  
QY 121 FGLIPETISDCCYEYKORRENERLMDNDSENNQSMPSLRQMMRAFEHPHST 179  
DB 121 FGLIPETISDCCYEYKORRENERLMDNDSENNQSMPSLRQMMRAFEHPHST 179  
QY 181 LALVYVYVTFGFIIVSVITNVETVPCGVPSKELPCGEYSVAFCPLDCAWIMFVE 240  
DB 181 LALVYVYVTFGFIIVSVITNVETVPCGVPSKELPCGEYSVAFCPLDCAWIMFVE 240  
QY 180 MALVYVYVTFGFIIVSVITNVETVPCGVPSKELPCGEYSVAFCPLDCAWIMFVE 239  
DB 180 MALVYVYVTFGFIIVSVITNVETVPCGVPSKELPCGEYSVAFCPLDCAWIMFVE 239  
QY 241 YLNLFLPAAPSRIRIRSVMSIIVVAIMPYYITGLVMTNNEVSGAFVTLRVFRVRIKF 300  
DB 241 YLNLFLPAAPSRIRIRSVMSIIVVAIMPYYITGLVMTNNEVSGAFVTLRVFRVRIKF 300  
QY 240 YLNLFLPAAPSRIRIRSVMSIIVVAIMPYYITGLVMTNNEVSGAFVTLRVFRVRIKF 299  
DB 240 YLNLFLPAAPSRIRIRSVMSIIVVAIMPYYITGLVMTNNEVSGAFVTLRVFRVRIKF 299  
QY 301 SRHSGARITIGYTKSCASELGLFLSLTMAIIPATMFAEKSSSKFTSIPASFWY 360  
DB 301 SRHSGARITIGYTKSCASELGLFLSLTMAIIPATMFAEKSSSKFTSIPASFWY 360  
QY 300 SRHSGARITIGYTKSCASELGLFLSLTMAIIPATMFAEKSSSKFTSIPASFWY 359  
DB 300 SRHSGARITIGYTKSCASELGLFLSLTMAIIPATMFAEKSSSKFTSIPASFWY 359  
QY 361 TIVMTTIGYDMVPKTIAGKIPGSGISGLSVLVIALFPVIVSNFSRIYHONRADRR 420  
DB 361 TIVMTTIGYDMVPKTIAGKIPGSGISGLSVLVIALFPVIVSNFSRIYHONRADRR 420  
QY 360 TIVMTTIGYDMVPKTIAGKIPGSGISGLSVLVIALFPVIVSNFSRIYHONRADRR 419  
DB 360 TIVMTTIGYDMVPKTIAGKIPGSGISGLSVLVIALFPVIVSNFSRIYHONRADRR 419

QY 421 AOK--KARLIRVAKGTSSNAVYLSKRNGLNEALLETGTPEE-EHMGTSLIESOH 477  
DB 420 AOKQKARLIRVAKGTSSNAVYLSKRNGLNEALLETGTPEE-EHMGTSLIESOH 478  
QY 478 HLHLEKTEKTLGYLVDPDPLSVRTSTIKNEHFIIDECQFEQNCMESSQNPSTRPSLS 537  
DB 479 HLHLEKTEKTLGYLVDPDPLSVRTSTIKNEHFIIDECQFEQNCMESSQNPSTRPSLS 538  
QY 538 SHPGITTTCCSRRSKTKTHLPNSNLPATRLSMOELSTIHIQSEOPSLTSSRLNKA 597  
DB 539 SEEGITGTCSSRRPKNIQPLNATHSTHNLQELSLMHIQCEBOQPLNTRSRSLNMS 578  
QY 598 DDGLRPNCKTS-QTTAIIISPTPPA---LTPEGESPPASPDPNNIPTSINVKV 652  
DB 579 DESGLNCKSSGLVITAIISIPPPSNNSRAPDPAPPEAP-PLIN-PSST-DVVKI 635  
QY 653 SVL 655  
DB 636 SAL 638

RESULT 9  
ID 08HYZ1 PRELIMINARY; PRT; 630 AA.  
AC 08HYZ1.  
DT 01-MAR-2003 (TREMREL. 23, Created)  
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)  
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)  
DE Voltage-gated potassium channel Kv4.2.  
OS Muscicula putorius furo (Ferret).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
OC Muscicula.  
RX NCBI\_TaxID=9669;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Patel S.P., Strauss H.C.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY147192; AANJ9878.1; -.  
DR HSP; Q63881; 156C.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR000210; BTB POZ.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K\_channel\_pore.  
DR InterPro; IPR004056; KV43channel.  
DR InterPro; IPR003968; Kv\_channel.  
DR InterPro; IPR003091; K\_channel.  
DR InterPro; IPR003131; K\_tetra.  
DR InterPro; IPR005820; M\_channel\_nlg.  
DR InterPro; IPR003975; Shal\_channel.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR Pfam; PF02214; K\_tetra; 1.  
DR PRINTS; PRO0169; KCHANNEL.  
DR PRINTS; PRO1517; KV42CHANNEL.  
DR PRINTS; PRO1491; KVCHANNEL.  
DR PRINTS; PRO1497; SHALCHANNEL.  
DR SMART; SM00225; BTB; 1.  
DR Ion transport; Ionic channel; Transmembrane; Transport.  
DR KW SEQUENCE 630 AA; 70565 MW; DA4CFD16998A9842 CRC64;  
SQ

Query Match 73.6%; Score 2510.5; DB 2; Length 630;  
Best Local Similarity 73.9%; Pred. No. 5e-149;  
Matches 488; Conservative 68; Mismatches 69; Indels 35; Gaps 7;

QY 1 MAAGVAAWLPFPAAALIGMPFVANCMPPLADKKNKRODELIIVLVSGRRFQWRTTLER 59  
DB 1 MAAGVAAWLPFPAAALIGMPFVANCMPPLADKKNKRODELIIVLVSGRRFQWRTTLER 60

QY 60 RYDPTLLGSTEKEFFENEDTKYFFDRDPEVRCVNFRTGKLYPRYECISAYDELA 119  
 DB 61 RYDPTLLGSSERDFPHPTQYFFDRDPDIPIHILNFRTGKLYPRHICISAYDELA 120  
 QY 120 FYGILPEIIGDCCEYEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWAFENPHT 178  
 DB 121 FYGILPEIIGDCCEYEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWAFENPHT 180  
 QY 179 STALVFFYVYTGFFIAVSVITNVETVPCGVPGS-KELPCGERYSVAFFCLDTACWIF 237  
 DB 181 STALVFFYVYTGFFIAVSVITNVETVPCGVPGS-KELPCGERYSVAFFCLDTACWIF 240  
 QY 238 TVEYLRLFAFAPRFRFRSVMSSIIDVVAIMPYYIIGLWMTNEDVSGAVTLVFRVFR 297  
 DB 241 TVEYLRLFAFAPRFRFRSVMSSIIDVVAIMPYYIIGLWMTNEDVSGAVTLVFRVFR 300  
 QY 298 FKRSRHSQGRIRIIGYTLKSCASELGFELFMAIIFAVVMPYAEKGSASAKFTSIPAS 357  
 DB 301 FKRSRHSQGRIRIIGYTLKSCASELGFELFMAIIFAVVMPYAEKGSASAKFTSIPAA 360  
 QY 358 FWTITVMTLGGDMVPTIAGKIFGSGISLGVIALPVPIVSNFRITHONORAD 417  
 DB 361 FWTITVMTLGGDMVPTIAGKIFGSGISLGVIALPVPIVSNFRITHONORAD 420  
 QY 418 KRPAAQKARLARIIVAKTGSSNAYLHKNGLNEALELTGTPEEBHMGKTSLSIESOH 477  
 DB 421 KRPAAQKARLARIIVAKTGSSNAYLHKNGLNEALELTGTPEEBHMGKTSLSIESOH 479  
 QY 478 HLHCEKKTGLSVLVDPLLSRTSTIKHNEPFIIDEMFONCESMOMVPESTRSPSLS 537  
 DB 480 HLHCEKKTGLSVLVDPLLSRTSTIKHNEPFIIDEMFONCESMOMVPESTRSPSLS 520  
 QY 538 SHPGLTTCSSRSRKTTHLPNSNLPATRLRSMOELSTIHQSGEOPSLTSSSLNLKA 597  
 DB 521 SOGQVSTCCSRHKKTRFRIPMANVSSHSGVOELSTIQRCYERPLSNSSSLNKA 580  
 QY 598 DDLGPNCKTSQITTAIISIPTPALPTEGESRP-PPASPGPNTNIPSTSNVVKVSVL 655  
 DB 581 BECVKNCQEPQVTTAIIISIPTPVPTPEGDDRESPEVSGG-----NIVRSAL 630

RESULT 10  
 KCD2\_RABIT STANDARD; PRT; 630 AA.  
 ID KCD2\_RABIT STANDARD; PRT; 630 AA.  
 AC P59955;  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated potassium channel subunit Kv4.2).  
 GN Name=KCNQ2;  
 OS Oryzolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand white; TISSUE=Cornea;  
 RA Rae J.L.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 SEQUENCE OF 15-614 FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=22117972; PubMed=12122138;  
 RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G., Obeo A., Genforinia M.D., Gonzalez C.;  
 RT "Molecular identification of Kv alpha subunits that contribute to the oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit carotid body.";  
 RT J. Physiol. (Lond.) 542:369-382(2002).  
 CC -1- FUNCTION: pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(to) current in heart and I(Sa) current in neurons. Channel properties

CC are modulated by interactions with other alpha subunits and with regulatory subunits.  
 CC -1- SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3. Associates with the regulatory subunits KCNP1, KCNP2, KCNP3 and KCNP4. Interacts with DPP6, DUG4 and FRGQ. Interacts with PLNA and PLNC (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Detected in brain frontal cortex.  
 CC -1- DOMAIN: The segment 54 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
 CC -1- PTM: Phosphorylated on serine and threonine residues (by similarity).  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF508735; AAM46929.1; -;  
 DR EMBL: AF493547; AAM46841.1; -;  
 DR InterPro: IPR005821; Ion trans.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR003131; K\_tetra.  
 DR InterPro: IPR005820; M+channel\_nlg.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR Pfam: PF02214; K\_tetra; 1.  
 DR Ion transport; Ionic channel; Multigene family; Phosphorylation; Potassium; Potassium channel; Potassium transport; Transmembrane; K+ transport; Voltage-gated channel.  
 KW DOMAIN 1  
 FT TRANSSEM 184 204  
 FT TRANSSEM 225 245  
 FT DOMAIN 246 259  
 FT TRANSSEM 260 280  
 FT TRANSSEM 290 310  
 FT DOMAIN 311 323  
 FT TRANSSEM 324 344  
 FT TRANSSEM 363 383  
 FT TRANSSEM 385 405  
 FT DOMAIN 406 630  
 FT SITS 370 375  
 FT MOD RES 38 38  
 FT MOD RES 552 552  
 FT MOD RES 602 602  
 FT MOD RES 607 607  
 FT MOD RES 616 616  
 FT CONFLICT 118 118  
 FT CONFLICT 379 379  
 SQ SEQUENCE 630 AA; 70613 MW; 5981C87A5E4C4D1 CRC64;  
 Query Match 73.4%; Score 2504.5; DB 1; Length 630;  
 Best Local Similarity 73.9%; Pred. No. 1,2e-148;  
 Matches 489; Conservative 69; Mismatches 65; Indels 39; Gaps 8;

QY 1 MAAGVAAWLPFAAALIGMPPVANCMPAPADKNR-ODELIVLVNSGRFPQTWTTLE 59  
 DB 1 MAAGVAAWLPFAAALIGMPPVANCMPAPADKNR-ODELIVLVNSGRFPQTWTTLE 60  
 QY 60 RYDPTLLGSTEKEFFENEDTKYFFDRDPEVRCVNFRTGKLYPRYECISAYDELA 119  
 DB 61 RYDPTLLGSSERDFPHPTQYFFDRDPDIPIHILNFRTGKLYPRHICISAYDELA 120  
 QY 120 FYGILPEIIGDCCEYEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWAFENPHT 178  
 DB 121 FYGILPEIIGDCCEYEYKORRENAERLMDNDSENNOES-MPSLSFRQTMWAFENPHT 180  
 QY 179 STALVFFYVYTGFFIAVSVITNVETVPCGVPGS-KELPCGERYSVAFFCLDTACWIF 237

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DB 161 STMALVFYTVGTFIAVSVIANVVEIVPGSSPGHKEIPGERRAVNAFECIDTACWIF 240
QY 238 TVEYLRLPAFBSRRPFRSWSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVPRVERI 297
DB 241 TVEYLRLAALAPSRYPFRSWSIIDVVAIMPYIIGLVMTNEDVSGAVTLRVPRVERI 300
QY 298 FKFSHSGGLRLIGTLKSCASELGFLLFSLTMAIITPTWPFVEYKSSASKFTSIPAS 357
DB 301 FKFSHSGGLRLIGTLKSCASELGFLLFSLTMAIITPTWPFVEYKSSASKFTSIPAS 360
QY 358 FWYITVMTTIGYGMVPEKTLAGKIFGSGICSLGVIALPVPVIVSNFSRIYHONORAD 417
DB 361 FWYITVMTTIGYGMVPEKTLAGKIFGSGICSLGVIALPVPVIVSNFSRIYHONORAD 420
QY 418 KRPAPKARLARIRVAKTGSSNAYASHKRNGLNLELITGPREE--HMGKTLISIQ 475
DB 421 KRPAPKARLARIRVAKTGSSNAYASHKRNGLNLELITGPREE--HMGKTLISIQ 477
QY 476 HHHLHLCLEKTTGSLVVDPLSLVSTIKHFEIDEMFEONCMESMOMYPTSPRS 535
DB 478 HHHLHLCLEKTTGSLVVDPLSLVSTIKHFEIDEMFEONCMESMOMYPTSPRS 538
QY 536 LSHHPGLTTTCCSRRSKKTLLPNLNLNLRSLRMOELSTIHIQSEOPSLTSSSLNL 595
DB 519 LSSQGVSTSTCSRHKKTFRIPNANVSGSGVQELSTIQRVERPLSNSSSLNA 578
QY 596 KADGLRPNCSTQITTAIISIPPPALTPGEGSRP--PPSPGPNTPISITSVAVXS 653
DB 579 KMEBCVKNCEQPVYTTAIISSIPPTTPGDDRPESPEYSGG-----NIVRVS 628
QY 654 VL 655
DB 629 AL 630

RESULT 11
KCD2_MOUSE STANDARD; PRT; 630 AA.
ID_KCD2_MOUSE Q920V2; Q8BSK3; Q8CHB7; Q9JUC0;
AC Q920V2; Q8BSK3; Q8CHB7; Q9JUC0;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
DE Potassium channel subunit Kv4.2).
GN Name=Kcnd2; Synonyms=Kiaa1044;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark R.B., Giles W.R.;
RT "Cloning and functional characterization of mouse heart K+ channel
RT alpha subunits, Kv1.5, Kv4.2 and Kv4.3."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Oseada N., Kuesda J., Tanuma R., Ito A., Hirata M., Sugano S.;
RA Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22353125; PubMed=12465718;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT 1. The complete nucleotide sequences of 100 mouse KIAA-homologues
RT cDNAs identified by screening of terminal sequences of cDNA clones

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RT randomly sampled from size-fractionated libraries."
RL DNA Res. 9:179-188(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Meiosephros, and Olfactory bulb;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki N., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oosato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yaegaki K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarini R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blaise J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher V., Forrest A.F., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grummond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongsway A., Kurochkin I.V., Lee Y., Lehman B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyrshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazune N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hare A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [5]
RP PHOSPHORYLATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20497051; PubMed=11040264;
RA Varga A.W., Anderson A.E., Adams J.P., Vogel H., Sweatt J.D.;
RT "Input-specific immunolocalization of differentially phosphorylated
RT Kv4.2 in the mouse brain."
RL Learn. Memory 7:321-332(2000).
RN [6]
RP INTERACTION WITH KCNIP3, MUTAGENESIS OF SER-552, AND PHOSPHORYLATION.
RX MEDLINE=22338839; PubMed=12451113;
RA Schrader L.A., Anderson A.E., Mayne A., Pfeiffer P.J., Sweatt J.D.;
RT "PKA modulation of Kv4.2-encoded A-type potassium channels requires
RT formation of a supramolecular complex."
RL J. Neurosci. 22:10123-10133(2002).
RN [7]
RP INTERACTION WITH KCND3 AND KCNIP2.
RX MEDLINE=21906624; PubMed=11909823;
RX DOI=10.1161/01.RES.0000012664.05949.E0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RA Nerbonne J.M.;
RT "Role of heteromultimers in the generation of myocardial transient
RT outward K+ currents."
RL Circ. Res. 90:586-593(2002).
RN [8]
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
RN inactivating A-type potassium channels. May contribute to (ITo)
RN current in heart and (Isa) current in neurons. Channel properties
RN are modulated by interactions with other alpha subunits and with
RN regulatory subunits.
RN -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
RN Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
RN KCNIP4. Interacts with DPP6, DLG4 and FREQ. Interacts with FLNA
RN and FLNC (by similarity).
RN -1- SUBCELLULAR LOCATION: Integral membrane protein.
RN -1- TISSUE SPECIFICITY: Detected in brain, especially in hippocampus,
RN medial habenular nucleus, striatum, amygdala, cortex and
RN cerebellum.
RN -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
RN characterized by a series of positively charged amino acids at

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RT "Modulation of A-type potassium channels by a family of calcium  
RT sensors.";  
RL Nature 403:553-556(2000).  
RN [4]  
RP INTERACTION WITH KCNIP1 AND FREO.  
RX MEDLINE=21532927; PubMed=11606724; DOI=10.1073/pnas.221168498;  
RA Nakamura T.Y., Pountney D.J., Ozalta A., Nandi S., Ueda S., Rudy B.,  
RA Coetzee W.A.;  
RT "A role for frequenin, a Ca2+-binding protein, as a regulator of Kv4  
RT K+-currents.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12808-12813(2001).  
RN [5]  
RP INTERACTION WITH KCNIP4.  
RX MEDLINE=21964093; PubMed=11847232; DOI=10.1074/jbc.M200897200;  
RA Morohashi Y., Hatano N., Ohya S., Takikawa R., Matsubara T.,  
RA Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.;  
RT "Molecular cloning and characterization of CALPKCNIP4, a novel EF-  
RT hand protein interacting with presenilin 2 and voltage-gated potassium  
RT channel subunit Kv4.";  
RL J. Biol. Chem. 277:14965-14975(2002).  
RN [6]  
RP MUTAGENESIS OF 627-VAL--LEU-630, AND INTERACTION WITH DLG4.  
RX MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;  
RA Wong W., Newell E.W., Ungloff D.G.M., Jones O.T., Schlichter L.C.;  
RT "Cell surface targeting and clustering interactions between  
RT heterologously expressed PSD-95 and the Shal voltage-gated potassium  
RT channel, Kv4.2.";  
RL J. Biol. Chem. 277:20423-20430(2002).  
RN [7]  
RP INTERACTION WITH DPP6.  
RX MEDLINE=22464931; PubMed=12575952; DOI=10.1016/S0896-6273(02)01185-6;  
RA Nadal M.S., Ozaite A., Amarillo Y., Vega-Saenz de Miera E., Ma Y.,  
RA Mo W., Goldberg B.M., Mismal Y., Ikemura Y., Neubert T.A., Rudy B.;  
RT "The CD26-related dipeptidyl aminopeptidase-like protein DPPX is a  
RT critical component of neuronal A-type K+ channels.";  
RL Neuron 37:449-461(2003).  
CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
CC inactivating A-type potassium channels. May contribute to I(TO)  
CC current in heart and I(Sa) current in neurons. Channel properties  
CC are modulated by interactions with other alpha subunits and with  
CC regulatory subunits.  
CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.  
CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
CC KCNIP4. Interacts with FLNA and FLNC (By similarity). Interacts  
CC with DPP6, DLG4 and FREO.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Interaction with  
CC DPP6, DLG4 or FREO may increase cell surface expression.  
CC -1- TISSUE SPECIFICITY: Highly expressed in heart and throughout the  
CC brain, with similar levels in cortex and hypothalamus, and much  
CC higher levels in hippocampus, dentate gyrus and the habenular  
CC nucleus of the thalamus. Detected at similar levels in heart  
CC atrium and ventricle. Detected in aorta, cardiac and smooth  
CC muscle.  
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at  
CC every third position.  
CC -1- PTM: Phosphorylated on serine and threonine residues (By  
CC similarity).  
CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)  
CC subfamily.  
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a  
CC frameshift in position 477.  
CC  
CC -----  
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CC  
CC EMBL; S64320; AAB19939.1; -;  
CC EMBL; M59980; AAA40929.1; ALT\_FRAME.

DR PIR; J00271; J00271.  
DR PDB; 1S6C; X-ray; B=1-30.  
DR InterPro; IPR003821; Ion\_trans.  
DR InterPro; IPR001622; K+-channel\_pore.  
DR InterPro; IPR003091; K\_channel.  
DR InterPro; IPR003131; K\_tetra.  
DR InterPro; IPR004055; Kv42channel.  
DR InterPro; IPR003968; Kv\_channel.  
DR InterPro; IPR003820; M4-channel\_nlg.  
DR InterPro; IPR003975; Shal\_channel.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR Pfam; PF02214; K\_tetra; 1.  
DR PRINTS; PR00169; KCHANNEL.  
DR PRINTS; PR01517; KV42CHANNEL.  
DR PRINTS; PR01491; KVCHANNEL.  
DR PRINTS; PR01497; SHALCHANNEL.  
DR 3D-structure; Ion transport; Ionic channel; Multigene family;  
KW Phosphorylation; Potassium; Potassium channel; Potassium transport;  
KW Transmembrane; Transport; Voltage-gated channel.  
FT DOMAIN 1 183  
FT TRANSMEM 184 204  
FT TRANSMEM 225 245  
FT DOMAIN 246 259  
FT TRANSMEM 260 280  
FT TRANSMEM 290 310  
FT DOMAIN 311 323  
FT TRANSMEM 324 344  
FT TRANSMEM 363 383  
FT TRANSMEM 385 405  
FT DOMAIN 406 630  
FT SITE 370 375  
FT MOD\_RES 38 38  
FT MOD\_RES 552 552  
FT MOD\_RES 602 602  
FT MOD\_RES 607 607  
FT MOD\_RES 616 616  
FT MUTAGEN 627 630  
SQ SEQUENCE 630 AA; 70548 MW; PDE57E8A5113BABR CMC64;  
Query Match 73.3%; Score 2499.5; DB 1; Length 630;  
Best Local Similarity 73.6%; Pred. No. 2,4e-148;  
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;  
QY 1 MAAGYAAMLPAPARAAGAGMVPVANCMPPLADAKKR-QDELIVYNSGRFPQRTTLE 59  
DB 1 MAAGYAAMLPAPARAAGAGMVPVANCMPPLADAKKR-QDELIVYNSGRFPQRTTLE 60  
QY RYPPTLLGSSSEKDFPHETQYFFDDPDIFRHLNFKYRGLKHPRAHECISAYDEBLA 120  
DB RYPPTLLGSSSEKDFPHETQYFFDDPDIFRHLNFKYRGLKHPRAHECISAYDEBLA 120  
QY FYGLIPETIGDCCEBYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENBPT 178  
DB FYGLIPETIGDCCEBYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENBPT 178  
QY 121 FFGILPELIGCCCEBYKDRRENAERLQDDADVDNNGESALPMTARQWRAPFENHT 180  
DB 121 FFGILPELIGCCCEBYKDRRENAERLQDDADVDNNGESALPMTARQWRAPFENHT 180  
QY 179 STALVFFYVYTGFIIVASVITNVVETVPCGTVGS-KELPCGERYSVAFCFLDPAQWIF 237  
DB 179 STALVFFYVYTGFIIVASVITNVVETVPCGTVGS-KELPCGERYSVAFCFLDPAQWIF 237  
QY 181 STMALVFFYVYTGFIIVASVITNVVETVPCGTVGS-KELPCGERYSVAFCFLDPAQWIF 240  
DB 181 STMALVFFYVYTGFIIVASVITNVVETVPCGTVGS-KELPCGERYSVAFCFLDPAQWIF 240  
QY 238 TVEYLILFLAPBSRYRFRSWSIIDVAIMPYYIGVMTNNEVSGAFVTLRFRVRI 297  
DB 238 TVEYLILFLAPBSRYRFRSWSIIDVAIMPYYIGVMTNNEVSGAFVTLRFRVRI 297  
QY 241 TVEYLILFLAPBSRYRFRSWSIIDVAIMPYYIGVMTNNEVSGAFVTLRFRVRI 300  
DB 241 TVEYLILFLAPBSRYRFRSWSIIDVAIMPYYIGVMTNNEVSGAFVTLRFRVRI 300  
QY 298 FKFSRHSQGLRIILGTYLTKSCASEGLFLFTMAIIIFATWFAEKGSASAKFTSPAS 357  
DB 298 FKFSRHSQGLRIILGTYLTKSCASEGLFLFTMAIIIFATWFAEKGSASAKFTSPAS 357  
QY 301 FKFSRHSQGLRIILGTYLTKSCASEGLFLFTMAIIIFATWFAEKGSASAKFTSPAS 360  
DB 301 FKFSRHSQGLRIILGTYLTKSCASEGLFLFTMAIIIFATWFAEKGSASAKFTSPAS 360  
QY 358 FWYITVMTTIGYGDMPKTIAGKIRGSGISLGSVYVIALPVPIYVNSFSIYHQNORAD 417  
DB 358 FWYITVMTTIGYGDMPKTIAGKIRGSGISLGSVYVIALPVPIYVNSFSIYHQNORAD 417  
QY 361 FWYITVMTTIGYGDMPKTIAGKIRGSGISLGSVYVIALPVPIYVNSFSIYHQNORAD 420  
DB 361 FWYITVMTTIGYGDMPKTIAGKIRGSGISLGSVYVIALPVPIYVNSFSIYHQNORAD 420  
QY 418 KRAQCKARLARIRIVATGSSNAYLHAKRNGCLNLEALVELNTPREEHNGKTTSLIESQH 477  
DB 418 KRAQCKARLARIRIVATGSSNAYLHAKRNGCLNLEALVELNTPREEHNGKTTSLIESQH 477

DB 421 KRAQKARLARIIRAKSGSANAWMOSKNGLLSNQIQ-SSDEPAFVSKSSGFFTOHH 479  
 QY 478 HLHAEKTEKTLGYLVDDPLLSVTRSTIKHFEFIDCOMFONCMSSMOMYPTSTRPSLS 537  
 DB 480 HLHAEKTEKTLGYLVDDPLLSVTRSTIKHFEFIDCOMFONCMSSMOMYPTSTRPSLS 520  
 QY 538 SHBGLTTCCSRSSKKTTHLPNSNLPATRLRSQMOELSTIHIQSGEOPSLTTSSSLNKA 597  
 DB 521 SQGGVSTCCSRHRKHSFRIPNANVSGSHGSGVOELSTIQRVCERTPLSNRSSLNAMK 580  
 QY 598 DDLRPNCKTSQTTTALISPTPALTPGESRP--PPAPGPRNTNPSITSNVVAKSV 655  
 DB 581 BECVKLNCEQPYVTALISIPTPVTTPEGDDRPESSEYSG-----NIVRSAL 630

RESULT 13  
 KCND2\_HUMAN STANDARD; PRT; 630 AA.  
 AC Q9NZV8; Q95012; Q9UBV7; Q9UN98; Q9UNH9;  
 DT 29-MAR-2004 (Ref. 43, Created)  
 DT 29-MAR-2004 (Ref. 43, Last sequence update)  
 DT 05-JUN-2004 (Ref. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated  
 DE potassium channel subunit Kv4.2).  
 GN Name=KCND2; Synonyms=KIAA1044;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99397452; PubMed=10470851;  
 RA Kikuno R., Nagase T., Ishikawa K.-I., Hirogawa M., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XIV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:197-205(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99397452; PubMed=10470851;  
 RA Kikuno R., Nagase T., Ishikawa K.-I., Hirogawa M., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XIV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:197-205(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20017432; PubMed=10551270;  
 RA Zhu X.-R., Wolf A., Schwarz M., Isbrandt D., Pongs O.;  
 RT "Characterization of human Kv4.2 mediating a rapidly-inactivating  
 RT transient voltage-sensitive K<sup>+</sup> current.";  
 RL Recept. Channels 6:387-400(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=20195625; PubMed=10729221; DOI=10.1006/gene.2000.6117;  
 RA Isbrandt D., Leichter T., Waldechmetz R., Zhu X.-R., Luhmann U.,  
 RA Michel U., Sauter K., Pongs O.;  
 RT "Gene structures and expression profiles of three human KCND (Kv4)  
 RT potassium channels mediating A-type currents I(TO) and I(SA).";  
 RL Genomics 64:144-154(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22616434; PubMed=12690205; DOI=10.1126/science.1083423;  
 RA Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayashi K.,  
 RA Herbrick J.-A., Carson A.R., Parker-Katiraei L., Skang J., Khaja R.,  
 RA Zhang J., Hudek A.K., Li M., Haddad M., Duggan G.B., Fernandez B.A.,  
 RA Kanemitsu E., Gentles S., Christopoulos C.C., Choufani S.,  
 RA Kasanitska D., Zheng X.H., Lai Z., Nusskern D., Zhang Q., Gu Z., Lu F.,  
 RA Zeeman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C.,  
 RA Weksberg R., Zackai E.H., Grebe T.A., Cox S.R., Kirkpatrick S.J.,

RA Rahman N., Friedman J.M., Heng H.H.Q., Pelicci P.G., Lo-Coco F.,  
 RA Belloni E., Shafer L.G., Pober B., Morton C.C., Gasella J.F.,  
 RA Brune G.A.P., Korf B.R., Quade B.J., Ligon A.H., Ferguson H.,  
 RA Higgins A.W., Leach N.T., Herrick S.R., Lemire E., Farra C.G.,  
 RA Kim H.-G., Summers A.M., Gripp K.W., Roberts W., Satalari P.,  
 RA Winsor E.J.T., Gzieschik K.-H., Teed A., Mhassian B.A., Kere J.,  
 RA Amengol L., Pujana M.A., Estivill X., Wilson M.D., Koop B.F.,  
 RA Tosi S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B.,  
 RA Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner H.,  
 RA Doehner K., Rommens J.M., Vincent J.B., Venter J.C., Li P.W.,  
 RA Mural R.J., Adams M.D., Tsui L.-C.;  
 RT "Human chromosome 7: DNA sequence and biology.";  
 RL Science 300:767-772(2003).  
 RN [6]  
 RP MUTAGENESIS OF 601-PRO--PRO-604, SUBCELLULAR LOCATION, AND INTERACTION  
 RP WITH FLNA AND FLNC.  
 RX MEDLINE=20556633; PubMed=11102480;  
 RA Petrecca K., Miller D.M., Shrier A.;  
 RT "Localisation and enhanced current density of the Kv4.2 potassium  
 RT channel by interaction with the actin-binding protein filamin.";  
 RL J. Neurosci. 20:8736-8744(2000).  
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
 CC inactivating A-type potassium channels. May contribute to I(TO)  
 CC current in heart and I(SA) current in neurons. Channel properties  
 CC are modulated by interactions with other alpha subunits and with  
 CC regulatory subunits.  
 CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.  
 CC Associates with the regulatory subunits KCNIP2, KCNIP3 and  
 CC KCNIP4. Interacts with DPP6, DLG4 and FROG (by similarity).  
 CC Interacts with FLNA and FLNC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Detected in  
 CC dendrites in cultured hippocampal neurons.  
 CC -1- TISSUE SPECIFICITY: Highly expressed throughout the brain.  
 CC Expression is very low or absent in other tissues.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- PTM: Phosphorylated on serine and threonine residues (by  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)  
 CC subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; AF121104; AAD22053.1; -.  
 DR EMBL; AB028967; BAA82996.2; ALT\_INIT.  
 DR EMBL; AJ010969; CAB56841.1; -.  
 DR EMBL; AF166008; AAF65618.1; -.  
 DR EMBL; AF166007; AAF65618.1; JOINED.  
 DR EMBL; AC004888; AAC83405.1; -.  
 DR EMBL; AC004946; -; NOT ANNOTATED\_CDS.  
 DR EMBL; AF142568; AAD52159.1; -.  
 DR HSSP; Q16968; 1A68.  
 DR GeneW; HGNC:6238; KCND2.  
 DR H-InvDB; HIX007027; -.  
 DR MIM; 605410; -.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K+channel.  
 DR InterPro; IPR003091; K+channel.  
 DR InterPro; IPR003131; Ktetra.  
 DR InterPro; IPR004055; KV42channel.  
 DR InterPro; IPR003968; KV channel.  
 DR InterPro; IPR005820; M+channel nlg.  
 DR InterPro; IPR003975; Shal channel.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PRO1517; KVA2CHANNEL.  
DR PRINTS; PRO1491; KVCCHANNEL.  
DR PRINTS; PRO1497; SHALCHANNEL.  
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
KW Potassium; Potassium channel; Potassium transport; Transmembrane;  
KW Transport; Voltage-gated channel.  
FT DOMAIN 1 183 Cytoplasmic (Potential).  
FT TRANSMEM 184 204 Segment S1 (Potential).  
FT TRANSMEM 225 245 Segment S2 (Potential).  
FT DOMAIN 246 259 Cytoplasmic (Potential).  
FT TRANSMEM 260 280 Segment S3 (Potential).  
FT TRANSMEM 290 310 Segment S4 (Potential).  
FT DOMAIN 311 323 Cytoplasmic (Potential).  
FT TRANSMEM 324 344 Segment S5 (Potential).  
FT TRANSMEM 363 383 Segment S6 (Potential).  
FT TRANSMEM 385 405 Segment S6 (Potential).  
FT DOMAIN 406 630 Cytoplasmic (Potential).  
FT SITE 370 375 Selectivity filter (By similarity).  
FT MOD\_RES 38 38 Phosphoserine (By similarity).  
FT MOD\_RES 552 552 Phosphoserine (By similarity).  
FT MOD\_RES 602 602 Phosphoserine (By similarity).  
FT MOD\_RES 607 607 Phosphoserine (By similarity).  
FT MOD\_RES 616 616 Phosphoserine (By similarity).  
FT MUTAGEN 601 604 PTPP->ATPA: Abolishes interaction with FLNC.  
FT CONFLICT 450 450 N -> S (in Ref. 1).  
FT CONFLICT 464 464 Q -> P (in Ref. 1).  
FT CONFLICT 550 550 Q -> R (in Ref. 1).  
FT CONFLICT 553 553 I -> V (in Ref. 1).  
SQ SEQUENCE 630 AA; 70536 MW; 0C1162FFA20421 CRC64;  
Query Match 73.2%; Score 2498.5; DB 1; Length 630;  
Best Local Similarity 73.6%; Pred. No. 2.8e-146;  
Matches 486; Conservative 69; Mismatches 70; Indels 35; Gaps 7;  
QY 1 MAAGAAAMLPPARAAAIIGMPVANCMPPLAPADKNKR-OBELIYLVNAGRRPOTWRTTLE 59  
DB 1 MAAGVAAALPPARAAAIIGMPVAGMPAPAPROEKRTODALIVNAGTRFOTWDTLE 60  
QY 60 RYPDTLLGSTEKEFFENEDTKEYFFRDPEVFCVNFYRTGKLHYRVECTISAYDELA 119  
DB 61 RYPDTLLGSSSRDFFHYHPETQOYFFRDPDIFRHLINFYRCKLHYRHECTISAYDELA 120  
QY 120 FYGLPEITIGDCCYEEYKDRKRENAERLMDNDSENNQES-MPSLSFRQTMRAFENPHT 178  
DB 121 FFGIIPETIGDCCYEEYKDRRENAERLQDDADDTJABSLPTMTAQRWRRAFENPHT 180  
QY 179 STLALVFYVYTGFFIAVSITNVVETVCGTVPGS-KELPCGERYSVAFCLDTACWIF 237  
DB 181 STMALVFYVYTGFFIAVSIVANVETVPCGSPGHIKELPCGERYAVAFCLDTACWIF 240  
QY 238 TVEYLRLFAAPSRRYRIRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRI 297  
DB 241 TVEYLRLFAAPSRRYRIRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRI 300  
QY 298 FKFSRHSGGLRILGYTLKSCASELGFLLFSUTMAIIPATVMFYAEKSSASKFTSIPAS 357  
DB 301 FKFSRHSGGLRILGYTLKSCASELGFLLFSUTMAIIPATVMFYAEKSSASKFTSIPAS 360  
QY 358 FWYIIVMTTIGYGDMPVKTIAGKIFGSIISGLVIALPVPVIVNSFSIHYONORAD 417  
DB 361 FWYIIVMTTIGYGDMPVKTIAGKIFGSIISGLVIALPVPVIVNSFSIHYONORAD 420  
QY 418 KRRAROKARLARIRVAKTGSSNAYLHRSKNGLLNEALRGTPREEHKGTSTLESQNH 477  
DB 421 KRRAROKARLARIRVAKTGSSNAYLHRSKNGLLNEALRGTPREEHKGTSTLESQNH 479  
QY 478 HLHLCLEKTTGLSTLVDPDLSVSTIKNEHFIDEQNFQONCHSSMONTPTSTRPSLS 537  
DB 480 HLHLCLEKTT-----NHEFVDEQVFEESCEVAATVNPSSSPSLS 520  
QY 538 SHPGITTCSSRSRKTTHLPNSNLPATRLRSMOGLSTIHIQGSQPSLITTSRSSLNKA 597

DB 521 SQGVSTSCSRHKKTPRIPANVSGSHQSIQELSTIQRCVERTPLSNRSSLNKM 580  
QY 598 DDGAPNCKTQITTAIISITPPALTPREGSRP--PASGCPNTNITSINSYKVSYL 655  
DB 581 BECVLNCQOPYVTTAIISITPPALTPREGSRP-----NIVRSAL 630  
RESULT 14  
Q8UW33 PRELIMINARY; PRT; 632 AA.  
AC Q8UW33;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Shal-like voltage-gated potassium channel.  
GN Name=Kva2.2;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
NCBI\_TaxID=9031;  
[1]  
RP SEQUENCE FROM N.A.  
RA Sakai Y., Sokolowski B.H.A.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF075160; AAL56633.1; -.  
DR HSSP; Q63881; 1S6C.  
DR GO; GO:0016021; C:Integral to membrane; IEA.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR Pfam; PF00520; Ion trans; 1.  
DR Pfam; PF02214; K tetra; 1.  
DR PRINTS; PRO0169; KCHANNEL.  
DR PRINTS; PRO1517; KVA2CHANNEL.  
DR PRINTS; PRO1491; KVCCHANNEL.  
DR PRINTS; PRO1497; SHALCHANNEL.  
DR SMART; SM00225; BTB; 1.  
KW Ion transport; Ionic channel; Transmembrane; Transport.  
SQ SEQUENCE 632 AA; 70982 MW; 147C92979F2297D9 CRC64;  
Query Match 73.2%; Score 2497.5; DB 2; Length 632;  
Best Local Similarity 74.0%; Pred. No. 3.3e-148;  
Matches 489; Conservative 62; Mismatches 75; Indels 35; Gaps 7;  
QY 1 MAAGAAAMLPPARAAAIIGMPVANCMPPLAPADKNKR-OBELIYLVNAGRRPOTWRTTLE 59  
DB 1 MAAGVAAALPPARAAAIIGMPVATGMPAPARORERKKSQSLIVNVSIGIOFOTWDTLE 60  
QY 60 RYPDTLLGSTEKEFFENEDTKEYFFRDPEVFCVNFYRTGKLHYRVECTISAYDELA 119  
DB 61 RYPDTLLGSSSRDFFHYHPETQOYFFRDPDIFRHLINFYRCKLHYRQECTISAYDELA 120  
QY 120 FYGLPEITIGDCCYEEYKDRKRENAERLMDNDSENNQES-SMPSLSFRQTMRAFENPHT 178  
DB 121 FFGIIPETIGDCCYEEYKDRRENAERLQDDADQDHTAESSLPMTARQRWRRAFENPHT 180  
QY 179 STLALVFYVYTGFFIAVSITNVVETVCGTVPGS-KELPCGERYSVAFCLDTACWIF 237  
DB 181 STLALVFYVYTGFFIAVSIVANVETVPCGSPGHIRELPCGERYAVAFCLDTACWIF 240  
QY 238 TVEYLRLFAAPSRRYRIRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRI 297  
DB 241 TVEYLRLFAAPSRRYRIRSVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRI 300  
QY 298 FKFSRHSGGLRILGYTLKSCASELGFLLFSUTMAIIPATVMFYAEKSSASKFTSIPAS 357  
DB 301 FKFSRHSGGLRILGYTLKSCASELGFLLFSUTMAIIPATVMFYAEKSSASKFTSIPAS 360  
QY 358 FWYIIVMTTIGYGDMPVKTIAGKIFGSIISGLVIALPVPVIVNSFSIHYONORAD 417









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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 00:35:45 ; Search time 482.789 Seconds  
(without alignments)  
509.498 Million cell updates/sec

Title: US-10-062-879-4

Perfect score: 3320

Sequence: 1 MAAQVAAWLPFARAATGMM.....PGPNTNIPSTSNVYKSVL 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	636	5	ABB79585 Human Kv4
2	3311	99.7	636	2	AAW79589 Human Kv
3	3300.5	99.4	655	5	ABB79584 Human Kv4
4	3291.5	99.1	655	2	AAW79590 Human Kv
5	3291.5	99.1	655	2	AAW79591 Human Kv
6	3285	98.9	636	2	AAW79591 Human Kv
7	3284.5	98.9	655	7	ADD48188 Rat Prote
8	3283.5	98.9	655	8	ADSL6294 Human VOI
9	3279.5	98.8	655	4	AAAB86321 Human Kv4
10	3055	92.0	611	7	ADBE1252 Rat Prote
11	2518	75.8	630	7	ADM10929 Human O64
12	2518	75.8	630	7	ADM10928 Human O64
13	2518	75.8	630	7	ADM10927 Human O64
14	2518	75.8	630	7	ADM10927 Human O64
15	2518	75.8	630	8	ADJ11257 Human ova
16	2518	75.8	630	8	ADJ11260 Human ova
17	2518	75.8	630	8	ADJ11258 Human ova
18	2518	75.8	630	8	ADJ11259 Human ova
19	2518	75.8	630	8	ADM43520 Human ova
20	2518	75.8	630	8	ADM43519 Human ova
21	2518	75.8	630	8	ADM43521 Human ova
22	2518	75.8	630	8	ADM43518 Human ova
23	2516	75.8	630	2	AAV13523 Amino aci
24	2513	75.7	629	4	AAAB86319 Human Kv4
25	2132.5	64.2	647	4	AAAM25597 Human pro

26	2127.5	64.1	646	4	AAAB86318 Human Kv4
27	2121.5	63.9	646	2	AAV34123 Human pot
28	1955	58.9	571	4	ABB71722 Drosophi
29	894	26.9	217	4	AAAB86320 Human Kv4
30	869	26.2	214	2	AAV13524 Amino aci
31	844.5	25.4	255	7	ADM10926 Human O64
32	844.5	25.4	255	8	ADJ11256 Human ova
33	844.5	25.4	255	8	ADM43517 Human ova
34	774.5	23.3	806	7	ADJ79875 CTKA_huma
35	766	23.1	911	7	ADJ69676 Human hea
36	758	22.8	985	8	ADJ30147 Drosophi
37	758	22.8	985	8	ADJ30143 Drosophi
38	750	22.6	854	6	ABP58354 Human pot
39	750	22.6	854	7	ADJ79874 CTKA_huma
40	750	22.6	858	2	AAV32015 Human cat
41	750	22.6	858	5	AAO17058 Human KCN
42	750	22.6	858	8	ADJ38328 Human cat
43	749	22.5	985	4	ABB57774 Drosophi
44	747	22.5	1019	4	ABB67198 Drosophi
45	746	22.5	149	8	ADJ25645 Voltage-g

## ALIGNMENTS

RESULT 1  
ABB79585 standard; protein, 636 AA.  
XX  
XX ABB79585;  
XX  
XX 01-OCT-2002 (first entry)  
XX  
XX Human Kv4.3 potassium channel (short form).  
XX  
XX Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;  
XX  
XX neurotropic; neuroprotective; cardiant; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US6395477-B1.  
XX  
XX 28-MAY-2002.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX 23-OCT-1998; 98US-00178109.  
XX  
XX (AMHP) AMERICAN HOME PROD CORP.  
XX  
XX Cockett MT, Dilks DW, Ling HC, Sokol PT;  
XX  
XX WPI: 2002-556093/59.  
XX  
XX N-PSDB; ABN84401.  
XX  
XX New isolated polynucleotide encoding human Kv4.3 potassium channel  
XX  
XX polypeptide, useful as probe in a diagnostic method for detecting nucleic  
XX  
XX acid encoding human Kv4.3, and for treating Alzheimer's and heart  
XX  
XX diseases.  
XX  
XX Claim 1; Col 23-26; 19pp; English.  
XX  
XX The present sequence is the protein sequence of the short isoform of  
XX  
XX novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been  
XX  
XX identified: a full-length form (hKv4.3 long) (see ABB79584); and the  
XX  
XX short form, which has a deletion of 19 amino acids in the carboxy domain  
XX  
XX after the predicted sixth transmembrane domain (hKv4.3 short). Human  
XX  
XX heart primarily expresses hKv4.3 long, whereas human brain contains both  
XX  
XX forms. The invention provides Kv4.3 polypeptides, polynucleotides, and  
XX  
XX methods for producing these polynucleotides. The Kv4.3 polypeptides and  
XX  
XX polynucleotides are useful in the diagnosis, treatment and screening of  
XX  
XX human diseases relating to an excess or deficiency of hKv4.3 activity,  
XX  
XX including Alzheimer's disease and heart disease

XX Sequence 636 AA;  
SQ

Query Match 100.0%; Score 3320; DB 5; Length 636;  
Best Local Similarity 100.0%; Pred. No. 1,6e-313; Indels 0; Gaps 0;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGVAAAMLPPFAAAAIAGMPVANCMPPLAPADKXKRODELYLVANSGRFFQWRITLER 60  
DB 1 MAAGVAAAMLPPFAAAAIAGMPVANCMPPLAPADKXKRODELYLVANSGRFFQWRITLER 60  
QY 61 YPDTLLGSTEKEFFEDTKEYFFDRDPEVFRCLVNFYRGKLIHYRPECISAYDELLAF 120  
DB 61 YPDTLLGSTEKEFFEDTKEYFFDRDPEVFRCLVNFYRGKLIHYRPECISAYDELLAF 120  
QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSPFQTMRAFEENPHST 180  
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSPFQTMRAFEENPHST 180  
QY 181 LALVFFVYVGFPAVSVITNVETVPCGTVPKSGKELPCGGRYSVAFFCLDTACVMTFTVE 240  
DB 181 LALVFFVYVGFPAVSVITNVETVPCGTVPKSGKELPCGGRYSVAFFCLDTACVMTFTVE 240  
QY 241 YLRLFAAPSRRYFIRSVMSIIDVVAIMPYYIGLVMTNEDVGAFTLRFVFRIFK 300  
DB 241 YLRLFAAPSRRYFIRSVMSIIDVVAIMPYYIGLVMTNEDVGAFTLRFVFRIFK 300  
QY 301 SRHSQGRILIGYLLKSCASELGFLLPSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
DB 301 SRHSQGRILIGYLLKSCASELGFLLPSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
QY 361 TIVMTLLGYGDMVPKTIAGKIFGSLSGVLVIALPVVIVSNFSRIYHONQADKRR 420  
DB 361 TIVMTLLGYGDMVPKTIAGKIFGSLSGVLVIALPVVIVSNFSRIYHONQADKRR 420  
QY 421 AOKKARLARIRVAKTSSNAYLHRSKRGGLNEALELTGTPEEEMGKTTSLISQHHLL 480  
DB 421 AOKKARLARIRVAKTSSNAYLHRSKRGGLNEALELTGTPEEEMGKTTSLISQHHLL 480  
QY 481 HCLEKTTNHEFIDQWFEONCMESMONYPSTRPSLSHPGLTTCCSRRSKKTTHLPN 540  
DB 481 HCLEKTTNHEFIDQWFEONCMESMONYPSTRPSLSHPGLTTCCSRRSKKTTHLPN 540  
QY 541 SNLPATRLRSWQELSTHIGSEBQPSLTSSSLNLKADGLRBNCKTSQITTAIISIP 600  
DB 541 SNLPATRLRSWQELSTHIGSEBQPSLTSSSLNLKADGLRBNCKTSQITTAIISIP 600  
QY 601 PPALTPEGESRPPASPGPNTNIPSLITSNVKVSVL 636  
DB 601 PPALTPEGESRPPASPGPNTNIPSLITSNVKVSVL 636

## RESULT 2

AAW79589  
ID AAW79589 standard; protein; 636 AA.

XX AAW79589;  
XX

DT 11-JAN-1999 (first entry)

DE Human Kv potassium channel hKv4.3 (shorter isoform).

KM Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
therapy; diagnosis.

XX Homo sapiens.  
XX OS

PN MO9842833-A2.  
XX

PD 01-OCT-1998.  
XX

PF 23-MAR-1998; 98WO-EP001901.  
XX

PR 27-MAR-1997; 97GB-00006377.  
PR 09-DEC-1997; 97BP-00402971.  
PR 11-DEC-1997; 97BP-00403007.  
XX  
XX (SMIK) SMITHKLINE BEECHAM LAB PHARM.  
XX  
XX Bril AM, Calmels TRG, Faivre JSP, Javre J, Rouanet S;  
PT MPI; 1998-542277/46.  
DR N-PSDB; AAV61571.  
XX

PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
PT polynucleotide(s) useful in the treatment of disorders including cardiac  
PT arrhythmias and Alzheimer's disease.

XX Claim 2; Page 25; 47pp; English.

CC This is the amino acid sequence for an isoform of human Kv potassium  
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3  
CC polynucleotide (see AAV61571), and has 99% identity with rat Kv4.3.  
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all  
CC Kv family related proteins. A longer isoform (see AAW79590) has been  
CC identified, which has an additional 19 amino acids inserted between amino  
CC acids 487 and 488. The invention relates to hKv4.3 polypeptides and  
CC polynucleotides, and to methods for producing such polypeptides by  
CC recombinant techniques. hKv4.3 polypeptides can be used to identify  
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also  
CC claimed are methods for utilizing such agonists and antagonists for the  
CC treatment of subjects in need of enhanced or reduced activity or  
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac  
CC arrhythmias and Alzheimer's disease. The invention can also be used to  
CC detect disease associated with inappropriate hKv4.3 expression or  
CC activity  
CC  
XX

SQ Sequence 636 AA;

Query Match 99.7%; Score 3311; DB 2; Length 636;  
Best Local Similarity 99.7%; Pred. No. 1,2e-312; Indels 0; Gaps 0;  
Matches 634; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAGVAAAMLPPFAAAAIAGMPVANCMPPLAPADKXKRODELYLVANSGRFFQWRITLER 60  
DB 1 MAAGVAAAMLPPFAAAAIAGMPVANCMPPLAPADKXKRODELYLVANSGRFFQWRITLER 60  
QY 61 YPDTLLGSTEKEFFEDTKEYFFDRDPEVFRCLVNFYRGKLIHYRPECISAYDELLAF 120  
DB 61 YPDTLLGSTEKEFFEDTKEYFFDRDPEVFRCLVNFYRGKLIHYRPECISAYDELLAF 120  
QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSPFQTMRAFEENPHST 180  
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSPFQTMRAFEENPHST 180  
QY 181 LALVFFVYVGFPAVSVITNVETVPCGTVPKSGKELPCGGRYSVAFFCLDTACVMTFTVE 240  
DB 181 LALVFFVYVGFPAVSVITNVETVPCGTVPKSGKELPCGGRYSVAFFCLDTACVMTFTVE 240  
QY 241 YLRLFAAPSRRYFIRSVMSIIDVVAIMPYYIGLVMTNEDVGAFTLRFVFRIFK 300  
DB 241 YLRLFAAPSRRYFIRSVMSIIDVVAIMPYYIGLVMTNEDVGAFTLRFVFRIFK 300  
QY 301 SRHSQGRILIGYLLKSCASELGFLLPSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
DB 301 SRHSQGRILIGYLLKSCASELGFLLPSLTMAIIFATVMFYAEKGSASAKFTSIIPASFWY 360  
QY 361 TIVMTLLGYGDMVPKTIAGKIFGSLSGVLVIALPVVIVSNFSRIYHONQADKRR 420  
DB 361 TIVMTLLGYGDMVPKTIAGKIFGSLSGVLVIALPVVIVSNFSRIYHONQADKRR 420  
QY 421 AOKKARLARIRVAKTSSNAYLHRSKRGGLNEALELTGTPEEEMGKTTSLISQHHLL 480  
DB 421 AOKKARLARIRVAKTSSNAYLHRSKRGGLNEALELTGTPEEEMGKTTSLISQHHLL 480  
QY 481 HCLEKTTNHEFIDQWFEONCMESMONYPSTRPSLSHPGLTTCCSRRSKKTTHLPN 540  
DB 481 HCLEKTTNHEFIDQWFEONCMESMONYPSTRPSLSHPGLTTCCSRRSKKTTHLPN 540

DB 481 HCLEKTHHEFIDQMFQNCMESSMONTPTSRPSLSHPGLTTCRRKTKTHLPN 540  
QY 541 SNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADDLGRPNCKTSQITTAIISPT 600  
DB 541 SNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADDLGRPNCKTSQITTAIISPT 600  
QY 601 PPALTPGESRPPSPGPNTPISITSNVAVSVL 636  
DB 601 PPALTPGESRPPSPGPNTPISITSNVAVSVL 636  
RESULT 3  
ABB79584  
ID ABB79584 standard; protein; 655 AA.  
XX ABB79584;  
AC ABB79584;  
XX 01-OCT-2002 (first entry)  
DT 01-OCT-2002 (first entry)  
XX Human Kv4.3 potassium channel (long form).  
DB Human Kv4.3 potassium channel (long form).  
XX Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;  
KW nootropic; neuroprotective; cardiac; gene therapy.  
XX Homo sapiens.  
OS Homo sapiens.  
PN US6395477-B1.  
XX 28-MAY-2002.  
PD 28-MAY-2002.  
XX 23-OCT-1998; 98US-00178109.  
PF 23-OCT-1998; 98US-00178109.  
XX 23-OCT-1998; 98US-00178109.  
PR 23-OCT-1998; 98US-00178109.  
XX (AMHP) AMERICAN HOME PROD CORP.  
PA (AMHP) AMERICAN HOME PROD CORP.  
XX Cockett MI, Dilks DW, Ling HC, Sokol PT;  
PI Cockett MI, Dilks DW, Ling HC, Sokol PT;  
XX WPI; 2002-556093/59.  
DR N-PSDB; ABN84400.  
XX New isolated polynucleotide encoding human Kv4.3 potassium channel  
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic  
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart  
PT diseases.  
XX Claim 1; Col 16-20; 19pp; English.  
XX The present sequence is the protein sequence of the long isoform of novel  
CC human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been  
CC identified: the present full-length form (hKv4.3 long); and a second form  
CC (see ABB79585), which has a deletion of 19 amino acids in the carboxy  
CC domain after the predicted sixth transmembrane domain (hKv4.3 short).  
CC Human heart primarily expresses hKv4.3 long, whereas human brain contains  
CC both forms. The invention provides Kv4.3 polypeptides, polynucleotides,  
CC and methods for producing these polynucleotides. The Kv4.3 polypeptides  
CC and polynucleotides are useful in the diagnosis, treatment and screening  
CC of human diseases relating to an excess or deficiency of hKv4.3 activity,  
CC including Alzheimer's disease and heart disease  
XX  
SQ Sequence 655 AA;  
Query Match 99.4%; Score 3300.5; DB 5; Length 655;  
Best Local Similarity 97.1%; Pred. No. 1.3e-311;  
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
QY 1 MAAGVAAALPPARRAALIGMPVANCMPMLAPADKXKRODELIVANVSGRRPQTATTLER 60  
DB 1 MAAGVAAALPPARRAALIGMPVANCMPMLAPADKXKRODELIVANVSGRRPQTATTLER 60  
QY 61 YPDLLGSTEKEFFENEDTKEFFPDQDEPFRVCVNFYRTGLAHYPRYCISAYDELAIF 120  
DB 61 YPDLLGSTEKEFFENEDTKEFFPDQDEPFRVCVNFYRTGLAHYPRYCISAYDELAIF 120

DB 61 YPDLLGSTEKEFFENEDTKEFFPDQDEPFRVCVNFYRTGLAHYPRYCISAYDELAIF 120  
QY 121 YGILPEIIGDCCYEEYKRRKRNARLMDNDSENQSSMPSLSRQTMWAFENPHST 180  
DB 121 YGILPEIIGDCCYEEYKRRKRNARLMDNDSENQSSMPSLSRQTMWAFENPHST 180  
QY 181 LALVYYTGFPIAVSVITNVEYVPCGVTFQSGKELPGGERSVAFPCIDTACWIFVE 240  
DB 181 LALVYYTGFPIAVSVITNVEYVPCGVTFQSGKELPGGERSVAFPCIDTACWIFVE 240  
QY 241 YLLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRIEKE 300  
DB 241 YLLRLFAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVRIEKE 300  
QY 301 SRHSGGLRILGTYLTKSCASEIGFLFSLTMAIITPATWMPFAKSSASKFTISIPASFY 360  
DB 301 SRHSGGLRILGTYLTKSCASEIGFLFSLTMAIITPATWMPFAKSSASKFTISIPASFY 360  
QY 361 TIVMTTGLGYDMPVKTAGKIFGSLGSLGVLTALPVPIVSNFSRIYHONORADKR 420  
DB 361 TIVMTTGLGYDMPVKTAGKIFGSLGSLGVLTALPVPIVSNFSRIYHONORADKR 420  
QY 421 AOKKARLARIRVAKTGSNAVLHSKRNGLINEALELCTPPEEHNGKTTSLIESQHHL 480  
DB 421 AOKKARLARIRVAKTGSNAVLHSKRNGLINEALELCTPPEEHNGKTTSLIESQHHL 480  
QY 481 HCLEKTT-----NHEFIDQMFQNCMESSMONTPTSRPSLSHP 521  
DB 481 HCLEKTT-----NHEFIDQMFQNCMESSMONTPTSRPSLSHP 521  
QY 522 GLTTCCGRRRKKTHLPNSNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADG 581  
DB 522 GLTTCCGRRRKKTHLPNSNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADG 581  
QY 541 GLTTCCGRRRKKTHLPNSNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADG 600  
DB 541 GLTTCCGRRRKKTHLPNSNLPATRLRSWQELSTIHIOGSEOPSLTSSSLNLKADG 600  
QY 582 LRPNCKTSQITTAIISPTPPALTPGESRPPSPGPNTPISITSNVAVSVL 636  
DB 582 LRPNCKTSQITTAIISPTPPALTPGESRPPSPGPNTPISITSNVAVSVL 636  
RESULT 4  
AAM79590  
ID AAM79590 standard; protein; 655 AA.  
XX AAM79590;  
AC AAM79590;  
XX 11-JAN-1999 (first entry)  
DT 11-JAN-1999 (first entry)  
XX Human Kv potassium channel hKv4.3 (longer isoform).  
DE Human Kv potassium channel hKv4.3 (longer isoform).  
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
KW therapy; diagnosis.  
XX Homo sapiens.  
OS Homo sapiens.  
PN Key location/Qualifiers  
FT Peptide 488..506  
FT /note="extra residues of longer hKv4.3 isoform"  
XX MO9842833-A2.  
XX 01-OCT-1998.  
PD 01-OCT-1998.  
XX 23-MAR-1998; 98WO-EP001901.  
XX 27-MAR-1997; 97GB-00006377.  
PR 09-DEC-1997; 97EP-00402971.  
PR 11-DEC-1997; 97EP-00403007.  
XX (SMK) SMITHKLINE BEECHAM LAB PHARM.  
PA Bril AWA, Calmels JPP, Faivre JSP, Javre J, Rouanet S;  
PI WPI, 1998-542277/46.  
XX

DR N-PSDB; AAV61572.

XX New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
PT polynucleotide(s) useful in the treatment of disorders including cardiac  
PS arrhythmias and Alzheimer's disease.

PS Claim 2; Page 26-27; 47pp; English.

XX This is the amino acid sequence for an isoform of human Kv potassium  
CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3  
CC polynucleotide (see AAV61572), and has 97% identity with rat Kv4.3.  
CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all  
CC Kv family related proteins. A shorter isoform (see AAV9589) has been  
CC identified, which lacks amino acid residues 488-506 of the longer  
CC isoform. The invention relates to hKv4.3 polypeptides and  
CC polynucleotides, and to methods for producing such polypeptides by  
CC recombinant techniques. hKv4.3 polypeptides can be used to identify  
CC agonists and antagonists of hKv4.3 and to raise specific antibodies. Also  
CC claimed are methods for utilizing such agonists and antagonists for the  
CC treatment of subjects in need of enhanced or reduced activity or  
CC expression of hKv4.3 polypeptide. These include the treatment of cardiac  
CC arrhythmias and Alzheimer's disease. The invention can also be used to  
CC detect disease associated with inappropriate hKv4.3 expression or  
CC activity

XX Sequence 655 AA;

Query Match 99.1%; Score 3291.5; DB 2; Length 655;

Best Local Similarity 96.8%; Pred. No. 1e-310; Mismatches 2; Indels 19; Gaps 1;

Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGVAAAMLPFAPRAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRRTLLER 60

DB 1 MAAGVAAAMLPFAPRAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRRTLLER 60

QY 61 YPDTLLGSTEKEFEFFNEDTKYFFDRDPEVFRCLANFYRQKLAHYPRYECISAYDELA 120

DB 61 YPDTLLGSTEKEFEFFNEDTKYFFDRDPEVFRCLANFYRQKLAHYPRYECISAYDELA 120

QY 121 YGILPEIIGCCVEYEDRKRENERLMDNDSENNESMPSLSFRQTMRAFPENPTST 180

DB 121 YGILPEIIGCCVEYEDRKRENERLMDNDSENNESMPSLSFRQTMRAFPENPTST 180

QY 181 LALVFYVVGFFLAVSYITNVVEVPCGVPGSKELPCGERSYVAFCLDTACMIFTV 240

DB 181 LALVFYVVGFFLAVSYITNVVEVPCGVPGSKELPCGERSYVAFCLDTACMIFTV 240

QY 241 YLRLFAAPSRKRYRFRSVMGIIDVVAIMPYIIGLWMTNNEVDGAFYTLRFRVRIK 300

DB 241 YLRLFAAPSRKRYRFRSVMGIIDVVAIMPYIIGLWMTNNEVDGAFYTLRFRVRIK 300

QY 301 SRHSGRIIGYTLKSCASSELGFLFSLTMAIIFATVMPFAEKSSASKPTSPASF 360

DB 301 SRHSGRIIGYTLKSCASSELGFLFSLTMAIIFATVMPFAEKSSASKPTSPASF 360

QY 361 TIVMTLTGYGDMVPKTIAGKIFGSIISLGLVIALPVPYVSNFRIYHONORAKRR 420

DB 361 TIVMTLTGYGDMVPKTIAGKIFGSIISLGLVIALPVPYVSNFRIYHONORAKRR 420

QY 421 AOKKARLARIRVAKTGSNNAYLHRSKNGLEALLETGPPEEHMGKTTSLIESQHLL 480

DB 421 AOKKARLARIRVAKTGSNNAYLHRSKNGLEALLETGPPEEHMGKTTSLIESQHLL 480

QY 481 HCLEKTT-----NHEFTIDQMFQNCMESSMOWPSTRSSLSHP 521

DB 481 HCLEKTTGLSYLVDDPLSVRTSTIKNHEFTIDQMFQNCMESSMOWPSTRSSLSHP 540

QY 522 GLATTCSSRSKTKTHPNSNLPAITRLSMQELSTIHQSEQPSLTSTRSLMLKADG 581

DB 522 GLATTCSSRSKTKTHPNSNLPAITRLSMQELSTIHQSEQPSLTSTRSLMLKADG 581

QY 582 LRPNCKTSQITTAIISITPPALTPEGESRPPASPENNTNPSITSNVAVSVL 636

DB 582 LRPNCKTSQITTAIISITPPALTPEGESRPPASPENNTNPSITSNVAVSVL 636

DB 601 LRPNCKTSQITTAIISITPPALTPEGESRPPASPENNTNPSITSNVAVSVL 655

RESULT 5  
ID ADF91398 standard; protein; 655 AA.

AC ADF91398;

DT 26-FEB-2004 (first entry)

DE Wild-type hKv4.3 #SEQ ID 5.

XX Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
KM tranquilizer; sedative; neuroprotective; nootropic; antiparkinsonian;  
KM nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
KM blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;  
KM tachycardia; congestive heart failure; epilepsy; stroke;  
KM traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
KM Parkinson's disease.

OS Homo sapiens.

PN WO2003097682-A1.

PD 27-NOV-2003.

PF 14-MAY-2003; 2003WO-IB002453.

PR 15-MAY-2002; 2002GB-00011123.

PR 15-MAY-2002; 2002US-0378076P.

PR 15-MAY-2002; 2002US-0378131P.

XX (DEVG-) DEVGEN NV.

PA Kalecta TJ, Dewulf NE, Plaetnick GKM,

DR WPI; 2004-061981/06.

DR N-PSDB; ADF91397.

PT New nematode worm expressing a heterologous nucleotide sequence encoding

PT a functional voltage-gated potassium channel of the Kv4 family, useful

PT for determining compounds that interact with the voltage-gated potassium

PT channel.

PS Example 1; SEQ ID NO 5; 82pp; English.

XX The invention relates to a nematode worm that expresses a heterologous  
CC nucleotide sequence encoding a functional voltage-gated potassium channel  
CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,  
CC part or fragment. The nematode worm is useful in determining whether a  
CC compound interacts with the voltage-gated potassium channel of the Kv4  
CC family or whether a compound is an agonist, antagonist, opener and/or  
CC blocker of the voltage-gated potassium channel expressed by the nematode  
CC worm. The methods are used for identifying and developing compounds that  
CC interact with voltage-gated potassium channels of the Kv4 family. The  
CC compounds may be used in the development and/or preparation of  
CC compositions for pharmaceutical, agrochemical and/or veterinary use.  
CC These may be used in preparing compositions for preventing or treating  
CC diseases or conditions such as arrhythmia, tachycardia, congestive heart  
CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,  
CC Alzheimer's disease or Parkinson's disease. The current sequence  
CC represents wild-type hKv4.3.

XX Sequence 655 AA;

Query Match 99.1%; Score 3291.5; DB 8; Length 655;

Best Local Similarity 96.8%; Pred. No. 1e-310; Mismatches 2; Indels 19; Gaps 1;

Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGVAAAMLPFAPRAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRRTLLER 60

DB 1 MAAGVAAAMLPFAPRAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRRTLLER 60

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QY 61 YPDTLLGSTRKEFFENEDTKEYEFDPRDPEVERCVLNFYRTGKLHYPRYECISAYDEDLAF 120
Db 61 YPDTLLGSTRKEFFENEDTKEYEFDPRDPEVERCVLNFYRTGKLHYPRYECISAYDEDLAF 120
QY 121 YGILPEIIGDCCYEBEYKDRKRENAERLMDNDSENNOESMPSLSRQTMWRAFENPHST 180
Db 121 YGILPEIIGDCCYEBEYKDRKRENAERLMDNDSENNOESMPSLSRQTMWRAFENPHST 180
QY 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVGSKELPCGERYSVAFCLDPAWMIFFVE 240
Db 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVGSKELPCGERYSVAFCLDPAWMIFFVE 240
QY 241 YLRLFAAPSRKRFIRSVMSIIDVAIMPYYIGLWMTNNEVSGAFVTLRFRVFRIRKF 300
Db 241 YLRLFAAPSRKRFIRSVMSIIDVAIMPYYIGLWMTNNEVSGAFVTLRFRVFRIRKF 300
QY 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASKFTSIPASFWY 360
Db 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIIVMTTLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONQADRR 420
Db 361 TIIVMTTLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONQADRR 420
QY 421 AOKKARLARIRIVAKTGSNNAYLHRSKRNGLNEALELGTPEEHNGKTTSLIESQHHL 480
Db 421 AOKKARLARIRIVAKTGSNNAYLHRSKRNGLNEALELGTPEEHNGKTTSLIESQHHL 480
QY 481 HCLEKTT-----NHEFIDQMFQONCMSSMONTPTSTRPSLSHP 521
Db 481 HCLEKTT-----NHEFIDQMFQONCMSSMONTPTSTRPSLSHP 521
QY 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGG 581
Db 522 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGG 581
QY 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGG 600
Db 541 GLTTCCSRRSKKTTHLPNSNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGG 600
QY 582 LRPCKTSQITTAIISITPTPALTPEGSRPPAPSGPNTNIPSTSNVVKVSVL 636
Db 601 LRPCKTSQITTAIISITPTPALTPEGSRPPAPSGPNTNIPSTSNVVKVSVL 655

RESULT 6
AAM79591
ID AAM79591 standard; procein; 636 AA.
AC AAM79591;
XX
XX 11-JAN-1999 (first entry)
DT
XX Human Kv potassium channel hkv4.3.
DE
XX Potassium channel; Kv; hkv4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis.
XX
XX Homo sapiens.
OS
XX MO9842833-A2.
PN
XX 01-OCT-1998.
PD
XX 23-MAR-1998; 98MO-EP001901.
PE
XX 27-MAR-1997; 97GB-00006377.
PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
XX (SMIK ) SMITHKLINE BEECHAM LAB PHARM.
PA
XX Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
FI WPI; 1998-542277/46.
XX
XX N-PSDB; AAV61573.
DR
```

```
XX New potassium channel polypeptides, hkv4.3 - and hkv4.3-encoding
PT polynucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
XX Claim 19; Page 28; 47pp; English.
XX
CC This is the amino acid sequence for an isoform of human Kv potassium
CC channel hkv4.3. The sequence was deduced from an isolated hkv4.3
CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3.
CC Hydrophobicity analysis indicates 6 transmembrane domains. Typical of all
CC Kv family related proteins, hkv4.3 isoforms (see AAM79589 and AAM79590)
CC are also claimed. The invention relates to hkv4.3 polypeptides and
CC polynucleotides, and to methods for producing such polypeptides by
CC recombinant techniques. hkv4.3 polypeptides can be used to identify
CC agonists and antagonists of hkv4.3 and to raise specific antibodies. Also
CC claimed are methods for utilizing such agonists and antagonists for the
CC treatment of subjects in need of enhanced or reduced activity or
CC expression of hkv4.3 polypeptide. These include the treatment of cardiac
CC arrhythmias and Alzheimer's disease. The invention can also be used to
CC detect disease associated with inappropriate hkv4.3 expression or
CC activity
CC
SQ Sequence 636 AA;

Query Match 98.9%; Score 3285; DB 2; Length 636;
Best Local Similarity 99.1%; Pred. No. 4.1e-310;
Matches 630; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAGVAAALPPARAALIGMMVPAACMPPLAADKNKRODELIVLNSGRFQTRTTER 60
Db 1 MAAGVAAALPPARAALIGMMVPAACMPPLAADKNKRODELIVLNSGRFQTRTTER 60
QY 61 YPDTLLGSTRKEFFENEDTKEYEFDPRDPEVERCVLNFYRTGKLHYPRYECISAYDEDLAF 120
Db 61 YPDTLLGSTRKEFFENEDTKEYEFDPRDPEVERCVLNFYRTGKLHYTRXECISAYDEDLAF 120
QY 121 YGILPEIIGDCCYEBEYKDRKRENAERLMDNDSENNOESMPSLSRQTMWRAFENPHST 180
Db 121 YGILPEIIGDCCYEBEYKDRKRENAERLMDNDSENNOESMPSLSRQTMWRAFENPHST 180
QY 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVGSKELPCGERYSVAFCLDPAWMIFFVE 240
Db 181 LALVFYVYTGFFIAVSVTNNVETVPCGTVGSKELPCGERYSVAFCLDPAWMIFFVE 240
QY 241 YLRLFAAPSRKRFIRSVMSIIDVAIMPYYIGLWMTNNEVSGAFVTLRFRVFRIRKF 300
Db 241 YLRLFAAPSRKRFIRSVMSIIDVAIMPYYIGLWMTNNEVSGAFVTLRFRVFRIRKF 300
QY 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASKFTSIPASFWY 360
Db 301 SRHSGRLILGYTLKSCASELGFLLFSLTMAIIIPATVMFYAEKSSASKFTSIPASFWY 360
QY 361 TIIVMTTLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONQADRR 420
Db 361 TIIVMTTLGYGDMVPKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONQADRR 420
QY 421 AOKKARLARIRIVAKTGSNNAYLHRSKRNGLNEALELGTPEEHNGKTTSLIESQHHL 480
Db 421 AOKKARLARIRIVAKTGSNNAYLHRSKRNGLNEALELGTPEEHNGKTTSLIESQHHL 480
QY 481 HCLEKTTNHEFIDQMFQONCMSSMONTPTSTRPSLSHPGLTTCCSRRSKKTTHLPN 540
Db 481 HCLEKTTNHEFIDQMFQONCMSSMONTPTSTRPSLSHPGLTTCCSRRSKKTTHLPN 540
QY 541 SNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGGLRPNCKTSQITTAIISITPT 600
Db 541 SNLPATRLRSQMOELSTIHIQSEOPSLTSSSLNKADGGLRPNCKTSQITTAIISITPT 600
QY 601 PPALTPEGSRPPAPSGPNTNIPSTSNVVKVSVL 636
Db 601 PPALTPEGSRPPAPSGPNTNIPSTSNVVKVSVL 636
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RESULT 7  
ADD48188  
ID ADD48188 standard; protein; 655 AA.  
XX  
AC ADD48188;  
XX  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein AAB53321, SEQ ID NO 13886.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
OS Unidentified.  
XX  
PN MO2003016475-A2.  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002MO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
XX DR GENBANK; AAB53321.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
PS Example 1; Page: 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity for identifying a compound or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a rat protein (described in Table 3  
XX of the specification) which is differentially expressed during pain.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 655 AA;  
XX  
Query Match 98.9%; Score 3284.5; DB 7; Length 655;  
Best Local Similarity 96.6%; Pred. No. 4.8e-310;

		Matches 633; Conservative 1; Mismatches 2; Indels 19; Gaps 1;			
Qy	1	MAAGVAAWLPFAFAAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRTTLRR	60		
Dd	1	MAAGVAAWLPFAFAAAAGMMPVANCMPPLAPADKXKRODELIVLVNSGRRFQWRTTLRR	60		
Qy	61	YPDTLIGSTKEKFFENEDTKYFFDRDPVFCVINFYRTGKLHPRYCISAYDELLAP	120		
Dd	61	YPDTLIGSTKEKFFENEDTKYFFDRDPVFCVINFYRTGKLHPRYCISAYDELLAP	120		
Qy	121	YGLPPEIIGDCCYEEKDKRRENAERLMDNSENNOESMPSLSPQTMRAFEENHTST	180		
Dd	121	YGLPPEIIGDCCYEEKDKRRENAERLMDNSENNOESMPSLSPQTMRAFEENHTST	180		
Qy	181	LALVFYVTGFFIAVSVINNVETVPCGTVPSCKEIPCGERYSAVAFCLDTACVMIFTE	240		
Dd	181	LALVFYVTGFFIAVSVINNVETVPCGTVPSCKEIPCGERYSAVAFCLDTACVMIFTE	240		
Qy	241	YLRLFAAPSRYRFRISVMSIIDVVAIMPYYIGLVNTNEDVSGAFVTLRVPRVPRIFK	300		
Dd	241	YLRLFAAPSRYRFRISVMSIIDVVAIMPYYIGLVNTNEDVSGAFVTLRVPRVPRIFK	300		
Qy	301	SRHSOGLRILGYTLKSCASELGFLLFSLTMATITPATMVFYAEKSSASKFTSIPASFV	360		
Dd	301	SRHSOGLRILGYTLKSCASELGFLLFSLTMATITPATMVFYAEKSSASKFTSIPASFV	360		
Qy	361	TIYVMTTLGGDMVPPTIAGKIFGSCISLGVVLALPVVIVSNFSRIYHONQADKRR	420		
Dd	361	TIYVMTTLGGDMVPPTIAGKIFGSCISLGVVLALPVVIVSNFSRIYHONQADKRR	420		
Qy	421	AQKARLARIRVAKTGSSNANVYHLSKNGLLNEALBELGTPEEHRMCKTSLIFSQHHLI	480		
Dd	421	AQKARLARIRVAKTGSSNANVYHLSKNGLLNEALBELGTPEEHRMCKTSLIFSQHHLI	480		
Qy	481	HCLEKTT-----NHRFIDQMEQKCMESMOMNYSTRSPSSHP	521		
Dd	481	HCLEKTTGSLYVDPLSVRTSTINKHEPIDQMEQKCMESMOMNYSTRSPSSHS	540		
Qy	522	GLTTCCSRRSKKTTHLPNSNLPRALRSMOELSTHIGSEOPSLTTSRSSINLRADG	581		
Dd	541	GLTTCCSRRSKKTTHLPNSNLPRALRSMOELSTHIGSEOPSLTTSRSSINLRADG	600		
Qy	582	LRENCKTSQITTAIISIPPPALTPGESRPPASGCPNTNIPSTSNVVKSVL	636		
Dd	601	LRENCKTSQITTAIISIPPPALTPGESRPPASGCPNTNIPSTSNVVKSVL	655		
RESULT 8					
ADSI6294					
ADSI6294 standard; protein; 655 AA.					
XX					
AC ADSI6294;					
XX					
DT 02-DEC-2004 (first entry)					
XX					
DE Human voltage-dependent potassium channel (Haapkv4.3) protein.					
XX					
KW Voltage-dependent ion channel; drug candidate;					
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;					
KW anticonvulsant; antiarrhythmic; human.					
XX					
OS Homo sapiens.					
XX					
FH Key					
FH Region					
FH /note=.206					
FH /note="Hydrophobic region (51)"					
FH Region					
FH /note=.248					
FH /note="Hydrophobic region (52)"					
FH Region					
FH /note=.281					
FH /note="Hydrophobic region (53)"					
FH Region					
FH /note=.305					
FH /note="Hydrophobic region (54)"					
FH Region					
FH /note=.343					



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FT      /note="Hydrophobic region (S5)"
FT      Region      355..365
FT      /note="Pore region (P)"
FT      Region      374..400
FT      /note="Hydrophobic region (S6)"
XX      US2004175761-A1.
XX      09-SEP-2004.
XX      01-MAR-2003; 2003US-00377139.
XX      01-MAR-2003; 2003US-00377139.
XX      01-MAR-2003; 2003US-00377139.
XX      (MACK/) MACKINNON R.
XX      (MACK/) MACKINNON A. L.
XX      (JIAN/) JIANG Y.
XX      (RUTA/) RUTA V.
XX      Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX      WPI: 2004-642122/62.
XX      GENBANK; AF120491.
XX      Screening drug candidates that target voltage dependent ion channel
XX      protein, involves contacting screening protein with chemical compound,
XX      which is drug candidate and determining whether chemical compound binds
XX      to screening protein.
XX      Disclosure; SEQ ID NO 6; 61bp; English.
XX      The invention relates to the composition of matter suitable for use in
XX      identifying chemical compounds that bind to voltage-dependent ion channel
XX      proteins. The composition comprises a screening protein that consists of
XX      an ion channel voltage sensor domain of the ion channel protein
XX      immobilised on a solid support. The invention is useful for identifying
XX      chemical compounds (drug candidate) that bind to voltage-dependent ion
XX      channel proteins. The drug candidate of the invention is utilised for
XX      treating a condition mediated by aberrant electrical activity that
XX      initiates uptake or release of neurotransmitters and contraction of
XX      muscles. The drug candidate of the invention is also utilised for
XX      treating epilepsy and arrhythmia. The present sequence is a voltage-
XX      dependent potassium (Kv) channel protein.
XX      Sequence 655 AA;
XX      Query Match      98.8%; Score 3283.5; DB 8; Length 655;
XX      Best Local Similarity 96.8%; Pred. No. 6,1e-310; Indels 19; Gaps 1;
XX      Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;
QY      1 MAAGVAAALPPARAAATGMPVANCMPPLAPADKKNKRODELIVLVNAGRRPQTWTTLLR 60
DB      1 MAAGVAAALPPARAAATGMPVANCMPPLAPADKKNKRODELIVLVNAGRRPQTWTTLLR 60
QY      61 YPDLTLLGSTEKEFFNEEDTKYFFPDREVEPRCVLNFRTGTLHPRECEISAYDELAIF 120
DB      61 YPDLTLLGSTEKEFFNEEDTKYFFPDREVEPRCVLNFRTGTLHPRECEISAYDELAIF 120
QY      121 YGILPEITIGDCCEYEYKDRKRENAERLMDNDSENNOSMPSLSRQTMMAFENPHST 180
DB      121 YGILPEITIGDCCEYEYKDRKRENAERLMDNDSENNOSMPSLSRQTMMAFENPHST 180
QY      181 LALVFFYYTGFPIAVSVITNVEVTPCGTVPQSKELPCGERYSVAFCLIDTACWIFTE 240
DB      181 LALVFFYYTGFPIAVSVITNVEVTPCGTVPQSKELPCGERYSVAFCLIDTACWIFTE 240
QY      241 YLRLFAAPSRBYRFRSVMSIIDVAIMPYIIGVMTNEDSGAFYTLARVPRVRIKF 300
DB      241 YLRLFAAPSRBYRFRSVMSIIDVAIMPYIIGVMTNEDSGAFYTLARVPRVRIKF 300
QY      301 SRHSGRLILIGYTLKSCASELGLFLSLTMAIIFATVFAEKSSASKFTSIPASFWY 360
DB      301 SRHSGRLILIGYTLKSCASELGLFLSLTMAIIFATVFAEKSSASKFTSIPASFWY 360

```

```

QY      361 TIVMTTTLGYGDMVPKTAGKIFGSIICSLGVLVIALPVPVIVNSFRIYHONORADRR 420
DB      361 TIVMTTTLGYGDMVPKTAGKIFGSIICSLGVLVIALPVPVIVNSFRIYHONORADRR 420
QY      421 AOKKARLARIRAVAKGSSNAYLHSCRNGLNEALSLTGPBEHNGKTTSLIESQHHL 480
DB      421 AOKKARLARIRAVAKGSSNAYLHSCRNGLNEALSLTGPBEHNGKTTSLIESQHHL 480
QY      481 HCLEKTYT-----NHEFIDEQMFQONCESSMONTPTSTRPSLSHP 521
DB      481 HCLEKTYTGLSYLVDDPLLSVTRSTIKNEHFIQMFQONCESSMONTPTSTRPSLSHP 540
QY      522 GLTTCCGRRSKKTHLNSULPATRLASMOELSTIHOQSOPSLTSTRSSLNKADGG 581
DB      541 GLTTCCGRRSKKTHLNSULPATRLASMOELSTIHOQSOPSLTSTRSSLNKADGG 600
QY      582 LRPNCKTSQITTAIISIPTPPALTPGEGSRPPSPGPNTPITSNVVKSVL 636
DB      601 LRPNCKTSQITTAIISIPTPPALTPGEGSRPPSPGPNTPITSNVVKSVL 655
XX      RESULT 9
XX      AAB86321
XX      ID AAB86321 standard; protein; 655 AA.
XX      AC AAB86321;
XX      DT 13-SEP-2001 (first entry)
XX      DE Human Kv4.3 protein.
XX      KW Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;
XX      neurodegenerative disease; ischemia; stroke; Alzheimer's disease;
XX      Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;
XX      learning capacity; protein kinase activator; anti-arrhythmic.
XX      OS Homo sapiens.
XX      PN DB19963612-A1.
XX      PD 12-JUL-2001.
XX      PF 29-DEC-1999; 99DE-01063612.
XX      PR 29-DEC-1999; 99DE-01063612.
XX      PA (GENI-) FORSCHUNGSSELLSCHAFT GENION MBH.
XX      DR WPI: 2001-426637/46.
XX      PT New potassium channel subunit proteins, useful for identifying and
XX      testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological
XX      agents.
XX      PS Claim 4; Page 32-33; 50pp; German.
XX      This invention describes a novel potassium channel protein (I) that is
XX      either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium
XX      channels containing (I) are used to identify and test: (i) compounds for
XX      treatment of neurodegenerative diseases (autism, epilepsy, ischemia,
XX      stroke, Alzheimer's, Parkinson's and Huntington's diseases) or cardiac
XX      arrhythmia, or those that improve learning capacity and memory; and (ii)
XX      activators of protein kinases. Host cells that express (I) can identify
XX      agents that do not interact significantly with channels and control I_t_o
XX      (a quickly activated transient current), so lack the side effects of
XX      known anti-arrhythmic agents. They also eliminate, or reduce, the need
XX      for testing on organ cultures
XX      Sequence 655 AA;
XX      Query Match      98.8%; Score 3279.5; DB 4; Length 655;
XX      Best Local Similarity 96.6%; Pred. No. 1.5e-309;

```

Matches	633;	Conservative	0;	Mismatches	3;	Indels	19;	Gaps	1;
QY	1	MAAGVAAAML	PFAPAAAIGMMPVANCMPPLAPADKNRQDELIVLANSGRRFQWRTTLER	60					
Db	1	MAAGVAAAML	PFAPAAAIGMMPVANCMPPLAPADKNRQDELIVLANSGRRFQWRTTLER	60					
QY	61	YPTTLGSTEKEPF	FNFEDTKEYFPDRDPEVRCVLNFRYTKLHYPRYECISAYDELA	120					
Db	61	YPTTLGSTEKEPF	FNFEDTKEYFPDRDPEVRCVLNFRYTKLHYPRYECISAYDELA	120					
QY	121	YGLPELIGDCC	EEYKDRRENAERLMDNDSENNQESMPSLSPFQTMRAENPHST	180					
Db	121	YGLPELIGDCC	EEYKDRRENAERLMDNDSENNQESMPSLSPFQTMRAENPHST	180					
QY	181	LALVFFVYTG	FFFAVSVITNVETVPCGVPGSKELPCGGRYVAFFCLDTACVMITVE	240					
Db	181	LALVFFVYTG	FFFAVSVITNVETVPCGVPGSKELPCGGRYVAFFCLDTACVMITVE	240					
QY	241	YLRLFAAPSR	RYFIRSVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVFRIFKF	300					
Db	241	YLRLFAAPSR	RYFIRSVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFVFRIFKF	300					
QY	301	SRHSGRLIG	YTLKSCASELGFLESLTMAIIIFATVMEYAKGSSASKFTSIIPASFWY	360					
Db	301	SRHSGRLIG	YTLKSCASELGFLESLTMAIIIFATVMEYAKGSSASKFTSIIPASFWY	360					
QY	361	TIYMTTLG	YGDWVPKTIAGKIRGSLCSLGSVLVIALPVPVIVSNFSRIYHONQADKRR	420					
Db	361	TIYMTTLG	YGDWVPKTIAGKIRGSLCSLGSVLVIALPVPVIVSNFSRIYHONQADKRR	420					
QY	421	AOKKARLAR	IRVAKTSSNAYLHSGKNGLINEALELTGPEEBHMKTTSLISQHHLL	480					
Db	421	AOKKARLAR	IRVAKTSSNAYLHSGKNGLINEALELTGPEEBHMKTTSLISQHHLL	480					
QY	481	HCELEKT	-----NHERIDQMEFONQESSMOMYPTSRPSLSHP	521					
Db	481	HCELEKT	-----NHERIDQMEFONQESSMOMYPTSRPSLSHP	521					
QY	522	GLTTCCSR	RSKKTTHLPNSNLPAIRLSMOELSTHIOGSEOPSLTSSSLNLKADG	581					
Db	522	GLTTCCSR	RSKKTTHLPNSNLPAIRLSMOELSTHIOGSEOPSLTSSSLNLKADG	581					
QY	582	LRPNCKTS	QITTAIISIPPPALTPEGESRPPAPSPGPNINIBSITSNVVKSVL	636					
Db	601	LRPNCKTS	QITTAIISIPPPALTPEGESRPPAPSPGPNINIBSITSNVVKSVL	636					
RESULT 10									
ADE61252									
ID ADE61252 standard; protein: 611 AA.									
ADE61252;									
29-JAN-2004 (first entry)									
Rat Proteoin AAA80459, SEQ ID NO 7170.									
Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;									
chronic constriction injury; CCI; spared nerve injury; SNI; Chung.									
Rattus norvegicus.									
W02003016475-A2.									
27-FEB-2003.									
14-AUG-2002; 2002WO-US025765.									
14-AUG-2001; 2001US-0312147P.									
01-NOV-2001; 2001US-0346382P.									
26-NOV-2001; 2001US-0333347P.									
(GEHO) GEN HOSPITAL CORP.									

PA	(FARB) BAYER AG.
XX	
PI	Woolf C, D'ureo D, Befort K, Coctigan M;
XX	
DR	WPI: 2003-268312/26.
DR	GENBANK: AAA80459.
PT	New composition comprising two or more isolated polypeptides, useful for
PT	preparing a medicament for treating pain in an animal.
XX	
PS	Claim 1; Page; 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC	therapy). The sequence presented is a rat protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	the sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 611 AA:
Query Match	92.0%; Score 3055; DB 7; Length 611;
Best Local Similarity	99.3%; Pred. No. 9, 6e-288;
Matches	584; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY	1 MAAGVAAAML
Db	1 MAAGVAAAML
QY	61 YPTTLGSTEKEPF
Db	61 YPTTLGSTEKEPF
QY	121 YGILPELIGDCC
Db	121 YGILPELIGDCC
QY	181 LALVFFVYTG
Db	181 LALVFFVYTG
QY	241 YLRLFAAPSR
Db	241 YLRLFAAPSR
QY	301 SRHSGRLIG
Db	301 SRHSGRLIG
QY	361 TIYMTTLG
Db	361 TIYMTTLG

QY 421 AOKKRLARIRVAKTSSNAVYLSKRNGLNLEALBELTGPBEEHMKTTSLIESQHHL 480  
DB 421 AOKKRLARIRVAKTSSNAVYLSKRNGLNLEALBELTGPBEEHMKTTSLIESQHHL 480  
QY 481 HCLEKTTNHEFIDEQMFECNCESSMOWNYPTSRPSLSHPGLTTCCSRRSKKTTHLPN 540  
DB 481 HCLEKTTNHEFIDEQMFECNCESSMOWNYPTSRPSLSHPGLTTCCSRRSKKTTHLPN 540  
QY 541 SNLPATRLRSMQELSTIHIGSEQPSLTTSSSLNLIKADGRLPNCKT 588  
DB 541 SNLPATRLRSMQELSTIHIGSEQPSLTTSSSLNLIKADGRLPNCKT 588

## RESULT 11

ADM10929  
ID ADM10929 standard; protein; 630 AA.  
AC ADM10929;  
XX 20-MAY-2004 (first entry)  
DT Human O647SgenomicContig3 homologue protein #4.  
DE  
XX  
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
KW cyostatic; gene therapy; human; ds.  
XX Homo sapiens.  
OS  
XX US2003206918-A1.  
PN  
XX 06-NOV-2003.  
PD  
XX 05-FEB-2003; 2003US-00361811.  
PF  
XX 10-SEP-1999; 99US-00394374.  
PR 01-MAY-2000; 2000US-00561778.  
PR 15-AUG-2000; 2000US-00640173.  
PR 07-SEP-2000; 2000US-00656668.  
PR 14-NOV-2000; 2000US-00713550.  
PR 03-APR-2001; 2001US-00825294.  
PR 02-OCT-2001; 2001US-00970966.  
PR 02-AUG-2002; 2002US-00212677.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Fanger GR, Fling SP;  
XX  
XX WPI: 2003-901037/82.  
XX N-PSDB; ADM10923.  
XX  
XX New polynucleotides encoding tumor proteins, treating or inhibiting the  
XX development of cancer, particularly ovarian cancer, and for stimulating  
XX and/or expanding T cells specific for a tumor protein.  
XX  
XX Example 12; SEQ ID NO 260; 221bp; English.  
XX  
XX This invention describes a novel ovarian tumour protein which can be used  
XX to detecting the presence of an ovarian cancer in a patient by  
XX stimulating and/or expanding T cells specific for the tumour protein. The  
XX products of the invention can also be used in a method to inhibit the  
XX development of a cancer in a patient comprising (a) incubating CD4+  
XX and/or CD8+ T cells isolated from a patient with at least one ovarian  
XX tumour protein, such that T cell proliferate and (b) administering to the  
XX patient the proliferated T cells. The cyostatic polynucleotides or  
XX polypeptides described in the invention are useful for treating or  
XX inhibiting the development of cancer, particularly ovarian cancer and for  
XX stimulating and/or expanding T cells specific for a tumour protein or for  
XX gene therapy.  
XX  
XX Sequence 630 AA;  
XX  
XX Query Match 75.8%; Score 2518; DB 7; Length 630;

Best Local Similarity 75.8%; Pred. No. 26-235;  
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY 1 MAAGVAAAMLPFAAALIGMPVANCMPPLADPKKR-ODELIYVNVSGRRQTRTTLE 59  
DB 1 MAAGVAAAMLPFAAALIGMPVANCMPPLADPKKR-ODELIYVNVSGRRQTRTTLE 60  
QY 60 RYPTDILLSTEKEPFENEDTKEYFPDRDPEVRCULNFRGKLYHPRCEISAVDEELA 119  
DB 61 RYPTDILLSTEKEPFENEDTKEYFPDRDPEVRCULNFRGKLYHPRCEISAVDEELA 120  
QY 120 FYGILPEIIGCCYEYKORRENAERLMDNDSENNOES-MSLSFRQTMRAFENPPT 178  
DB 121 FFGILPEIIGCCYEYKORRENAERLMDNDSENNOES-MSLSFRQTMRAFENPPT 180  
QY 179 STLALVFYVTVGFFLAIVSVITNVETVPCGVPGS-KELPCGERYSVAFCLDTACWIF 237  
DB 181 STMALVFYVTVGFFLAIVSVITNVETVPCGVPGS-KELPCGERYSVAFCLDTACWIF 240  
QY 238 TVEYLLRLPAAPSRRYRFRSVMSIIDVVAIMPYTGTMTNEDVSGAFVTLRVRVPT 297  
DB 241 TVEYLLRLPAAPSRRYRFRSVMSIIDVVAIMPYTGTMTNEDVSGAFVTLRVRVPT 300  
QY 298 FKFSRHSQGLRIIGYTLKSCASELGFLEPSLTMAIIFPATVMPYAEKSSASKFTSIPAS 357  
DB 301 FKFSRHSQGLRIIGYTLKSCASELGFLEPSLTMAIIFPATVMPYAEKSSASKFTSIPAS 360  
QY 358 FWYITVITMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVVIVNSFSRIYHONORAD 417  
DB 361 FWYITVITMTLGYGDMVPKTIAGKIFGSI CSLSGVLVIALPVVIVNSFSRIYHONORAD 420  
QY 418 KRRACKKRLARIRVAKTSSNAVYLSKRNGLNLEALBELTGPBEEHMKTTSLIESQH 477  
DB 421 KRRACKKRLARIRVAKTSSNAVYLSKRNGLNLEALBELTGPBEEHMKTTSLIESQH 479  
QY 478 HHLHCLKTTNHEFIDEQMFECNCESSMOWNYPTSRPSLSHPGLTTCCSRRSKKTTH 537  
DB 480 HHLHCLKTTNHEFIDEQMFECNCESSMOWNYPTSRPSLSHPGLTTCCSRRSKKTTH 539  
QY 538 LPNSNLPAATRLRSMQELSTIHIGSEQPSLTTSSSLNLIKADGRLPNCKTSQITTAIS 597  
DB 540 LPNSNLPAATRLRSMQELSTIHIGSEQPSLTTSSSLNLIKADGRLPNCKTSQITTAIS 599  
QY 598 IPTPPALTPEGSRP--PPASBPPTNIPSTISNVKYSVL 636  
DB 600 IPTPPALTPEGSRP--PPASBPPTNIPSTISNVKYSVL 630  
RESULT 12  
ADM10928  
ID ADM10928 standard; protein; 630 AA.  
AC ADM10928;  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human O647SgenomicContig3 homologue protein #3.  
DE  
XX  
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
KW cyostatic; gene therapy; human; ds.  
XX  
XX Homo sapiens.  
OS  
XX US2003206918-A1.  
PN  
XX 06-NOV-2003.  
PD  
XX 05-FEB-2003; 2003US-00361811.  
PF  
XX 10-SEP-1999; 99US-00394374.  
PR 01-MAY-2000; 2000US-00561778.  
PR 15-AUG-2000; 2000US-00640173.  
PR 07-SEP-2000; 2000US-00656668.



```
Db      1 MAAGVAAWLPPARAALIGMPVAGSMPAPPROEKRKTODALIVNVSGRFQWDTTLE 60
Qy      RYPTLLGSTEKEEFENDTKEVEFPDRDEVRCLNPFKTKLHYPRRECSAAYDELLA 119
Db      61 RYPTLLGSSERDFPHETQYFPDRDPDIFRHILNFRKGLHYPRRECSAAYDELLA 120
Qy      120 FYGILPEIIGCCYEYKDRKRENAERLMDNDSENNQES--MPSLSFQTMRAEPENPT 178
Db      121 FFGILPEIIGCCYEYKDRRENAERLQDDADDTAGSALPTMTAKORVRAENPHHT 180
Qy      179 STALVFFYVTGFFIAVSVINNVETVPCGIVPGS--KELPCGERYSVAFFCLDTACWIMF 237
Db      181 STMALVFFYVTGFFIAVSVINNVETVPCGSSPGHIKELPCGERYVAFAFFCLDTACWIMF 240
Qy      238 TVEYLRLFAAPRSRRFRIRSVMSIIDVAIMPYITGLVMTNNEDEVSGAFVTLRVRVRI 297
Db      241 TVEYLRLFAAPRSRRFRIRSVMSIIDVAIMPYITGLVMTNNEDEVSGAFVTLRVRVRI 300
Qy      298 FKFSRHSGRLILGTYLKSASBELGFLPSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db      301 FKFSRHSGRLILGTYLKSASBELGFLPSLTMAIIFATVMFYAEKSSASKFTSIPAS 360
Qy      358 FWYITVMTTLLGYGDMVEPKTIAGKIFGSIICSLSGVLVIALPVPVIVSNFSRIYHONRAD 417
Db      361 FWYITVMTTLLGYGDMVEPKTIAGKIFGSIICSLSGVLVIALPVPVIVSNFSRIYHONRAD 420
Qy      418 KRRQOKKARLARIRVAKTGSSNAYLHSGKNGILNLELTGPREEHNGKTSLESQHH 477
Db      421 KRRQOKKARLARIRVAKTGSSNAYLHSGKNGILNLELTGPREEHNGKTSLESQHH 479
Qy      478 HLHCLKETTTHHEFIDEQMPFONCMESMOMVPTSRPSLSHSGLTTCSSRRSKTKTH 537
Db      480 HLHCLKETTTHHEFIDEQMPFONCMESMOMVPTSRPSLSHSGLTTCSSRRSKTKTH 539
Qy      538 LPNSNLPATRLRSMQELSTHIOGSEOPSLTTRSSSLNKLKDDGLRPNCCKTSQITTAIIS 597
Db      540 LPNSNLPATRLRSMQELSTHIOGSEOPSLTTRSSSLNKLKDDGLRPNCCKTSQITTAIIS 599
Qy      598 IPTPPALTPGEGSRP--PPASPGPNTNIPSTISNVVAKSVL 636
Db      600 IPTPPALTPGEGSRP--PPASPGPNTNIPSTISNVVAKSVL 636

RESULT 14
ADM10927
ID      ADM10927 standard; protein; 630 AA.
XX      ADM10927;
XX      20-MAY-2004 (first entry)
XX      Human O647SgenomicContig3 homologue protein #2.
XX      ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX      cyclostatic; gene therapy; human; ds.
OS      Homo sapiens.
XX      US2003206918-A1.
XX      06-NOV-2003.
XX      05-FEB-2003; 2003US-00361811.
XX      10-SEP-1999; 99US-00394374.
XX      01-MAY-2000; 2000US-00561778.
XX      15-AUG-2000; 2000US-00640173.
XX      07-SEP-2000; 2000US-00656668.
XX      14-NOV-2000; 2000US-00713550.
XX      03-APR-2001; 2001US-00825294.
XX      02-OCT-2001; 2001US-00970966.
XX      02-AUG-2002; 2002US-00212677.
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PA      (CORI-) CORIXA CORP.
XX
PI      Fanger GR, Fling SP;
XX
DR      WPI; 2003-901037/82.
XX      N-PSDB; ADM10921.
XX
PT      New polynucleotides encoding tumor proteins, treating or inhibiting the
PT      development of cancer, particularly ovarian cancer, and for stimulating
PT      and/or expanding T cells specific for a tumor protein.
XX
PS      Example 12; SEQ ID NO 258; 221bp; English.
XX
CC      This invention describes a novel ovarian tumour protein which can be used
CC      to detecting the presence of an ovarian cancer in a patient by
CC      stimulating and/or expanding T cells specific for the tumour protein. The
CC      products of the invention can also be used in a method to inhibit the
CC      development of a cancer in a patient comprising (a) incubating CD4+
CC      and/or CD8+ T cells isolated from a patient with at least one ovarian
CC      tumour protein, such that T cell proliferate and (b) administering to the
CC      patient the proliferated T cells. The cyclostatic polynucleotides or
CC      polypeptides described in the invention are useful for treating or
CC      inhibiting the development of cancer, particularly ovarian cancer and for
CC      stimulating and/or expanding T cells specific for a tumour protein or for
CC      gene therapy.
XX
SQ      Sequence 630 AA;
XX
Query Match          75.8%; Score 2518; DB 7; Length 630;
Best Local Similarity 75.8%; Pred. No. 2e-235;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy      1 MAAGVAAWLPPARAALIGMPVANCMPMLPADKXKR--ODELIVNVSGRRRPQWRTTLE 59
Db      1 MAAGVAAWLPPARAALIGMPVAGSMPAPPROEKRKTODALIVNVSGRFQWDTTLE 60
Qy      60 RYPTLLGSTEKEEFENDTKEVEFPDRDEVRCLNPFKTKLHYPRRECSAAYDELLA 119
Db      61 RYPTLLGSSERDFPHETQYFPDRDPDIFRHILNFRKGLHYPRRECSAAYDELLA 120
Qy      120 FYGILPEIIGCCYEYKDRKRENAERLMDNDSENNQES--MPSLSFQTMRAEPENPT 178
Db      121 FFGILPEIIGCCYEYKDRRENAERLQDDADDTAGSALPTMTAKORVRAENPHHT 180
Qy      179 STALVFFYVTGFFIAVSVINNVETVPCGIVPGS--KELPCGERYSVAFFCLDTACWIMF 237
Db      181 STMALVFFYVTGFFIAVSVINNVETVPCGSSPGHIKELPCGERYVAFAFFCLDTACWIMF 240
Qy      238 TVEYLRLFAAPRSRRFRIRSVMSIIDVAIMPYITGLVMTNNEDEVSGAFVTLRVRVRI 297
Db      241 TVEYLRLFAAPRSRRFRIRSVMSIIDVAIMPYITGLVMTNNEDEVSGAFVTLRVRVRI 300
Qy      298 FKFSRHSGRLILGTYLKSASBELGFLPSLTMAIIFATVMFYAEKSSASKFTSIPAS 357
Db      301 FKFSRHSGRLILGTYLKSASBELGFLPSLTMAIIFATVMFYAEKSSASKFTSIPAS 360
Qy      358 FWYITVMTTLLGYGDMVEPKTIAGKIFGSIICSLSGVLVIALPVPVIVSNFSRIYHONRAD 417
Db      361 FWYITVMTTLLGYGDMVEPKTIAGKIFGSIICSLSGVLVIALPVPVIVSNFSRIYHONRAD 420
Qy      418 KRRQOKKARLARIRVAKTGSSNAYLHSGKNGILNLELTGPREEHNGKTSLESQHH 477
Db      421 KRRQOKKARLARIRVAKTGSSNAYLHSGKNGILNLELTGPREEHNGKTSLESQHH 479
Qy      478 HLHCLKETTTHHEFIDEQMPFONCMESMOMVPTSRPSLSHSGLTTCSSRRSKTKTH 537
Db      480 HLHCLKETTTHHEFIDEQMPFONCMESMOMVPTSRPSLSHSGLTTCSSRRSKTKTH 539
Qy      538 LPNSNLPATRLRSMQELSTHIOGSEOPSLTTRSSSLNKLKDDGLRPNCCKTSQITTAIIS 597
Db      540 LPNSNLPATRLRSMQELSTHIOGSEOPSLTTRSSSLNKLKDDGLRPNCCKTSQITTAIIS 599
Qy      598 IPTPPALTPGEGSRP--PPASPGPNTNIPSTISNVVAKSVL 636
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:58:11 ; Search time 104.44 Seconds  
(without alignments)  
454.585 Million cell updates/sec

Title: US-10-062-879-4

Perfect score: 3320

Sequence: 1 MAAGVAAWLPFARAALIGMM.....PCPNNTISITSNVKSVL 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCPUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	636	3	US-09-178-109-4 Sequence 4, Appl1
2	3311	99.7	636	3	US-09-142-791A-2 Sequence 2, Appl1
3	3300.5	99.4	655	3	US-09-178-109-2 Sequence 2, Appl1
4	3291.5	99.1	655	3	US-09-142-791A-4 Sequence 4, Appl1
5	3285	98.9	636	3	US-09-142-791A-6 Sequence 6, Appl1
6	2518	75.8	630	4	US-09-949-016-6828 Sequence 6828, Ap
7	2121.5	63.9	646	3	US-09-336-643A-10 Sequence 10, Appl
8	865.5	26.1	260	4	US-09-949-016-8327 Sequence 8327, Ap
9	774.5	23.3	806	4	US-09-833-466-113 Sequence 13, Appl
10	750	22.6	854	4	US-09-833-466-112 Sequence 12, Appl
11	750	22.6	858	4	US-09-275-252A-6 Sequence 6, Appl1
12	726.5	21.9	539	1	US-08-464-340A-13 Sequence 13, Appl
13	723	21.8	616	4	US-09-275-252A-4 Sequence 4, Appl1
14	719	21.7	552	4	US-09-949-016-8164 Sequence 8164, Ap
15	718	21.6	523	4	US-09-949-016-6195 Sequence 6195, Ap
16	712.5	21.5	528	2	US-08-527-152-2 Sequence 2, Appl1
17	710.5	21.4	495	4	US-09-275-252A-5 Sequence 5, Appl1
18	704	21.2	446	4	US-10-162-012-8 Sequence 8, Appl1
19	703	21.2	601	3	US-09-336-643A-4 Sequence 4, Appl1
20	704	21.2	532	4	US-10-162-012-13 Sequence 13, Appl
21	696	21.0	757	4	US-09-949-016-7121 Sequence 7121, Ap
22	695	20.9	532	1	US-08-288-405A-10 Sequence 10, Appl
23	689	20.8	556	4	US-09-275-252A-8 Sequence 8, Appl1
24	678	20.4	159	2	US-08-606-143-45 Sequence 45, Appl
25	675	20.3	529	4	US-09-949-016-6196 Sequence 6196, Ap
26	675	20.3	538	4	US-09-949-016-8017 Sequence 8017, Ap
27	635.5	19.1	162	2	US-08-606-143-44 Sequence 44, Appl

28	632	19.0	490	3	US-09-336-643A-6 Sequence 6, Appl1
29	632	19.0	491	4	US-09-181-339-12 Sequence 12, Appl
30	632	19.0	507	4	US-09-949-016-9860 Sequence 9860, Ap
31	629	18.9	494	4	US-09-949-016-7475 Sequence 7475, Ap
32	627.5	18.9	491	4	US-09-181-339-7 Sequence 7, Appl1
33	622	18.7	494	1	US-08-464-340A-4 Sequence 4, Appl1
34	622	18.7	494	3	PCR-US94-08449A-4 Sequence 4, Appl1
35	614	18.5	499	3	US-09-336-643A-8 Sequence 8, Appl1
36	598	18.0	513	4	US-09-949-016-10288 Sequence 10288, A
37	597	18.0	477	3	US-09-336-643A-18 Sequence 18, Appl
38	584	17.6	513	1	US-08-464-340A-2 Sequence 2, Appl1
39	584	17.6	513	5	PCR-US94-08449A-2 Sequence 2, Appl1
40	569	17.1	506	4	US-09-719-919A-1 Sequence 1, Appl1
41	564	17.0	519	4	US-09-719-919A-17 Sequence 17, Appl
42	557.5	16.8	545	4	US-09-833-466-3 Sequence 3, Appl1
43	529	15.9	497	4	US-09-181-339-3 Sequence 3, Appl1
44	410	12.3	423	4	US-09-181-339-9 Sequence 9, Appl1
45	370.5	11.2	256	4	US-09-181-339-5 Sequence 5, Appl1

ALIGNMENTS

RESULT 1									
US-09-178-109-4									
Sequence 4, Application US/09178109									
Patent No. 6395477									
GENERAL INFORMATION:									
APPLICANT: Cockett, Mark I.									
APPLICANT: Dilke, Daniel W.									
APPLICANT: Chang Ling, Hui-Ping									
APPLICANT: Soko, Patricia T.									
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and									
TITLE OF INVENTION: Polypeptides and Uses Therefor									
FILE REFERENCE: ahp-98089									
CURRENT APPLICATION NUMBER: US/09/178,109									
CURRENT FILING DATE: 1998-10-23									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 4									
LENGTH: 636									
TYPE: PRT									
ORGANISM: human									
US-09-178-109-4									
Query Match									
Best Local Similarity 100.0%; Score 3320; DB 3; Length 636;									
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	61	YPTDLGSTTEKPEFNEDETKYFPDDEVEPRCVLNFRTGKHYPRECTSAVDLAF	120						
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DB	121	YGLPEITIGDCYEEYKRRKRNARLMDDDSENNOSSMPSLSTROTMRFAFENPHST	180						
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DB	181	LALVYYTGTGFIASVITNVETVPCGTVPQSGKELPCGERYSVAFCLDPAQWIFVE	240						
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DB	241	YLLRFAAPSRYPFRSVMSIIDVAIMPYYIGLMTNNEDVSGAFVTLRVRVRIRPKF	300						
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Db 541 SNLPATRLRSMOBLSTIHIQSEQPSLTTSRSSLNKADGRLPNCKTSQITTAIISPT 600
QY 601 PPALTPGEGSRPPASPGRPNTNIPSTISNVKXSVL 636
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Db 601 PPALTPGEGSRPPASPGRPNTNIPSTISNVKXSVL 636
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## RESULT 2

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US-09-142-791A-2
; Sequence 2, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmele
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouane
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142, 791A
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-2
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Query Match 99.7%; Score 3311; DB 3; Length 636;

Best Local Similarity 99.7%; Pred. No. 8.4e-309; Matches 634; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 YPDTLLGSTEKEFFENEDTKEYFFDRDPEVRCVLPYRGTGKLHYRPECISAYDELA 120
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Db 121 YGILPELIGCCYEEYKDRKRENAERLMDNDSENNOESMPSLSFRQTMRAFAENPHTST 180
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Db 181 LALVFFVYVTFGLFVAVITNVVETVPCGTVPSSKELPCGGRYSVAFFCLDTACVMI 240
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Db 601 PPALTPGEGSRPPASPGRPNTNIPSTISNVKXSVL 636
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## RESULT 3

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US-09-178-109-2
; Sequence 2, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dicks, Daniel W.
; APPLICANT: Sokol, Patricia T.
; APPLICANT: Chang Ling, Hual-Ping
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178, 109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: human
US-09-178-109-2
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Query Match 99.4%; Score 3300.5; DB 3; Length 655;

Best Local Similarity 97.1%; Pred. No. 9e-308; Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

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Db 601 LRPNCKTSQITTAIISITPPALTPEGESRPPASPGENTNIPSTSNVVKYVL 655
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RESULT 4  
US-09-142-791A-4  
Sequence 4, Application US/09142791A  
Patent No. 6368823

## GENERAL INFORMATION:

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APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Caimels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 655
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-4
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Query Match 99.1%; Score 3291.5; DB 3; Length 655;  
Best Local Similarity 96.8%; Pred. No. 6.6e-307;  
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

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RESULT 5  
US-09-142-791A-6  
Sequence 6, Application US/09142791A  
Patent No. 6368823

## GENERAL INFORMATION:

```
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Caimels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-142-791A-6
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Query Match 98.9%; Score 3285; DB 3; Length 636;  
Best Local Similarity 99.1%; Pred. No. 2.6e-306;  
Matches 630; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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DB 241 YLRLFAAPSRVFRISVMSIIDVVAIMPYIGLWMTNNEVSGAFVTLRVPRVFR 300
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RESULT 6
US-09-949-016-6828
; Sequence 6828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6828
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6828
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Query Match 75.8%; Score 2518; DB 4; Length 630;
Best Local Similarity 75.8%; Pred. No. 1,2e-232;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
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QY 1 MAAGVAAALPFAAALIGMPVANCMPPLADPNKR-ODELIYLVNSGRRFQTRWTTLE 59
DB 1 MAAGVAAALPFAAALIGMPVASCMPVAPRQRRKRTQDALIVLVNSGTRFQWQDTLE 60
QY 60 RYPTLLIGSTKEFFNFBDTKEVFFDRDDEYFRCVLANFYRGKLAHYRPECISAYDEELA 119
DB 61 RYPTLLIGSSERDFEYHPEETOQYFFDRDDPDIFRHILNFYRGKLAHYRPECISAYDEELA 120
```

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QY 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAEFENPHT 178
DB 121 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNQSMPSLSFRQTMRAEFENPHT 180
QY 179 STIALVFYVYVGFIAVSVITNVETVPCGYVPGSKELPCGERVAVAFCLDTACVMIF 237
DB 181 STIALVFYVYVGFIAVSVITNVETVPCGYVPGSKELPCGERVAVAFCLDTACVMIF 240
QY 238 TVEYLRLFAAPSRVFRISVMSIIDVVAIMPYIGLWMTNNEVSGAFVTLRVPRVFR 297
DB 241 TVEYLRLFAAPSRVFRISVMSIIDVVAIMPYIGLWMTNNEVSGAFVTLRVPRVFR 300
QY 298 FKFSRHSOGIRLIGYTLKSCASELGLFSLTMAIIIFATVMEYAEKGSASAKFTSIPAS 357
DB 301 FKFSRHSOGIRLIGYTLKSCASELGLFSLTMAIIIFATVMEYAEKGSASAKFTSIPAS 360
QY 358 FWTYITMTTLLGYDMVPPRTIAGKIFGSLGSLGVVIALPVPVIVSNFSRIYHQRAD 417
DB 361 FWTYITMTTLLGYDMVPPRTIAGKIFGSLGSLGVVIALPVPVIVSNFSRIYHQRAD 420
QY 418 KRAOKKARLARIKAVKTGSSNAVYLHSKRNGLNEALELTGTPEEBHMGKTSLSISOH 477
DB 421 KRAOKKARLARIKAVKTGSSNAVYLHSKRNGLNEALELTGTPEEBHMGKTSLSISOH 479
QY 478 HLEKTTNHEFIDQWFEQNCMESSMONTPTSPSLSHPGTLTTCSSRSKKTTHLPN 537
DB 480 HLEKTTNHEFIDQWFEQNCMESSMONTPTSPSLSHPGTLTTCSSRSKKTTHLPN 539
QY 538 LPSNLPATRLRMQELSTHIGSEQPSLTSSSLNKADGDLRPNCKTSQITTAIISPT 597
DB 540 LPSNLPATRLRMQELSTHIGSEQPSLTSSSLNKADGDLRPNCKTSQITTAIISPT 599
QY 598 IPTPPALTPGESRPPASPGPNTNIPSTSNVVKVSVL 636
DB 600 IPTPPALTPGESRPPASPGPNTNIPSTSNVVKVSVL 630
```

```
RESULT 7
US-09-336-643A-10
; Sequence 10, Application US/09336643A
; Patent No. 639761
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURRAN, Mark Edward
; APPLICANT: HU, Ping
; APPLICANT: RUTTER, Marc
; APPLICANT: WANG, Jian-Wang
; TITLE OF INVENTION: No. 639761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 646
; TYPE: PRT
; ORGANISM: H. sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(646)
; OTHER INFORMATION: xaa = Any Amino Acid
US-09-336-643A-10
```

```
Query Match 63.9%; Score 2121.5; DB 3; Length 646;
Best Local Similarity 65.1%; Pred. No. 1.5e-194;
Matches 428; Conservative 78; Mismatches 116; Indels 35; Gaps 13;
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```
QY 1 MAAGVAAALPFAAALIGMMPVANCMPMLPADKAKKRODELIVLVNSGRRFQMTTLER 60
DB 1 MAAGATLPLPFAAALVGMPLPAOQPLPAPGVKASRGDXVUVVNSGRRFETWKATLDR 60
QY 61 YPDTLLGSTEKEFFENEDTKEYFDRDPEVFRVCLNFYRTGKLHYPRYECISAYDELA 120
DB 61 YPDTLLGSEKKEFFDADSGEYFDRDPMFHVILNFRTGRLHCPROGCIQAPBELAF 120
QY 121 YGILPEITIGDCCYEEYKORKEKNAERLMDNDSENNQSMPSL---SFRQMTMAFENP 176
DB 121 YGILPELVGDCCLEBYRDKKENAERLMBDEBAEQAGG-PALPAGSSIRQKIMBAFENP 179
QY 177 HTSLTAIVFYVVTGFEIIVSVTVTVETVPC--GVTPSGKELPCGERVSAFCDTACV 234
DB 180 HTSLTAIVFYVVTGFEIIVSVTVTVETVPCGARSRRSEQPCGERPQAFCDTACV 239
QY 235 MIFVEYLLRLPAPASRYRFRISVMSIIDVVAIMPYIGLVMTNNEDEVSAGAFVTLRFRV 294
DB 240 LITGEYLLRLPAPASRCRFLRSVMSLIDVVAIIPYIGLVKPDVSGAFVTLRFRV 299
QY 295 FRIFKFSHSGQLRILGYTLKSCASELGPLLSLTMALIIIFATVMPYAEKSSASKFTSI 354
DB 300 FRIFKFSHSGQLRILGYTLKSCASELGPLLSLTMALIIIFATVMPYAEKGTNKTFTSI 359
QY 355 PASFYVITVMTTLLGYGMVPEKTIAGKIFGSCISGLVVLALPVPVIVNSFRYHONQ 414
DB 360 PAAFYVITVMTTLLGYGMVPESTAGKIFGSCISGLVVLALPVPVIVNSFRYHONQ 419
QY 415 RADKRAQKARLARIRVAKTGSSNAVYLSKRNGLLNEALDTGTPEEHM-GKTTSLIE 473
DB 420 RADKRAQKARLARIRAKSGTTAFLQYKONG---GLEBSGGEQALCVRRSAPE 475
QY 474 SQHHLLHCLKETTNEEFIDQMFQONCESSMONYPTSPSLSSHP---GLTTTCCS 529
DB 476 QOHHLHLCKEKTCHETDELTFSE-ALGAVSPGARTSRSTSVSQVPGPSLSSCCP 534
QY 530 RRSK-KTHLPLNSNIPATRLSMOELSTIHQSGSQPSLTTRSSSLNAKADGLRPNCKT 588
DB 535 RRARRAIRLANSTASVSR-GSMOELDM--LAGLRSHAPQSRSSLNKPHDSLIDLNDS 591
QY 589 SQITTAISITPPALTPEGESRPPASPG-----PNTNIPSTISNVVYVS 634
DB 592 RDPVAIIISITPPANTPD-ESQ--PSSPGGGAGAGSTLRNSSLGTCPLPFTYKIS 645

RESULT 8
US-09-949-016-8327
; Sequence 8327, Application US/09949016
; Patent No. 6612339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8327
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8327

Query Match 26.1%; Score 865.5; DB 4; Length 260;
Best Local Similarity 64.2%; Pred. No. 1,4e-74;
```

```
Matches 174; Conservative 35; Mismatches 49; Indels 13; Gaps 3;
QY 368 LGYGMVKTITAGKIFGSCISGLVLTALPVPVIVNSFRYHONONADRRACKARL 427
DB 1 LRYGMVKTITAGKIFGSCISGLVLTALPVPVIVNSFRYHONORADRRACKARL 60
QY 428 ARIIRAKTGSSNAVYLSKRNGLLNEALDTGTPEEHMKTTSLESQHHLLHCLKETT 487
DB 61 ARIIRAKGSANAYVQSRKNGLLSNQLO--SSEDEAPVPSKSSSFTQHHLLHCLKETT 119
QY 488 NHEFIDQMFQONCESSMONYPTSPSLSSHPGLTTTCCSRKSKTTHLPNSNLPATR 547
DB 120 NHEFVDEQVPFESSCNEVATVVRPSHSPSLSSQGVSTCCSRRAKTFRIIPNAVSGH 179
QY 548 LRSQELSTIHQSGSQPSLTTRSSSLNAKADGLRPNCKTSQITTAIISITPPALPPE 607
DB 180 QGSIOELSTIQRCHERTPLNSNRSLSLNAKMECVKLNCEQPYVTTAISITPPVTPPE 239
QY 608 GESRP--PPASGPVNTNIPSTISNVVYVSVL 636
DB 240 GDDRPESPEYSGG-----NIVRSAL 260

RESULT 9
US-09-833-466-13
; Sequence 13, Application US/09833466
; Patent No. 6727353
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.2
US-09-833-466-13

Query Match 23.3%; Score 774.5; DB 4; Length 806;
Best Local Similarity 27.7%; Pred. No. 4.7e-65;
Matches 220; Conservative 116; Mismatches 243; Indels 215; Gaps 26;
QY 27 MPLAPAD--KMKRODELIVLVNSGRRFOT-WRTTLERYPDTLLG-----STEKEFF---- 74
DB 20 LPPEVVDIIRKTSGRKRVKIVNGLNHEVLMR-ITDLRIPRRLKLRQCNTHESILEYCD 78
QY 75 -FNEDTKEYFDRDPEVFRVCLNFYRTGKLHYPRYECISAYDELAFGILPEITIGDCY 133
DB 79 DYNLNENEYFDRDHPGAFSTILNFYRTGKLHMEEMCALSGQELDYGIDIEIYLESCQ 138
QY 134 EBYDRK-----RENAERLMDNDSENNQSMPSLFRQMTMARAFENPHTSTLALVF 186
DB 139 ARYHQKEQKNEELRRELEVTDRDEGEFDDTCCPDK--RKQMDLLEKPNSSVAAKTLA 196
QY 187 YVTGFFIAVSITNVVETVP-----CGTVPSGKELPCGERVSAFCDTACVMIPTV 239
DB 197 IVSTLIFVLSTIALSINTLPELOQTDGQNDNRQLA-----HVEAVCIAMFTM 246
QY 240 EYLLRLPAPASRYRFRISVMSIIDVVAIMPYIGLVMTNN-----EDVSGAFVTLRVF 292
DB 247 EYLLRFLSSPKWKRFPGPLNVLDLALIPYVITIFLTESKSVLQGVQVRRVVOIFRIM 306
QY 293 RVPRIFKFSRSGQLRILGYTLKSCASELGPLLSLTMALIIIFATVMPYAEKSSASKFT 352
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Db 307 RIIRILKLARHSTGLOSLGTLRRLSYNELGLILFLAMGIMIFSSLVFPAEKDEDAITKT 366  
Qy 353 SIPASFYITVTITLGYDMVEPKTIAGKIFGSIICSLGVLVIALPVYIVNSFSRIYHQ 412  
Db 367 SIPASFYITVTITLGYDMVEPKTIAGKIFGSIICSLGVLVIALPVYIVNSFSRIYHQ 426  
Qy 413 NQPADK---RRQOKAR-----LARIYAKTGS-----MAY 441  
Db 427 QKQOEKAIKRRERLERKRGSIYSNMLKDAFARSMELIIVAVEKAGESANTDSDNH 486  
Qy 442 LH-----SKRNGLINEALFELGTPEEBHMGKTSL-----ISQHHHLH-- 481  
Db 487 LSPSRKMKARKALSETISSNKSFEKYOESQKDSHEQLNNTFSSPOHLSAQKLEMYNE 546  
Qy 482 -----CLEKTTNHEFIDE--QMFQONCMESM---QNYSTRSPSLSHPGI 523  
Db 547 ITKTOPHSHNPQOEKRRERPSAYEBIEHEVVCQEOQLAVQTVIYVMKTSISDSF 606  
Qy 524 TTTCCSRRSKKTTHLPNSNLPAFRLRSMQELSTIHIQSEQ-----PSLTTSR----- 571  
Db 607 TS---CATDFETETERSP---LPPPSASHLQMKFPTDLETEEHQARAGPPLTLISREKQPA 661  
Qy 572 -----SSL-----NLKA 578  
Db 662 ARDGTLEAVDITVINIDASGQGLHSPLOSDNANDSPKSSILKSNPLKXNFKE 721  
Qy 579 DDGLRPNCKTS-----QITTAIISIPPPAL-----TPEGESRP----- 612  
Db 722 NRSAPOTPPSTARPLPVTTNADFSLTTPQIHISTILLEETPSQGBRPMALRQRLVADLP 781  
Qy 613 ---PPASPGPNTNI 623  
Db 782 KGCPCGPFPSRNCSL 795

RESULT 10  
US-09-833-466-12  
; Sequence 12, Application US/09833466  
; Patent No. 6727353  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy James  
; APPLICANT: IChogen, Inc.  
; TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From  
; FILE REFERENCE: 018512-005910US  
; CURRENT APPLICATION NUMBER: US/09/833, 466  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,793  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 854  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human voltage-gated potassium channel Kv2.1  
; US-09-833-466-12

Query Match 22.6%; Score 750; DB 4; Length 854;  
Best Local Similarity 29.2%; Pred. No. 1.2e-62;  
Matches 189; Conservative 114; Mismatches 220; Indels 124; Gaps 18;  
Qy 27 MPLAPAD--KNKQDELIVNVSGRRPQT--WRTTLERYPDTLLG-----STEKEFF----- 74  
Db 12 LPPEPMIVSKACSRVRRLNVGGLAHEVLMR--TLDRLPRTRLGKLDNCNTHSLLEVCD 70  
Qy 75 -FNEDTKEYFFDDPDEVFRVCLNFYRTGKLHYPRYECISADDELAFLYGLIPETIGCCY 133  
Db 71 DYSLDDNEYFFDRHPGAFTSLINFYRTGRLHMEEMCALFSQGLDWGIDELIYLESCQ 130  
Qy 134 EBYDKRENAERLMDNDSENNOE-----SMPSLSRQTMWRAFENDPHSTALVYVYV 188

Db 131 ARYHQKQEOHMBELKREAEFTLBERGSEPDNTCAEKRRKMLDLLEKPNSSVAAKLAI 190  
Qy 189 TGEFIVASYITNVVETPCGTVPKSGKELPCGRYSVA-----FFCLDTACVMIFTVEYLL 243  
Db 191 SIMFIYLSITLISINTLP-----ELQSLDFEGQSTONPOLAHAVEAVCIAMFTWEYLL 242  
Qy 244 RLFAAPSRFRFRISVMSIIDVVALMRYIYGLVMTNN-----EDVSGAFVTLRVRVR 296  
Db 243 RLFSBPKKRRFFGQPLNADILALIPYVYIIFLTSEINKSVLOFQNRVRVVOJFRIMRILR 302  
Qy 297 IFKFSHSGGLRLIGYTLKSCASELGEFLFSLTMAIIFATVAFVEKGSASAKFTSIPA 356  
Db 303 ILKLADHSTGLOSLGTLRRLSYNELGLILFLAMGIMIFSSLVFPAEKDEDTKFSIRA 362  
Qy 357 SFWYITVTITLGYDMVEPKTIAGKIFGSIICSLGVLVIALPVYIVNSFSRIYHQORA 416  
Db 363 SFWMATITMTYGYGDIYKRTILGKIVGGLCCAGLVIALPIPIVNNPSEBYKQKQ 422  
Qy 417 DKRAQKARLARIRVAKTGGSSNAYHSHRNGLL-----NEALBELTGPDEERH 464  
Db 423 EKAIKREAA-LER-----AKRNGSIYSNMNKDAFARSIEEMWDIVERKNGEN 467  
Qy 465 MGKTTLSIESQHHLHLEKTTNHEFIDEQMFQONCMESMOMNYSTRSPSLSHPGI 524  
Db 468 MGKDDYV---QDNHLSPNKMKMTKRTL--SETSSKSFEFKQGSPEK----- 510  
Qy 525 TTTCCSRRSKKTTHLPNSNLPAFRLRSMQELSTIHIQSEOPSLTTRSSINLKAQDLRP 584  
Db 511 ---ARSSSPQGL-----NVQQLDEMVMNMAQTQOPIINTMESAAQSPKREL-- 556  
Qy 585 NCKTSQITTAIISIPPPALTPEGESRPPASGPPNTNIPISITSNV 631  
Db 557 -----EMBSIPSPVAP-----LPTRRGVI 576

RESULT 11  
US-09-275-252A-6  
; Sequence 6, Application US/09275252A  
; Patent No. 6641997  
; GENERAL INFORMATION:  
; APPLICANT: Mackinnon, Roderick  
; APPLICANT: The Rockefeller University  
; TITLE OF INVENTION: Assays for Screening Compounds which Interact with  
; TITLE OF INVENTION: Calcium Channel Proteins, Mutant Prokaryotic Calcium  
; FILE REFERENCE: 018512-002901US  
; CURRENT APPLICATION NUMBER: US/09/275, 252A  
; CURRENT FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 09/045, 529  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: US 09/054, 347  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 858  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-275-252A-6

Query Match 22.6%; Score 750; DB 4; Length 858;  
Best Local Similarity 29.2%; Pred. No. 1.2e-62;  
Matches 189; Conservative 114; Mismatches 220; Indels 124; Gaps 18;  
Qy 27 MPLAPAD--KNKQDELIVNVSGRRPQT--WRTTLERYPDTLLG-----STEKEFF----- 74  
Db 16 LPPEPMIVSKACSRVRRLNVGGLAHEVLMR--TLDRLPRTRLGKLDNCNTHSLLEVCD 74  
Qy 75 -FNEDTKEYFFDDPDEVFRVCLNFYRTGKLHYPRYECISADDELAFLYGLIPETIGCCY 133  
Db 71 DYSLDDNEYFFDRHPGAFTSLINFYRTGRLHMEEMCALFSQGLDWGIDELIYLESCQ 134

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QY 134 BEYKDKRENAERLMDNDSENNOE-----SMPSLSPQTMRAFPENPTSTLALVPPYV 188
DB 135 ARYHOKKQOMBELKREBAETLREGEEDPNTCCAEKRRKMDLLEKPNSSVAAKILATIS 194
QY 189 TGFPIAVSVITVVEVPCGTVPGSKELPCGERISVA-----FPCIDTACWMTFTVEYLL 243
DB 195 SIMFVLSTIALSLNTLP-----ELQSLDFEGOSTDNPOLAHVEAVCIAMFTMEYLL 246
QY 244 RLPAAPSRFRFRSVMSIIDVVAIMPYIIGLVMTNN-----EDVSGAFVTLRVFRVR 296
DB 247 RFLSPKMKKFKPGPLNAIDLALIPYVITIFLTESNKSVLQFQVVRVAVQIFRIIRILR 306
QY 297 IFKFSRHSQGLRIGVTLKSCASELGFLLFSLTMIIIPATWFAEKSSASKTSIPA 356
DB 307 ILKARHSTGLQSLGFTLRSTYNEGLLFLPLAMGIMFSLVFAEKDEDTKKSLIPA 366
QY 357 SFMYITVMTTLGYGDMVPKTIAGKIFGSGISLGVLYALPVYIVSNFSRIYHONORA 416
DB 367 SPWATITMTVYGDYIPKTLIGKIVGGLCCIAGVLYALPIIIVNFSSEFYKQKRO 426
QY 417 DKRAOKKARLARIRVAKTGSSNAYLHSKRNGLL-----NEALBELGTPEEBER 464
DB 427 EKAKRREA-LER-----AKRNGSIVSMNMKAFAFSIEMMDIIVEKNGEN 471
QY 465 MGKTSILBSQHHLHLCLEKTTNHEFIDQMFQONCMHSSMONTPTSTRPSLSHPGLT 524
DB 472 MGKDKV---QDNHLSPNKMKWTKRTL--SETSSSKSFETKQGSPEK----- 514
QY 525 TTCRSRREKKTTHLPNSNLPATRLRSMOELSTIHHQSGSEPSLTJRSRSLNKKADGLRP 584
DB 515 -----ARSSSSPQHL-----NVQOLEDMYKMAKTOSQPLINTKESAAQKPEEL-- 560
QY 585 NCKTSQITTAIISPTPALTPEGESRPPASPGENTMIPSITSNVV 631
DB 561 -----EMESIPSPVAP-----LPTREGV 580

RESULT 12
US-08-464-340A-13
; Sequence 13, Application US/08464340A
; Patent No. 5710019
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,340A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

```

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; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-464-340A-13

Query Match      21.9%; Score 726.5; DB 1; Length 539;
Best Local Similarity 32.1%; Pred. No. 1e-60;
Matches 172; Conservative 100; Mismatches 193; Indels 71; Gaps 15;

QY 27 MFLPAD--KMKQBELVLVAVSGRRPQT-WRTTLERPDTLG-----STKEPF---- 74
DB 15 LPPEPMEIVRSACSPRLNVLGAAHVLMR-TLDRLPRTLGLRDCNTHDSILEYCD 73
QY 75 -FNEDTKVEFPDRDEVRVCLNFRYRTKLAHYPRCEISAYDDELAIFYGILPEIGDCCY 133
DB 74 DYSLDNBEYFPDRHGATSLINFRYTRGLHMEEMCALSPQELDYWGIDBIYIESCCQ 133
QY 134 BEYKDKRENAERLMDNDSENNOE-----SMPSLSPQTMRAFPENPTSTLALVPPYV 189
DB 135 ARYHOKKQOMBELKREBAETLREGEEDPNTCCAEKRRKMDLLEKPNSSVAAKILATIS 193
QY 190 GPFIVASVITVVEVPCGTVPGSKELPCGERISVA-----FPCIDTACWMTFTVEYLL 244
DB 194 IMFVLSTIALSLNTLP-----ELQSLDFEGOSTDNPOLAHVEAVCIAMFTMEYLL 245
QY 245 LPAAPSRFRFRSVMSIIDVVAIMPYIIGLVMTNN-----EDVSGAFVTLRVFRVR 297
DB 246 FLSPKMKKFKPGPLNAIDLALIPYVITIFLTESNKSVLQFQVVRVAVQIFRIIRILR 305
QY 298 FFKFSRHSQGLRIGVTLKSCASELGFLLFSLTMIIIPATWFAEKSSASKTSIPAS 357
DB 306 LKLAHSTGLQSLGFTLRSTYNEGLLFLPLAMGIMFSLVFAEKDEDTKKSLIPAS 365
QY 358 SFMYITVMTTLGYGDMVPKTIAGKIFGSGISLGVLYALPVYIVSNFSRIYHONORA 417
DB 366 FWWATITMTVYGDYIPKTLIGKIVGGLCCIAGVLYALPIIIVNFSSEFYKQKRO 425
QY 418 KRAOKKARLARIRVAKTGSSNAYLHSKRNGLL-----NEALBELGTPEEBER 465
DB 426 KAKRREA-LER-----AKRNGSIVSMNMKAFAFSIEMMDIIVEKNGEN 470
QY 466 GKTSLBSQHHLHLCLEKTTNHEFIDQMFQONCMHSSMONTPTSTRPSLSHPGLT 520
DB 471 GKDKV---QDNHLSPNKMKWTKRTL--SETSSSKSFETKQGSPEKARSSSSPQH 521

RESULT 13
US-09-275-252A-4
; Sequence 4, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 616

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TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-275-252A-4

Query Match 21.8%; Score 723; DB 4; Length 616;

Best Local Similarity 32.3%; Pred. No. 2,7e-60; Indels 96; Gaps 13;  
Matches 170; Conservative 105; Mismatches 156;

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QY 40 ELIVLVNNGRRFQMTTLTTERYPDTLLGSTEKEF-FENEDTKEYFPDRDEVRCLVNFY 98
DB 97 ERVIVNNGRRFQMTTLTTERYPDTLLGSTEKEF-FENEDTKEYFPDRDEVRCLVNFY 156
QY 99 RT-GKLYHRYECISAYDELAAYGILPEIIGCCCEEYKDRKRENAERLMDNSENQ 157
DB 157 QSGGRRLRPVNVPLDVFSSEIKFEY-----LQDAINKFRE-----DEGFIKEE 201
QY 158 ESMPSLSFRQTMRAPEHNTSTLALVYVVGFLAVSVITNVETP----- 206
DB 202 RPLPDEKORRWLLEFPSSQARVALISVILLSTVICTLETLPEPKHYKVENTT 261
QY 207 -CGTVGSKELPCGERYSVAFCLDTACWMTFVEYLLRLFAAPSRYFRYSWISIDVY 265
DB 262 TNGTKLEDEVP---DITDFPLEITCITWTFELTVRFLACPNKLNFCRDVNAVYDI 318
QY 266 AIMPYITGLV-----MTNEDVSGAFV-TLRFVRVRIKFSRH 303
DB 319 AIIPIYFITTALVAEEDDTLNPAPVSPQDKSSNQMSLAILRVLRLVAVFRLKLSRH 378
QY 304 SGLRLITGLTKSCASGLFLSLMAIIFATWYIAKSSASFTSIPASFWYTIY 363
DB 379 SKGLQILGRITKSKRELGLIFFLFGVLFSSAVFAAGSENSFKIIPDAFWAVV 438
QY 364 TMTTLGDMVPKTIAGKIGSICSLGVLVIALPVIVSNFSRIYHONQADKRAAK 423
DB 439 TMTTVGDMTPVPGFMKTIKSLCVIAGVLTIALPVIVSNFRYFHRADDEMQSON 498
QY 424 KARLARIKATGSSNAYL-----HSKRNGL-----LNEALELTGPREEHNGKT 468
DB 499 FNVH-----TSCSYLFGALGOHLKSSLSSESSDIDMDLDGIDATPGALDTGTR- 548
QY 469 TSLIESQHHLHLCLEKTTNHEFIDQMFEONCMESSMNYPSTRSP 515
DB 549 -----HMVPEFLR-----TOOSFEKQQLQLQLQOQSQSP 578

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## RESULT 14

US-09-949-016-8164  
Sequence 8164, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8164  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8164

Query Match 21.7%; Score 719; DB 4; Length 552;  
Best Local Similarity 31.2%; Pred. No. 5.5e-60;  
Matches 176; Conservative 105; Mismatches 172; Indels 112; Gaps 16;

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QY 18 GMPVAVNC-----PMP--LAPADKNKRODELIVLVNNGRRFQMTTLTTERYPDTLL 66
DB 48 GAPPGCGCGGGGDDRRYELPPLSLPAAGEODCCGERVININISGRIFETQKLCQFETLL 107
QY 67 GSTEKEF-FENEDTKEYFPDRDEVRCLVNFYRT-GKLYHRYECISAYDELAAYGIL 124
DB 108 GDEKRMRYFDPLRNRYFPDRNRPSPDALIYYQSGRRPVPNVVIDIFSEIRFYQ-- 165
QY 125 PELIGDCCCEEYKDRKRENAERLMDNSENQSMPSLSFQTMRAPEHNTSTLALV 184
DB 166 ---LGEAMKRE-----DEGFLREERPLPRDFOQVWLLLEFPSSQAPAG 212
QY 185 FYVVTGFLAVSVITNVETPVGTVGSKELPC-----GER-----YGV 224
DB 213 IAVSVLVILISIVICTLETLF--BERDKDYPASTQDSFEAGNSTGSRAGASSFS 270
QY 225 AFPCLDTCWMTFVEYLLRLFAAPSRYFRYSWISIDVVAIMPYITGLV-----T 277
DB 271 PEFVETLCTIWFSPFLVRFACPKATFSRNIMLIDIVAIIPYITLGTLELRQGN 330
QY 278 NNEVDGAFV-TLRFVRVRIKFSRHSGQLRIIGYTLKSCASGLFLSLMAIIFRA 336
DB 331 GQAMSLALIRYLRVLRVFRIRKLSHSGQLIGQTLKASRELGLIFFLTGYLTS 390
QY 337 TWAFYAEKSSASKFTSIPASFWYTIYMTTLGDMVPKTIAGKIGSICSLGVLVIA 396
DB 391 SAYFADDPDPSGFSIPDAFWMAVVTMTYVGYDMHPTVIGKIVGSLCAIAGVLTIA 450
QY 397 LPVPYVSNFSRIYHONQADKRAAKKARLARIKATGSSNAYLHSKRNGLNEALEL 456
DB 451 LPVPYVSNFSRIYHONQADKRAAKKARLARIKATGSSNAYLHSKRNGLNEALEL 485
QY 457 TGPREHNGKTTSLIESQHHLHLCLEKTTNHEFIDQMFEONCMESSMNYPSTRSP 516
DB 486 SSSAEELRKARSNTLSKSEIYVIE--EGAMNSAPFOTPFK----- 525
QY 517 LSSHPLGTTTCCSRRSKKTTHLPNS 541
DB 526 ----TGNSTATCT-----TNNPNS 541

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## RESULT 15

US-09-949-016-6195  
Sequence 6195, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6195  
LENGTH: 523  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6195

Query Match 21.6%; Score 718; DB 4; Length 523;  
Best Local Similarity 31.2%; Pred. No. 6.3e-60;  
Matches 176; Conservative 105; Mismatches 172; Indels 112; Gaps 16;

Db 19 GAPPGCGGGGCDRYEPLPSLPAGBODCCGERVINISGVREPTQLKLCQPPETLL 78  
 QY 67 GSTEKEF-FENEDTKEVEFEDRDPEVRCVNFYRT-GKLIHYPRYCISAYDELAFYGL 124  
 Db 79 GDPKRRMYFPDLRNEFFDRNRPSPFDALLYYQSGGRIRRPVNPIDIFSEIRFYQ-- 136  
 QY 125 PEIIGDCCYEYKDKRENAERIMDNDSENNQESMPSISFROTMWRAFENPHTSTLALV 184  
 Db 137 ---LGEAMEKEFRE-----DEGFLREERPLPRRDFQRYWLFYEPSSGPARG 183  
 QY 185 FYYVTGFFIAVSVITNVETVPCGTVPGSKELPC-----GER-----YSV 224  
 Db 184 IAIYSVLVILISIVFCLETLF--EFREKDYPASTSQDSFEAGNSTSGSRAGASPSFD 241  
 QY 225 AFPCIDTACWMLFTVEYLRLPAAPSRIRFIRSVMSIIDVVAIMPYYIGLVH-----T 277  
 Db 242 PFFVETLCIIMFSPFELLVRFEPACPSKATFSRNIMLIDIVAIIPYFTLTGTELAEROGN 301  
 QY 278 NNEDVSGAFV-TLRVFRVRIFFKFRHSQGLRIIGVTLKSCASELGFLLFSLTMAIIPA 336  
 Db 302 GQQMSLAILRVIRLVFRIFKLSRHSKGLQILGQTLKASRELGLIFLFTGVILFS 361  
 QY 337 TVMFAEKSSASKETSIPASFVYTIYMTTLGYGDMVPKTIAGKIFGSIKSLGVLVIA 396  
 Db 362 SAVYFAEADDPISGFSIPDAFWMAVMTTGYGDMHPVTIGKIVGSLCALAGVLITA 421  
 QY 397 LPVPYIVNFSRIYHQNRADKRAQKARLARIRVAKTSSNAYLHSHKRNGLNEALEL 456  
 Db 422 LPVPYIVNFMFYFHRETEGEEQ-----SQYMH-----VSCQHL 456  
 QY 457 TGTPEEHMGKTSLIESQHHLHLCKEKTNHEFIDQMFEQNCMESSMONYPTRSPS 516  
 Db 457 SSSAEELKARSNSTLSKSEYVIE--EGGMNHSAPQTPFK----- 496  
 QY 517 LSHPGLTTCSSRRSKKTHLPNS 541  
 Db 497 ----TGNSTATCT-----TNNNPNS 512

Search completed: April 6, 2005, 07:21:30  
 Job time : 106.44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 07:13:52 ; Search time 442.392 Seconds

(without alignments)  
477.292 Million cell updates/sec

Title: US-10-062-879-4

Perfect score: 3320

Sequence: 1 MAAGVAAWLPFARAALGWM.....PGPNTNITSITSNVKSVL 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*

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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	636	US-10-062-879-4	Sequence 4, Appli
2	3300.5	99.4	655	US-10-062-879-2	Sequence 2, Appli
3	3283.5	98.9	655	US-10-377-139-6	Sequence 6, Appli
4	2518	75.8	630	US-10-212-677-258	Sequence 258, App
5	2518	75.8	630	US-10-212-677-259	Sequence 259, App
6	2518	75.8	630	US-10-212-677-260	Sequence 260, App
7	2518	75.8	630	US-10-212-677-261	Sequence 261, App
8	2518	75.8	630	US-10-361-811-258	Sequence 258, App
9	2518	75.8	630	US-10-361-811-259	Sequence 259, App
10	2518	75.8	630	US-10-361-811-260	Sequence 260, App
11	2518	75.8	630	US-10-361-811-261	Sequence 261, App
12	2518	75.8	630	US-10-369-186-258	Sequence 258, App
13	2518	75.8	630	US-10-369-186-259	Sequence 259, App

14	2518	75.8	630	US-10-369-186-260	Sequence 260, App
15	2518	75.8	630	US-10-369-186-261	Sequence 261, App
16	2132.5	64.2	647	US-10-296-115-1112	Sequence 1112, App
17	2121.5	63.9	646	US-10-121-746-10	Sequence 10, Appli
18	844.5	25.4	255	US-10-212-677-257	Sequence 257, App
19	844.5	25.4	255	US-10-361-811-257	Sequence 257, App
20	844.5	25.4	255	US-10-369-186-257	Sequence 257, App
21	774.5	23.3	806	US-10-833-466-13	Sequence 13, Appli
22	774.5	23.3	806	US-10-199-869-6	Sequence 6, Appli
23	774.5	23.3	806	US-10-815-297-13	Sequence 15, Appli
24	766	23.1	911	US-10-408-765A-1482	Sequence 1482, App
25	758	22.8	854	US-10-154-086-20	Sequence 20, Appli
26	750	22.6	854	US-09-833-466-12	Sequence 12, Appli
27	750	22.6	854	US-10-199-869-5	Sequence 5, Appli
28	750	22.6	854	US-10-815-297-12	Sequence 12, Appli
29	736.5	22.2	857	US-10-377-139-5	Sequence 5, Appli
30	735	22.1	656	US-10-377-139-4	Sequence 4, Appli
31	726.5	21.9	539	US-10-325-891-13	Sequence 13, Appli
32	721.5	21.7	456	US-09-993-811-2	Sequence 2, Appli
33	721.5	21.7	456	US-09-974-712-2	Sequence 2, Appli
34	721.5	21.7	456	US-09-989-920-15	Sequence 175, App
35	721.5	21.7	456	US-10-254-010-4	Sequence 4, Appli
36	721	21.7	539	US-09-804-014A-27	Sequence 27, Appli
37	721	21.7	539	US-09-804-014A-8	Sequence 8, Appli
38	719	21.7	523	US-09-804-014A-32	Sequence 32, Appli
39	719	21.7	523	US-10-408-765A-2015	Sequence 2015, App
40	719	21.7	523	US-10-772-636-10	Sequence 10, Appli
41	718.5	21.6	525	US-09-804-014A-33	Sequence 33, Appli
42	717.5	21.6	585	US-10-400-435A-2	Sequence 2, Appli
43	717	21.6	499	US-10-322-281-766	Sequence 766, App
44	715.5	21.6	524	US-10-322-281-93	Sequence 93, Appli
45	715	21.5	499	US-10-322-281-763	Sequence 763, App

# ALIGNMENTS

RESULT 1

US-10-062-879-4

Sequence 4, Application US/10062879

Publication No. US20020127649A1

GENERAL INFORMATION:

APPLICANT: Cockett, Mark I.

APPLICANT: Dilks, Daniel W.

APPLICANT: Chang, Ling, Hui-Ping

APPLICANT: Sokol, Patricia T.

TITLE OF INVENTION: Human Potassium Channel Polynucleotides and

TITLE OF INVENTION: Polypeptides and Uses Therefor

FILE REFERENCE: ahp-98083

CURRENT APPLICATION NUMBER: US/10/062, 879

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: US/09/178,109

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 636

TYPE: PRT

ORGANISM: human

US-10-062-879-4

Query Match

Best Local Similarity 100.0%; Score 3320; DB 13; Length 636;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

1 MAAGVAAWLPFARAALGWMVFANCPMPPLAADKNKODELIYVNSGRFQRTTTER 60

1 YPDITLSTGEKFFPNEDTKYFFDRDPEVRVCYINFRYTKLHYPRYCISAYDELIAF 120

61 YPDITLSTGEKFFPNEDTKYFFDRDPEVRVCYINFRYTKLHYPRYCISAYDELIAF 120

61 YPDITLSTGEKFFPNEDTKYFFDRDPEVRVCYINFRYTKLHYPRYCISAYDELIAF 120

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QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAEPENPTST 180
DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAEPENPTST 180
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DB 181 LAIVFYVVGPFPAVAVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFVE 240
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DB 301 SRHSGRLIGYTLKSCASELGFLLFSLTMAIIIFATVMEFAEKGSASAKFTSIPASFMY 360
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DB 361 TIYMTTLGVDWVPKTIAGKIFGSLGSLGVVIALPVPVIVSNRSRIYHQORADKRR 420
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DB 421 AOKKARLARIRVAKTSSNAYLHRSKRGVLEALGTPEEEMGKTTSLIESQHHL 480
QY 481 HCLEKTTNHEFIDQMEFQNCMESSMONTYSTRSPSLSSHGTLTTCSSRSKKTTHLPN 540
DB 481 HCLEKTTNHEFIDQMEFQNCMESSMONTYSTRSPSLSSHGTLTTCSSRSKKTTHLPN 540
QY 541 SNLPATLRSMQELSTHIGSEBPSLTSSSLNLKADGCRNCTTSQTTAIIISPT 600
DB 541 SNLPATLRSMQELSTHIGSEBPSLTSSSLNLKADGCRNCTTSQTTAIIISPT 600
QY 601 PPALTPGESRPPASPGPNTNIPSTSNVYKSVL 636
DB 601 PPALTPGESRPPASPGPNTNIPSTSNVYKSVL 636

RESULT 2
US-10-062-879-2
; Sequence 2, Application US/10062879
; Publication No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang ling, Hual-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062, 879
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: human
US-10-062-879-2

Query Match 99.4%; Score 3300.5; DB 13; Length 655;
Best Local Similarity 97.1%; Pred. No. 7.3e-277;
Matches 636; Conservative 0; Mismatches 0; Indels 19; Gaps 1;
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DB 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAEPENPTST 180
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DB 181 LAIVFYVVGPFPAVAVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFVE 240
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DB 241 YLRLFAAPSRYPFRFISVMSIIDVVAIMPYYIGLVMTNNEVDGAFVTLRVFRVRIFFKF 300
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QY 361 TIYMTTLGVDWVPKTIAGKIFGSLGSLGVVIALPVPVIVSNRSRIYHQORADKRR 420
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DB 481 HCLEKTTGSLYVDLDSVSTIRNHEFIDQMEFQNCMESSMONTYSTRSPSLSSH 540
QY 522 GLTTCSSRSKKTTHLPNSNLPATLRSMQELSTHIGSEBPSLTSSSLNLKADG 581
DB 541 GLTTCSSRSKKTTHLPNSNLPATLRSMQELSTHIGSEBPSLTSSSLNLKADG 600
QY 582 LRNCKTSQTTAIIISIPPALTPGESRPPASPGPNTNIPSTSNVYKSVL 636
DB 601 LRNCKTSQTTAIIISIPPALTPGESRPPASPGPNTNIPSTSNVYKSVL 655
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RESULT 3
US-10-377-139-6
; Sequence 6, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; PRIOR FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1 -
; SEQ ID NO 6
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-139-6
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Query Match 98.9%; Score 3283.5; DB 16; Length 655;
Best Local Similarity 96.8%; Pred. No. 2.2e-275;
Matches 634; Conservative 0; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGVAAWLPFAAAAIAGMPVANCMPPLADADKRRQDELIVLVNSGRRFQTRTTLER 60
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QY 121 YGILPEIIGDCYEEYKDRKRENAERLMDNDSENNQESMPSLSFRQTMRAEPENPTST 180
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Db 121 YGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOSMPSLSFQTMRAFAENPHST 180
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Db 121 STMALVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 240
Qy 121 LALVYVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 240
Db 241 YLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 297
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Qy 241 YLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 297
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Qy 361 TIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 417
Db 361 TIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 417
Qy 361 TIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 417
Db 421 AOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Qy 421 AOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Db 421 AOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Qy 421 AOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Db 481 HCLEKTT-----NHBFIDQMFQONCMSSMONTPTSPSLSSHP 537
Qy 481 HCLEKTT-----NHBFIDQMFQONCMSSMONTPTSPSLSSHP 537
Db 481 HCLEKTT-----NHBFIDQMFQONCMSSMONTPTSPSLSSHP 537
Qy 481 HCLEKTT-----NHBFIDQMFQONCMSSMONTPTSPSLSSHP 537
Db 522 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 597
Qy 522 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 597
Db 522 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 597
Qy 522 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 597
Db 541 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 600
Qy 541 GLTTCCSRRSKTTHTLNSNIPATRLASMOELSTHIOGSEOPSLTSSSLNKADKG 600
Db 582 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Qy 582 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Db 601 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 655

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RESULT 4

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US-10-212-677-258
; Sequence 258, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenaule, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-258

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```

Query Match 75.8%; Score 2518; DB 14; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
Qy 1 MAAGVAAWLPARAAAIAGMPPVANCMPPLADKXKR-ODELIIVANSGRRPQTWRTTLE 59
Db 1 MAAGVAAWLPARAAAIAGMPPVANCMPPLADKXKR-ODELIIVANSGRRPQTWRTTLE 59
Qy 60 RYPTLLGSTEKEPENEDTKEYFEDDPEVRCVLTNFRGKLAHYPRYECISAYDDELA 119
Db 60 RYPTLLGSTEKEPENEDTKEYFEDDPEVRCVLTNFRGKLAHYPRYECISAYDDELA 119
Qy 61 RYPTLLGSSSRDFFHETQYFDRDPEDFRHLNFRGKLAHYPRYECISAYDDELA 120
Db 61 RYPTLLGSSSRDFFHETQYFDRDPEDFRHLNFRGKLAHYPRYECISAYDDELA 120
Qy 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 178
Db 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 178
Qy 121 FFGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 180
Db 121 FFGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 180

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Qy 179 STMALVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 237
Db 179 STMALVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 237
Qy 121 LALVYVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 240
Db 121 LALVYVYVYVGFIAVSITNVVETPCGTVPGS - KEGIKELPCGERYSVAFPCLDTCWMI 240
Qy 238 TVEYLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 297
Db 238 TVEYLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 297
Qy 241 TVEYLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 300
Db 241 TVEYLRLFAAPSRFRFRSVMISIDVVAIMPYYIGLWMTNEDVSGAFVTLRVRVRIRIFK 300
Qy 298 FKFSHSGOGLILGYTLKSCASELGFLLPSLTMAIIPATVWFYAEKSSASKFTSIPAS 357
Db 298 FKFSHSGOGLILGYTLKSCASELGFLLPSLTMAIIPATVWFYAEKSSASKFTSIPAS 357
Qy 301 FKFSHSGOGLILGYTLKSCASELGFLLPSLTMAIIPATVWFYAEKSSASKFTSIPAS 360
Db 301 FKFSHSGOGLILGYTLKSCASELGFLLPSLTMAIIPATVWFYAEKSSASKFTSIPAS 360
Qy 358 FMYTIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 417
Db 358 FMYTIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 417
Qy 361 FMYTIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 420
Db 361 FMYTIVMTTIGYGMVKTAGKIFGSIICSLGVLVIALPVPVVSNSRIRYHONORAD 420
Qy 418 KRAOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Db 418 KRAOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 477
Qy 421 KRAOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 479
Db 421 KRAOKKARLARIRAKTSSNAAYLSKRNGLNEALGTGPEEHGKTTSLIESQHHLL 479
Qy 478 HILHCLEKTTNHEFIDQMFQONCMSSMONTPTSPSLSSHPGLTTCCSRRSKTTHT 537
Db 478 HILHCLEKTTNHEFIDQMFQONCMSSMONTPTSPSLSSHPGLTTCCSRRSKTTHT 537
Qy 480 HILHCLEKTTNHEFIDQMFQONCMSSMONTPTSPSLSSHPGLTTCCSRRSKTTHT 539
Db 480 HILHCLEKTTNHEFIDQMFQONCMSSMONTPTSPSLSSHPGLTTCCSRRSKTTHT 539
Qy 538 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Db 538 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Qy 540 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 659
Db 540 LRPNCKTSQITTAIISPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 659
Qy 598 IPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Db 598 IPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 636
Qy 600 IPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 655
Db 600 IPTPALTEGESRPPASGPPTNIPSTSNVVKYSL 655

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RESULT 5

```

US-10-212-677-259
; Sequence 259, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenaule, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212.677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-677-259

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```

Query Match 75.8%; Score 2518; DB 14; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;
Qy 1 MAAGVAAWLPARAAAIAGMPPVANCMPPLADKXKR-ODELIIVANSGRRPQTWRTTLE 59
Db 1 MAAGVAAWLPARAAAIAGMPPVANCMPPLADKXKR-ODELIIVANSGRRPQTWRTTLE 59
Qy 60 RYPTLLGSTEKEPENEDTKEYFEDDPEVRCVLTNFRGKLAHYPRYECISAYDDELA 119
Db 60 RYPTLLGSTEKEPENEDTKEYFEDDPEVRCVLTNFRGKLAHYPRYECISAYDDELA 119
Qy 61 RYPTLLGSSSRDFFHETQYFDRDPEDFRHLNFRGKLAHYPRYECISAYDDELA 120
Db 61 RYPTLLGSSSRDFFHETQYFDRDPEDFRHLNFRGKLAHYPRYECISAYDDELA 120
Qy 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 178
Db 120 FYGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 178
Qy 121 FFGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 180
Db 121 FFGILPEIIGDCCYEYKDRKRENAERLMDNDSENNOS -MPSLSFQTMRAFAENPH 180

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Db 181 STMALVFYVYTGTFIAVSIVIANVETVPCGSSPGHIKELPCGERYAVAFCLDTACWMI 240
Qy 238 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 297
Db 241 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 357
Db 301 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 360
Qy 358 FMYTIVMTTIGYGMVPEKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONORAD 417
Db 361 FMYTIVMTTIGYGMVPEKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONORAD 420
Qy 418 KRRACKARLARIRAKTGSSNAYLHAKRNGLLNLEALGTPEEHNKKTSLIESQHH 477
Db 421 KRRACKARLARIRAKTGSSNAYLHAKRNGLLNLEALGTPEEHNKKTSLIESQHH 479
Qy 478 HLHLCLEKTTNHEFIDEQMFECNOMESSMOMYPSTRSPSLSSHPLTTCCSRKKTTH 537
Db 480 HLHLCLEKTTNHEFIDEQMFECNOMESSMOMYPSTRSPSLSSHPLTTCCSRKKTTH 539
Qy 538 LPSNLTPLTRLSMOELSTIHIOGSEOPSLTTSRSSLLMKADGRLPNCCKTSQITTAIIS 597
Db 540 LPSNLTPLTRLSMOELSTIHIOGSEOPSLTTSRSSLLMKADGRLPNCCKTSQITTAIIS 599
Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 636
Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 630

RESULT 8
US-10-361-811-258
; Sequence 258, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-258

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAAMLPPARAALIGMMPVANCMPPLAPADKNKR-ODELIVINSGRRFQTRTLE 59
Db 1 MAAGVAAAMLPPARAALIGMMPVASCMPAPAPROERKKTQDALIVINSGTRFQTRTLE 60
Qy 60 RYPTLLGSTKEKFPENEDTKEYFPDRDPEVRCVLNFRYTKGLHYPRYECISAYDEBELA 119
Db 61 RYPTLLGSTKEKFPENEDTKEYFPDRDPEVRCVLNFRYTKGLHYPRYECISAYDEBELA 120
Qy 120 FYGLIPELIIGCCYEEYKDRKRENAERLMDNDSENNOES--NPSLSFQOTMRAFENHT 178
Db 121 FYGLIPELIIGCCYEEYKDRKRENAERLMDNDSENNOES--NPSLSFQOTMRAFENHT 180
Qy 179 STLALVFYVYTGTFIAVSIVIANVETVPCGTVPGS-KELPCGERYAVAFCLDTACWMI 237
Db 181 STLALVFYVYTGTFIAVSIVIANVETVPCGTVPGS-KELPCGERYAVAFCLDTACWMI 240
Qy 238 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 297
Db 241 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
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Db 241 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 357
Db 301 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 360
Qy 358 FMYTIVMTTIGYGMVPEKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONORAD 417
Db 361 FMYTIVMTTIGYGMVPEKTIAGKIFGSI CSLGVLVIALPVPIVSNFSRIYHONORAD 420
Qy 418 KRRACKARLARIRAKTGSSNAYLHAKRNGLLNLEALGTPEEHNKKTSLIESQHH 477
Db 421 KRRACKARLARIRAKTGSSNAYLHAKRNGLLNLEALGTPEEHNKKTSLIESQHH 479
Qy 478 HLHLCLEKTTNHEFIDEQMFECNOMESSMOMYPSTRSPSLSSHPLTTCCSRKKTTH 537
Db 480 HLHLCLEKTTNHEFIDEQMFECNOMESSMOMYPSTRSPSLSSHPLTTCCSRKKTTH 539
Qy 538 LPSNLTPLTRLSMOELSTIHIOGSEOPSLTTSRSSLLMKADGRLPNCCKTSQITTAIIS 597
Db 540 LPSNLTPLTRLSMOELSTIHIOGSEOPSLTTSRSSLLMKADGRLPNCCKTSQITTAIIS 599
Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 636
Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSTSNVVKSVL 630

RESULT 9
US-10-361-811-259
; Sequence 259, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-259

Query Match 75.8%; Score 2518; DB 15; Length 630;
Best Local Similarity 75.8%; Pred. No. 4.7e-209;
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAAMLPPARAALIGMMPVANCMPPLAPADKNKR-ODELIVINSGRRFQTRTLE 59
Db 1 MAAGVAAAMLPPARAALIGMMPVASCMPAPAPROERKKTQDALIVINSGTRFQTRTLE 60
Qy 60 RYPTLLGSTKEKFPENEDTKEYFPDRDPEVRCVLNFRYTKGLHYPRYECISAYDEBELA 119
Db 61 RYPTLLGSTKEKFPENEDTKEYFPDRDPEVRCVLNFRYTKGLHYPRYECISAYDEBELA 120
Qy 120 FYGLIPELIIGCCYEEYKDRKRENAERLMDNDSENNOES--NPSLSFQOTMRAFENHT 178
Db 121 FYGLIPELIIGCCYEEYKDRKRENAERLMDNDSENNOES--NPSLSFQOTMRAFENHT 180
Qy 179 STLALVFYVYTGTFIAVSIVIANVETVPCGTVPGS-KELPCGERYAVAFCLDTACWMI 237
Db 181 STLALVFYVYTGTFIAVSIVIANVETVPCGTVPGS-KELPCGERYAVAFCLDTACWMI 240
Qy 238 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 297
Db 241 TVEYLLRLFAASRRPFRSVMGIIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
Qy 298 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 357
Db 301 FKFSSHSGGLRILGTLTKSCASELGFLLPSLTMAIIIFATVMFAEKSSASKFTSIPAS 360
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Db 301 FKFSRHSQGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMFAEKSSASAKFTSIPAA 360  
 Qy 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 417  
 Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420  
 Qy 418 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 477  
 Db 421 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 479  
 Qy 478 HLHCKEKTTHNEHFIDEQMFONCMESSMONTPTSTRPSLSHPGLTTCCSRRSKKTTH 537  
 Db 480 HLHCKEKTTHNEHFIDEQMFONCMESSMONTPTSTRPSLSHPGLTTCCSRRSKKTTH 539  
 Qy 538 LPSNLPATRLSMOBLSTIHIQGSQPSLTSTRSLNLKADGLRPNKCTOITTAIIS 597  
 Db 540 IPANAVSGSHQSGIQLSTIQIRCVERTPLSNRSLSLNKMBECVLIANCQOPYVTTAIIS 599  
 Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTISNVKSVL 636  
 Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSTISNVKSVL 630

RESULT 10  
 US-10-361-811-260  
 ; Sequence 260, Application US/10361811  
 ; Publication No. US20030206918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C8  
 ; CURRENT APPLICATION NUMBER: US/10/361.811  
 ; CURRENT FILING DATE: 2003-02-05  
 ; NUMBER OF SEQ ID NOS: 293  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 260  
 ; LENGTH: 630  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-361-811-260

Query Match 75.8%; Score 2518; DB 15; Length 630;  
 Best Local Similarity 75.8%; Pred. No. 4.7e-209;  
 Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAMLPFARAAAIIGMMPVANCMPPLAPADKNKR-ODELIVLVNNGRRFQTRTTLLE 59  
 Db 1 MAAGVAAMLPFARAAAIIGMMPVANCMPPLAPADKNKR-ODELIVLVNNGRRFQTRTTLLE 60  
 Qy 60 RYDPTLLGSTEKEKFFNEDTKYFFPDRDPEVRCVNLNFRYTGKLAHYRHCISAYDELA 119  
 Db 61 RYDPTLLGSSERDFFYHPTQYFFPDRDPEVRCVNLNFRYTGKLAHYRHCISAYDELA 120  
 Qy 120 FYGLIPEIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFQTMRAFENPHT 178  
 Db 121 FFGIIPFIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFQTMRAFENPHT 180  
 Qy 179 STALALFYVYTGFFIAVSIVTNNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACMIF 237  
 Db 181 STALALFYVYTGFFIAVSIVTNNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACMIF 240  
 Qy 238 TVEYLRLPAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFR 297  
 Db 241 TVEYLRLPAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFR 300  
 Qy 298 FKFSRHSQGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMFAEKSSASAKFTSIPAS 357  
 Db 301 FKFSRHSQGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMFAEKSSASAKFTSIPAS 360  
 Qy 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 417  
 Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420

Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420  
 Qy 418 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 477  
 Db 421 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 479  
 Qy 478 HLHCKEKTTHNEHFIDEQMFONCMESSMONTPTSTRPSLSHPGLTTCCSRRSKKTTH 537  
 Db 480 HLHCKEKTTHNEHFIDEQMFONCMESSMONTPTSTRPSLSHPGLTTCCSRRSKKTTH 539  
 Qy 538 LPSNLPATRLSMOBLSTIHIQGSQPSLTSTRSLNLKADGLRPNKCTOITTAIIS 597  
 Db 540 IPANAVSGSHQSGIQLSTIQIRCVERTPLSNRSLSLNKMBECVLIANCQOPYVTTAIIS 599  
 Qy 598 IPTPPALTPEGESRP--PPASPGPNTNIPSTISNVKSVL 636  
 Db 600 IPTPPALTPEGESRP--PPASPGPNTNIPSTISNVKSVL 630

RESULT 11  
 US-10-361-811-261  
 ; Sequence 261, Application US/10361811  
 ; Publication No. US20030206918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C8  
 ; CURRENT APPLICATION NUMBER: US/10/361.811  
 ; CURRENT FILING DATE: 2003-02-05  
 ; NUMBER OF SEQ ID NOS: 293  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 261  
 ; LENGTH: 630  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-361-811-261

Query Match 75.8%; Score 2518; DB 15; Length 630;  
 Best Local Similarity 75.8%; Pred. No. 4.7e-209;  
 Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAMLPFARAAAIIGMMPVANCMPPLAPADKNKR-ODELIVLVNNGRRFQTRTTLLE 59  
 Db 1 MAAGVAAMLPFARAAAIIGMMPVANCMPPLAPADKNKR-ODELIVLVNNGRRFQTRTTLLE 60  
 Qy 60 RYDPTLLGSTEKEKFFNEDTKYFFPDRDPEVRCVNLNFRYTGKLAHYRHCISAYDELA 119  
 Db 61 RYDPTLLGSSERDFFYHPTQYFFPDRDPEVRCVNLNFRYTGKLAHYRHCISAYDELA 120  
 Qy 120 FYGLIPEIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFQTMRAFENPHT 178  
 Db 121 FFGIIPFIIGDCCYEEYKDRKRENAERLMDNDSENNOES-MPSLSFQTMRAFENPHT 180  
 Qy 179 STALALFYVYTGFFIAVSIVTNNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACMIF 237  
 Db 181 STALALFYVYTGFFIAVSIVTNNVETVPCGTVPGS-KELPCGERYSVAFFCLDTACMIF 240  
 Qy 238 TVEYLRLPAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFR 297  
 Db 241 TVEYLRLPAAPSRYPFRISVMSIIDVVAIMPYYIGLVMTNNEVSGAFVTLRVFRVFR 300  
 Qy 298 FKFSRHSQGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMFAEKSSASAKFTSIPAS 357  
 Db 301 FKFSRHSQGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMFAEKSSASAKFTSIPAS 360  
 Qy 358 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 417  
 Db 361 FWTTIVMTTLGYGDMVPKTIAGKIFGSIICSLSGVLVIALPVPIVSNFSRIYHONORAD 420  
 Qy 418 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 477  
 Db 421 KRAQOKKARLARIIVAKTGSSNAYLHKSNGNLNEALELTGTPEEHMGKTTLSLSQHH 479

Db 421 KRAQKARLARIRAKSGSANAYMOSKNGLLSNQIQ-SSDEQAFVSKSGSFETQHH 479

Qy 478 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 537

Db 480 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 539

Qy 538 LPSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNKADGRLPNCCKTSOITTAIS 597

Db 540 IPNAVSSGHOSIQELSTIQRCYERPTLSNRSRLNAKMECEVKNCEOPVTTAIIIS 599

Qy 598 IPTPALPEGESRP--PPASDPNTNIPSTSNVVKSVL 636

Db 600 IPTPVTTPEGDPRPESPEYSGG-----NIVRSAL 630

RESULT 12

US-10-369-186-258

Sequence 258, Application US/10369186

Publication No. US20030232056A1

GENERAL INFORMATION:

APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 258

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

US-10-369-186-258

Query Match

Best Local Similarity 75.8%; Score 2518; DB 15; Length 630;

Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Db 480 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 539

Qy 538 LPSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNKADGRLPNCCKTSOITTAIS 597

Db 540 IPNAVSSGHOSIQELSTIQRCYERPTLSNRSRLNAKMECEVKNCEOPVTTAIIIS 599

Qy 598 IPTPALPEGESRP--PPASDPNTNIPSTSNVVKSVL 636

Db 600 IPTPVTTPEGDPRPESPEYSGG-----NIVRSAL 630

RESULT 13

US-10-369-186-259

Sequence 259, Application US/10369186

Publication No. US20030232056A1

GENERAL INFORMATION:

APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 259

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

US-10-369-186-259

Query Match

Best Local Similarity 75.8%; Score 2518; DB 15; Length 630;

Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAWLPPARAAALIGMPVANCMPMLAPADKKR-ODELIVLVNSGRPFQWRTTLE 59

Db 1 MAAGVAAWLPPARAAALIGMPVANCMPMLAPADKKR-ODELIVLVNSGRPFQWRTTLE 60

Qy 60 RYPTDLTSGTEKEPFNEDTKEYFPDRDPEVRCVLANFYRTGKLHYPRYECISAYDELA 119

Db 61 RYPTDLTSGSRDPEFYHETQOYFPDRDPEFRHLINFYRTGKLHYPRHECISAYDELA 120

Qy 120 FYGLIPETIIGDCCEYEDKRENAERLMDNDSENQES--MPSLSFQOTMRAENPHY 178

Db 121 FYGLIPETIIGDCCEYEDKRENAERLMDNDSENQES--MPSLSFQOTMRAENPHY 180

Qy 179 STLALVFYVYVGFPAVAVINNVETVPCGVPGS--KELPCGERYSVAFFCLDTACWIF 237

Db 181 STLALVFYVYVGFPAVAVINNVETVPCGVPGS--KELPCGERYSVAFFCLDTACWIF 240

Qy 238 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVRI 297

Db 241 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVRI 300

Qy 298 FKFSHSGQLRILGTTKSCASELGFLLFSLTMAIIIPATWFAEKSSASAKFTSIPAS 357

Db 301 FKFSHSGQLRILGTTKSCASELGFLLFSLTMAIIIPATWFAEKSSASAKFTSIPAS 360

Qy 358 FMYTIVMTTLLGYGDMVPEKTAGKIFGSIISGLVIALPVPIVSNFSRIYHONORAD 417

Db 361 FMYTIVMTTLLGYGDMVPEKTAGKIFGSIISGLVIALPVPIVSNFSRIYHONORAD 420

Qy 418 KRAQKARLARIRAKTSSNAYLHAKRNGLLNLEALBTGPBEHMGKTTSLIESQHH 477

Db 421 KRAQKARLARIRAKTSSNAYLHAKRNGLLNLEALBTGPBEHMGKTTSLIESQHH 479

Qy 478 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 537

Qy 1 MAAGVAAWLPPARAAALIGMPVANCMPMLAPADKKR-ODELIVLVNSGRPFQWRTTLE 59

Db 1 MAAGVAAWLPPARAAALIGMPVANCMPMLAPADKKR-ODELIVLVNSGRPFQWRTTLE 60

Qy 60 RYPTDLTSGTEKEPFNEDTKEYFPDRDPEVRCVLANFYRTGKLHYPRYECISAYDELA 119

Db 61 RYPTDLTSGSRDPEFYHETQOYFPDRDPEFRHLINFYRTGKLHYPRHECISAYDELA 120

Qy 120 FYGLIPETIIGDCCEYEDKRENAERLMDNDSENQES--MPSLSFQOTMRAENPHY 178

Db 121 FYGLIPETIIGDCCEYEDKRENAERLMDNDSENQES--MPSLSFQOTMRAENPHY 180

Qy 179 STLALVFYVYVGFPAVAVINNVETVPCGVPGS--KELPCGERYSVAFFCLDTACWIF 237

Db 181 STLALVFYVYVGFPAVAVINNVETVPCGVPGS--KELPCGERYSVAFFCLDTACWIF 240

Qy 238 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVRI 297

Db 241 TVEYLRLFAAPSRFRFRSVMISIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVRVRI 300

Qy 298 FKFSHSGQLRILGTTKSCASELGFLLFSLTMAIIIPATWFAEKSSASAKFTSIPAS 357

Db 301 FKFSHSGQLRILGTTKSCASELGFLLFSLTMAIIIPATWFAEKSSASAKFTSIPAS 360

Qy 358 FMYTIVMTTLLGYGDMVPEKTAGKIFGSIISGLVIALPVPIVSNFSRIYHONORAD 417

Db 361 FMYTIVMTTLLGYGDMVPEKTAGKIFGSIISGLVIALPVPIVSNFSRIYHONORAD 420

Qy 418 KRAQKARLARIRAKTSSNAYLHAKRNGLLNLEALBTGPBEHMGKTTSLIESQHH 477

Db 421 KRAQKARLARIRAKTSSNAYLHAKRNGLLNLEALBTGPBEHMGKTTSLIESQHH 479

Qy 478 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 537

Db 480 HLHCLKLEKTNHFEIDQMFQFONCMSSMONTPTSRPSLSHPGLTTCCSRBKKTTH 539

Qy 538 LPSNLPATRLRSMOELSTIHIOGSEOPSLTTSRSSSLNKADGRLPNCCKTSOITTAIS 597

Db 540 IPNANVSGHSGIOELSTIQIRCVERTPLNSRSSLNAMKECVLANCEQPYTTAIIIS 599  
Qy 598 IPTPPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 636  
Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRVSL 630

RESULT 14  
US-10-369-186-260  
; Sequence 260, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 260  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-260

Query Match 75.8%; Score 2518; DB 15; Length 630;  
Best Local Similarity 75.8%; Pred. No. 4.7e-209;  
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAMLPPARAAAIIGMPVANCMPPLAPADKNR-ODELIVLVNSGRPFQMTTLE 59  
Db 1 MAAGVAAMLPPARAAAIIGMPVASGMPAPRQERKRTQDALIVLVNSGRFQMTDILE 60

Qy 60 RYPTDLTGSTEKEFFFNEDTKEYFFDRDPEVFCVINFRTGKLAHYPRYECISAYDELA 119  
Db 61 RYPTDLTGSSERDFFHYFETQYFFDRDPDIFPHIINFRTGKLAHYPRHECISAYDELA 120

Qy 120 FYGLPEIIGDCCYEEYKDKRENAERLMDNDSENNQES-MESLSFRQTMRAFERPHT 178  
Db 121 FFGIIPRIIGDCCYEEYKDKRENAERLQDDADTDGTAGSALPTMTARQVMAFENPHT 180

Qy 179 STLALVYVYTGFFIAVSVTNVETVPCGTVGS-KEIPCGERYSVAFFCLDTACVMIF 237  
Db 181 STLALVYVYTGFFIAVSIVANVETVPCGSSPGHKEIPCGERYAVAFCLDTACVMIF 240

Qy 238 TVEYLRLFAAPSRIRYRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFRVRI 297  
Db 241 TVEYLRLFAAPSRIRYRISVMSIIDVVALPYIIGLWMTNEDVSGAFVTLRVFRVRI 300

Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 357  
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSASAKFTSIPAA 360

Qy 358 FWYTIIVMTTLGYDWMVKTIAGKIFGSLCSLGSVLVIALPVPIVINSRRIYHONRAD 417  
Db 361 FWYTIIVMTTLGYDWMVKTIAGKIFGSLCSLGSVLVIALPVPIVINSRRIYHONRAD 420

Qy 418 KRRQAOKARLARIRVATGSSNAYLHRSKRGLINEALELTGPBEEHMGKTSILIESQHH 477  
Db 421 KRRQAOKARLARIRVATGSSNAYLHRSKRGLINEALELTGPBEEHMGKTSILIESQHH 479

Qy 478 HLHLCLEKTTNHEFIDQMFQONCESSMONYPTSTSPSLSHRGLTTTCCSRRSKKTTH 537  
Db 480 HLHLCLEKTTNHEFIDQMFQONCESSMONYPTSTSPSLSHRGLTTTCCSRRSKKTTH 539

Qy 538 LPNSNLPTATRLRSMOELSTIHIOGSEQPSLTSSSLNLAKADGLRPNCKTSQITTAIIIS 597  
Db 540 IPNANVSGHSGIOELSTIQIRCVERTPLNSRSSLNAMKECVLANCEQPYTTAIIIS 599

Qy 598 IPTPPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 636  
Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRVSL 630

Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRVSL 630

RESULT 15  
US-10-369-186-261  
; Sequence 261, Application US/10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C9  
; CURRENT APPLICATION NUMBER: US/10/369,186  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 293  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 261  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-186-261

Query Match 75.8%; Score 2518; DB 15; Length 630;  
Best Local Similarity 75.8%; Pred. No. 4.7e-209;  
Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

Qy 1 MAAGVAAMLPPARAAAIIGMPVANCMPPLAPADKNR-ODELIVLVNSGRPFQMTTLE 59  
Db 1 MAAGVAAMLPPARAAAIIGMPVASGMPAPRQERKRTQDALIVLVNSGRFQMTDILE 60

Qy 60 RYPTDLTGSTEKEFFFNEDTKEYFFDRDPEVFCVINFRTGKLAHYPRYECISAYDELA 119  
Db 61 RYPTDLTGSSERDFFHYFETQYFFDRDPDIFPHIINFRTGKLAHYPRHECISAYDELA 120

Qy 120 FYGLPEIIGDCCYEEYKDKRENAERLMDNDSENNQES-MESLSFRQTMRAFERPHT 178  
Db 121 FFGIIPRIIGDCCYEEYKDKRENAERLQDDADTDGTAGSALPTMTARQVMAFENPHT 180

Qy 179 STLALVYVYTGFFIAVSVTNVETVPCGTVGS-KEIPCGERYSVAFFCLDTACVMIF 237  
Db 181 STLALVYVYTGFFIAVSIVANVETVPCGSSPGHKEIPCGERYAVAFCLDTACVMIF 240

Qy 238 TVEYLRLFAAPSRIRYRISVMSIIDVVAIMPYYIGLWMTNEDVSGAFVTLRVFRVRI 297  
Db 241 TVEYLRLFAAPSRIRYRISVMSIIDVVALPYIIGLWMTNEDVSGAFVTLRVFRVRI 300

Qy 298 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSASAKFTSIPAS 357  
Db 301 FKFSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSASAKFTSIPAA 360

Qy 358 FWYTIIVMTTLGYDWMVKTIAGKIFGSLCSLGSVLVIALPVPIVINSRRIYHONRAD 417  
Db 361 FWYTIIVMTTLGYDWMVKTIAGKIFGSLCSLGSVLVIALPVPIVINSRRIYHONRAD 420

Qy 418 KRRQAOKARLARIRVATGSSNAYLHRSKRGLINEALELTGPBEEHMGKTSILIESQHH 477  
Db 421 KRRQAOKARLARIRVATGSSNAYLHRSKRGLINEALELTGPBEEHMGKTSILIESQHH 479

Qy 478 HLHLCLEKTTNHEFIDQMFQONCESSMONYPTSTSPSLSHRGLTTTCCSRRSKKTTH 537  
Db 480 HLHLCLEKTTNHEFIDQMFQONCESSMONYPTSTSPSLSHRGLTTTCCSRRSKKTTH 539

Qy 538 LPNSNLPTATRLRSMOELSTIHIOGSEQPSLTSSSLNLAKADGLRPNCKTSQITTAIIIS 597  
Db 540 IPNANVSGHSGIOELSTIQIRCVERTPLNSRSSLNAMKECVLANCEQPYTTAIIIS 599

Qy 598 IPTPPALTPGESRP--PPASPGPNTNIPSTSNVVKSVL 636  
Db 600 IPTPPVTTPEGDDRPESPEYSGG-----NIVRVSL 630

Search completed: April 6, 2005, 08:34:00



Thu Apr 7 08:08:07 2005

us-10-062-879-4.apr5.rapb

Page 9

Job time : 443.392 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 04:45:50 ; Search time 114.785 Seconds  
(without alignments)  
533.115 Million cell updates/sec

Title: US-10-062-879-4

Sequence: 1 MAAQVAAALPPARAALIGMM.....PGPNTNIPSTSNVYKSVL 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2519	75.9	630	2 J00271	voltage-sensitive
2	2141.5	64.5	651	2 A39372	potassium channel
3	1915.5	57.7	490	2 A35312	potassium channel
4	1103	33.2	236	2 I57681	potassium channel
5	770	23.2	802	2 JH0595	potassium channel
6	750	22.6	858	2 S31761	potassium channel
7	736.5	22.2	643	2 S00480	potassium channel
8	736.5	22.2	853	1 CHRTD1	potassium channel
9	736	22.2	602	2 JH0166	potassium voltage-
10	736	22.2	656	2 JH0193	potassium channel
11	735.5	22.2	924	2 S12746	potassium channel
12	726.5	21.9	857	2 I56529	potassium channel
13	719	21.7	598	2 S66669	potassium channel
14	719	21.7	602	2 A49507	potassium channel
15	718.5	21.6	525	2 A43531	potassium channel
16	718	21.6	523	2 A38101	potassium channel
17	717.5	21.6	585	2 A39395	potassium channel
18	717	21.6	499	2 A77466	delayed rectifier
19	716.5	21.6	924	2 B41359	potassium channel
20	715	21.5	499	2 I84204	potassium channel
21	715	21.5	499	2 A33814	potassium channel
22	715	21.5	769	2 I56546	Shaw type potassiu
23	712.5	21.5	528	2 I54205	potassium channel
24	712	21.4	489	2 I51532	potassium channel
25	711.5	21.4	495	2 A40090	potassium channel
26	711.5	21.4	495	2 B39113	potassium channel
27	710.5	21.4	495	2 I57680	potassium channel
28	707.5	21.3	511	2 A46020	potassium channel
29	707	21.3	460	2 T27759	hypothetical prote

30	706.5	21.3	511	2 S07095	potassium channel
31	705	21.2	476	2 S21144	potassium channel
32	705	21.2	597	2 S51212	BAK5 protein - bov
33	701.5	21.1	498	2 A41359	potassium channel
34	700	21.1	679	2 A42073	potassium channel
35	699.5	21.1	489	2 J04787	Shaw protein - Cal
36	699	21.1	499	2 JH0313	potassium channel
37	699	21.1	499	2 A48672	delayed rectifier
38	697.5	21.0	625	2 S13919	potassium channel
39	697	21.0	581	2 S17150	potassium channel
40	696	21.0	613	2 A39402	potassium channel
41	694.5	20.9	660	2 S24125	potassium channel
42	692.5	20.9	624	2 S22703	voltage-gated pota
43	692.5	20.9	653	2 A39922	potassium channel
44	692.5	20.9	654	2 S11049	potassium channel
45	691	20.8	558	2 T23991	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

J00271 voltage-sensitive potassium channel protein [validated] - rat

N.Alternate names: rat sha/1

C.Species: Rattus norvegicus (Norway rat)

C.Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C.Accession: J00271; A39113

R.Baldwin, T.J.; Tsaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.

Neuron 7, 471-483, 1991

A.Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K+ c

A.Reference number: J00271; MUID:92000693; PMID:1840649

A.Accession: J00271

A.Molecule type: mRNA

A.Residues: 1-630 <BAU>

A.Experimental source: hippocampus

R.Roberde, S.L.; Tamkun, M.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A>Title: Cloning and tissue-specific expression of five voltage-gated potassium channel

A.Reference number: A39113; MUID:91156694; PMID:1705709

A.Accession: A39113

A>Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>

A.Cross-references: GB:M59980; NID:9203467; PIDN:AAA40929.1; PID:9203468

C.Function:

A>Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [valida

C.Superfamily: potassium channel protein drk1

C.Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel

F.38/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #sta

F.54,280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status

F.70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta

F.101,166,251,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status

F.113,265,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase

F.592/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 75.9%; Score 2519; DB 2; Length 630;  
Best Local Similarity 75.8%; Pred. No. 6.6e-186;

Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;

QY	1	MAAGVAAALPPARAALIGMMFVANCMPFLADADKKR-QDEILVINSGRPRQWRTTLE	59
DB	1	MAAGVAAALPPARAALIGMMFVAGPMPAPPROBKRTQDALIVLVNAGTRFQWQDTLE	60
QY	60	RYPTLLGSTEKEPPENDTKEYFPDRBYFRCLNRYRGKLYHPYECISAYDDSLA	119
DB	61	RYPTLLGSSSRDFFPHETQYFFDRDPDIFRHLNRYRGKLYHPYECISAYDESLA	120
QY	120	FYGLIPELLIGDCYCEYKORRENAERLMDNDSENNQES-MPSLSPFQITWRAFENPHT	178
DB	121	FFGLIPELLIGDCYCEYKORRENAERLQDDADTDNTGESALPTWTARQVWRAFENPHT	180

Qy	179	STALIVFYVMGFLFVAVITVMVETVPCGATPGS-KELPCGERSVAFPCIDTACMIF	237
Db	181	STMALVFFYVVGFFFLFVAVIANVVETVPCGSSPGHikelPCERYAVAFPCIDTACMIF	240
Qy	238	TVEYLLRLFAAPSRRYFTRSVMSIIDVVAIMYVYIGLVMTNNEDVSGAEVTLRVFRPRI	297
Db	241	TVEYLLRLFAAAPSRRYFTRSVMSIIDVVAILEYVYIGLVMTNEDVSGAEVTLRVFRPRI	300
Qy	298	EKFSHSGGRLILGTTKSCASEIGFLLPSLTMAITIPATVMFVAKGSSASAKFTSIPAS	357
Db	301	EKFSHSGGRLILGTTKSCASEIGFLLPSLTMAITIPATVMFVAKGSSASAKFTSIPAA	360
Qy	358	FWYITVMTTIGYGDVMPKTIAGKIFGSCISLSGVVLIALPVPVIVSNFSRIYHONORAD	417
Db	361	FWYITVMTTIGYGDVMPKTIAGKIFGSCISLSGVVLIALPVPVIVSNFSRIYHONORAD	420
Qy	418	KRPAPKARLARIRVAKTGSSNAYLHSKRNGLLNEALBELGTPEEBEHMGKTTSLIBSOHH	477
Db	421	KRPAPKARLARIRAPKSGSANAYMQSKNGLLSNOLQ-SSEDEPAFVSKSSSEFETQHH	479
Qy	478	HLHLLEKTTNHEFIDDEOMFEONCMSSMONYPSPRSPSLSHHPGLTTCGSRRSKXTH	537
Db	480	HLHLLEKTTNHEFIDDEOVFEESCEHVALVNPSPSSPBLSSQOGVSTTCGSRRHAKSR	539
Qy	538	LPNSULPATRLSRMOELSTIHIOGSEOPSLTTSRSLMLKADGRLPNCKTSQITTAIIS	597
Db	540	IPNAVSGSHRSVQELSTIQRCVERFTPLSNRSRLNAKMECVYLANCEOPYVTTAIIS	599
Qy	598	IPTPALTPEGESRP--PPASRGPMTNIPSLITSNVKVSYVL 636	
Db	600	IPTPEVTTPEGGDRPESPEYSG-----NIVRSAL 630	

RESULT 2  
A39372  
potassium channel protein Shall - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: A39372  
R/Pak, M.D.; Baker, K.; Govarrubias, M.; Butler, A.; Ratcliffe, A.; Salzkoff, L.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991  
A/Title: Mshal, a subfamily of A-type K(+) channel cloned from mammalian brain.  
A/Reference number: A39372; MUID:91239573; PMID:2034678  
A/Accession: A39372  
A/Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-651 <PAK>  
A:Cross-references: UNIPROT:003719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813

Query Match	64.5%	Score 2141.5;	DB 2;	Length 651;
Best Local Similarity	65.7%;	Pred. No. 8.2e-157;		
Matches	434;	Conservative	76;	Indels 35; Gaps 13
Qy	1	MAAGVAAALPFAARAALGMMVAVANCMPPLADPKKKRODELIVANVSGRRPQWRTTLRR	60	
Db	1	MAAGVATWLPFAARAALVGMPLPAQODLPALPAEYKSRGSEVAVLVANVSGRRPFETWKTDLR	60	
Qy	61	YPDTLTSGTEKEFFENEDTKEYFFPRDPEVFCVNLFFYTGKLIHYPRYECISAYDDELAF	120	
Db	61	YPTDLTSSSEKEFFFDABEGEYFFPRDPEMFHVLNFFYTGKLIHCRQCIQAFFDELAF	120	
Qy	121	YGIPEIIGDCCYEYBKORKRENAERLMDNDSENNOESMPSL---SFRQTMRAFENP	176	
Db	121	YGLVELVGDCCLEEYRDRKKENARLDAEBAQEGEG-PALPAGSLRQRLMRAFENP	179	
Qy	177	HTSTLALVFYTTGFIANSVTTNVEYVPCGTVP--GSEKLPCGERISVAFPCLDTACV	234	
Db	180	HTSTALVFYTTGFIANSVIANVETIIPCRGTPRMPSPKESOCGRPFETAFECMDTACV	239	
Qy	235	MEFTVEYLRLFAASRPFIRISWSIIDVVALMPYITGLVNTNNDSVGAFAFTLLRPFV	294	
Db	240	LIFTEBYLRLFAASRRCFLRISWSIIDVVALLPYITGLFPAKNDVSGAFAFTLLRPFV	299	

QY	295	FRIRKFSHSGCLRLIGVTLKSCASELGLPSLTMALIIIPATWPMVAREKSSASKEFTSI	354
Db	300	FRIFPSSHSGCLRLIGVTLKSCASELGLPSLTMALIIIPATWPMVAREKSGSKTNFTSI	359
QY	355	PASFMYTIVMTTIGYGDMPVKTTAGKIFGSIICSLSGVLVIALPVVIVSNFSRIYHQNQ	414
Db	360	PAAFMYTIVMTTIGYGDMPVSTIAGKIFGSIICSLSGVLVIALPVVIVSNFSRIYHQNQ	419
QY	415	RADRRRAQKRLARIRVAKTGSSNAVYHSKRNGLINLELGTTPPEEHHM-GKTTSLIE	473
Db	420	RADRRRAQKRLARIRLAKSGTTNAFLQYKONG---GLBPSGGDGMCLVRSRSAFE	475
QY	474	SOHHHLHLCLEKTNHFEPIIDQMEPQONMESSMQUVPTSRPSLSMHP---GLTTCCS	529
Db	476	QOHHLHLHLCLEKTCHEFTDELTPSEALGAVSLGRTS-RSTSVSSQEPGPGSLRSSCCS	534
QY	530	RR-SKTTTHLPNSLNPATRLRSMDLSTHIOGSEOPSLTSSRLNLKADGLRPNCKT	588
Db	535	RRVRRRAIRLANSTASVSR-GSMQDLDT--LAGLARSPAPQVRRSSLNAPPHSDLDLNCOS	591
QY	589	SOITTAIISITPPALPEGBSRPPAPG-----PNTNI-----PSTISNVYKVSU	635
Db	592	RDPAVAALISITPPANTPD-ESQPSRSSGGGSGGTPNTTLNNSLIGTFCCLPETHKISS	650
QY	636	L 636	
Db	651	L 651	

RESULT 3  
A35312  
potassium channel protein Shal2 - fruit fly (*Drosophila melanogaster*)  
C|Species: *Drosophila melanogaster*  
C|Date: 14-Sep-1990 #sequence\_revision 06-Nov-1992 #ext\_change 09-Jul-2004  
C|Accession: A35312, S12747  
R|Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salikoff, L.  
Science 248, 599-603, 1990  
A|Title: K+ current diversity is produced by an extended gene family conserved in *Drosophila*  
A|Reference number: A35312; MUID:90239553; PMID:2333511  
A|Accession: A35312  
A|Molecule type: mRNA  
A|Residues: 1-490 <MEI>  
A|Cross-references: UNIPROT: P17971; GB: M32660; NID: g158456; PID: g158457  
R|Butler, A., Wei, A., Salikoff, L., 1990  
Nucleic Acids Res. 18, 2173-2174.  
A|Title: Shal, Shab, and Shaw: three genes encoding potassium channels in *Drosophila*.  
A|Reference number: S12746; MUID:90245668; PMID:2336395  
A|Accession: S12747  
A|Molecule type: mRNA  
A|Residues: 1-490 <BUT>  
A|Cross-References: EMBL: M32660; NID: g158456; PID: g158457  
C|Genetics:  
A|Gene: shal2  
A|Cross-references: FlyBase: FBgn0005564  
C|Superfamily: potassium channel protein drkl  
C|Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

	Query Match	57.7%	Score 1915.5	DB 2	Length 490
	Best Local Similarity	73.6%	Pred. No. 1.4e-139		
	Matches	360	Conservative	61	Indels 5; Gaps 4
Qy	3	AGVAAAMLFPPAAAAAGMMPVANCMPMLPLPADNKKQ--DELIVLVNVSGRGFQRTWTLER	60		
Db	2	ASVAAAMLFPPAAAAAGWPIATHPLPPPPMKDRKTKDEKLLVNSGRFPEWRNTLLEK	61		
Qy	61	YPDTLLSSTEKEFPFNNEDTKKEYFEDRDDEVFRCVINFRTGKLAHPRYCISAYDELAFL	120		
Db	62	YPDTLLSSENEEEFFEDDECKEYFFRDRDPDIPHHIINYYTGKLAHKECHLTSYDEELAF	121		
Qy	121	YGIILPEITGDCCYEYKDKRKENARLMDNDNSENNOESMBEL-SFRQTMWTAFFENPHAS	179		
Db	122	FGIMEDVITGDCCYEYKDRKRENAARLMDDKLSENGDQOOLTNRRQKRWRAFFENPHAS	181		

Qy 180 TLALVYVYVGFIAVSVITNVEVPCGVG-SKEPLCGERYSAVAFCLDTACVMT 238  
 Db 182 TSALVYVYVGFIAVSVITNVEVPCGVG-SKEPLCGERYSAVAFCLDTACVMT 241  
 Qy 229 VEYLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLVFRVFRIF 298  
 Db 242 AEYLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTLVFRVFRIF 301  
 Qy 229 KFSRHSQGRILIGYTLKSCASELGLFVSLMAAIIIFAVVMPYAKKNVGNFTSIPAA 361  
 Db 302 KFSRHSQGRILIGYTLKSCASELGLFVSLMAAIIIFAVVMPYAKKNVGNFTSIPAA 361  
 Qy 359 WYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVSNFSRIYHONORDK 418  
 Db 362 WYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVSNFSRIYHONORDK 421  
 Qy 419 RPAQKARLARIKAVKGTSSNAYLHSGKNGLINEALELGTPEEHMKTTSLISQHH 478  
 Db 422 RKAQKARLARIKAVKGTSSNAYLHSGKNGLINEALELGTPEEHMKTTSLISQHH 480  
 Qy 479 LTHCEKTT 487  
 Db 481 LTRCEKTT 489

## RESULT 4

potassium channel protein - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 02-Aug-1996 #sequence 02-Aug-1996 #text\_change 03-Nov-2000  
 C:Accession: 157681  
 R:Rudy, B.; Kentros, C.; Vega-Saenz de Miera, E.C.  
 Mol. Cell. Neurosci. 2, 89-102, 1991  
 A:Title: Families of potassium channel genes in mammals: Toward an understanding of the  
 A:Reference number: 157681  
 A:Accession: 157681  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <RES>  
 A:Cross-references: GB:M74898; NID:g205040; PIDN:AAA41468.1; PID:g205041  
 C:Superfamily: potassium channel protein drkl

Query Match 33.2% Score 1103; DB 2; Length 236;  
 Best Local Similarity 93.2%; Pred. No. 1.9e-77;  
 Matches 219; Conservative 2; Mismatches 14; Indels 0; Gaps 0;  
 Qy 170 WRAPENPHTSLALVFYVVGFFIAVSVITNVEVPCGVGSKELPCGERYSVAFCL 229  
 Db 1 WRAPENPHTSLALVFYVVGFFIAVSVITNVEVPCGVGSKELPCGERYSVAFCL 60  
 Qy 230 DTACVMTTVEYLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTL 289  
 Db 61 DTACVMTTVEYLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTNEDVSGAFVTL 120  
 Qy 290 RVFRFRIRFKFSRHSQGRILIGYTLKSCASELGLFVSLMAAIIIFAVVMPYAEKSSAS 349  
 Db 121 RVFRFRIRFKFSRHSQGRILIGYTLKSCASELGLFVSLMAAIIIFAVVMPYAEKSSAS 180  
 Qy 350 KFTSIPASFYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVS 404  
 Db 181 KFTSIPASFYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVS 235

## RESULT 5

JH0595  
 potassium channel protein cdcr - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 17-Jul-1997 #sequence 17-Jul-1997 #text\_change 20-Aug-1999  
 C:Accession: JH0595  
 R:Huwang, P.M.; Glac, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H.  
 Neuron 8, 473-481, 1992  
 A:Title: A novel K+ channel with unique localizations in mammalian brain: molecular clon  
 A:Reference number: JH0595; MUID:92198655; PMID:1550672

A:Accession: JH0595  
 A:Molecule type: mRNA  
 A:Residues: 1-802 <HNA>  
 A:Cross-references: GB:M7482; NID:g203395; PIDN:AAA40905.1; PID:g203396  
 A:Experimental source: circumvallate papillae  
 C:Superfamily: potassium channel protein drkl  
 C:Keywords: glycoprotein; phosphoprotein; transmembrane protein  
 F:193-212/Domain: transmembrane #status predicted <TM1>  
 F:233-254/Domain: transmembrane #status predicted <TM2>  
 F:265-286/Domain: transmembrane #status predicted <TM3>  
 F:299-320/Domain: transmembrane #status predicted <TM4>  
 F:335-356/Domain: transmembrane #status predicted <TM5>  
 F:397-418/Domain: transmembrane #status predicted <TM6>  
 F:187,287,419,446/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:448,500/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 23.2% Score 770; DB 2; Length 802;  
 Best Local Similarity 29.9%; Pred. No. 4.6e-51;  
 Matches 212; Conservative 116; Mismatches 256; Indels 126; Gaps 24;  
 Qy 27 MFLAPAD--KKNRDELIVLVNLSGRFRQT-WRTTLERIPDTLLG-----STEKEF----- 74  
 Db 20 LPPEVVDIIRSKTSRRVKINVGILNHEVLR-TLDRILPRTRIGLRDQNTHESLLEVCD 78  
 Qy 75 -FNEPTKEVFPDRDPEVFRVCLNFRTRGKLHYPRPRECISAVDELAFYGLPEIIGDCCY 133  
 Db 79 DYNLENVEYFPDRHGAFTSLNFRTRGKLHMEBMCALSGQELDYGIDETIYESCCQ 138  
 Qy 134 EYKDRK-----RENARLMDNDSENNOBSPSLSFQTMWRAPENPHTSLALVFY 186  
 Db 139 ARYHQKQNMELRLREAFETMRDGESEFDTCCBEK--RKKLMDLEKPPSSVAAKILA 196  
 Qy 187 YVTEFFIAVSVITNVEVPCGVGSKELPCGERY-----SVAFCLDTACVMTFVEY 241  
 Db 197 IVSILFIVLSTIALSLNLP-----ELQENDEFGQPSDNKRLAHEAVCIAMFTMEY 248  
 Qy 242 LLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTN-----EDVSGAFVTLVFRV 294  
 Db 249 LLRLPAAPRRYFIRSVMSIIDVAIMPYYIGLVMTN-----EDVSGAFVTLVFRV 294  
 Qy 295 FRIFKFSRHSQGRILIGYTLKSCASELGLFVSLMAAIIIFAVVMPYAEKSSASKFTSI 354  
 Db 309 LRILKLAHSGTGLSIGFTLRSYNELGLLPLAMGMISLIVFAFKEDAKTKFTSI 368  
 Qy 355 PASFVYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVSNFSRIYHONQ 414  
 Db 369 PASFVYTIYMTTLGVDWVPKTIAGKIFGSLSGVLIALPVPVIVSNFSRIYHONQ 428  
 Qy 415 RADK---RPAQKAR-----LARIRAKTGSS-----NAYLH 443  
 Db 429 ROEKAIRKREALEKRGKSVSNLKDAPARSMELIDVAVEKAGESANIKOSVDNHL 488  
 Qy 444 SKRGLNLEAL-----ELTGPEEHMKTTSLISQHHHLACLE----- 484  
 Db 489 PSRKMARKALSTSSSNKSYENKIQEVSQKSHQNLNTSS--SSPQLHSQKLEMLYNE 546  
 Qy 485 --KTTNHE-----FIDE-QMEONCMSSM--QNYBTRSPSLSSHPGL 523  
 Db 547 ITTKQTHSHPPDCOEQEPERSAYEEIEHEBVCPOQQLVAQTEVIVDMKSTSSIDSF 606  
 Qy 524 TTCCSRKSKTTHLPNSNLPAATRLRSQDELSTHIGQSEDPSSLTSSSLNKLADDLR 583  
 Db 607 TS--CAIDFETERSP--LPPPSASHQMKFPTDLPGMDHQRVRAFPFLLLRDKG-- 659  
 Qy 584 PNCKTSQITTAIISITP-PALTPREGESRPPASGPNTNIPSTISNVK 632  
 Db 660 PAABEALDVAIPIDITVNLMDGASHGPIQPSADSPSSSLK--SNPLK 707

## RESULT 6

S31761  
 potassium channel protein DRK1 - human  
 C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S31761  
 R/Albrecht, B.; Loria, C.; Stocker, K.; Pongs, O.  
 submitted to the EMBL Data Library, September 1992  
 A/Description: Cloning, expression and chromosomal localization of the delayed rectifier  
 A/Reference number: S31761  
 A/Molecule type: DNA  
 A/Accession: S31761  
 A/Residues: 1-858 <ALB>  
 A/References: UNIPROT:Q14721; EMBL:X68302; NID:G30892; PIDN:CAA48374.1; PID:G30892  
 C/Genetic:  
 A/Gene: GDB:KCNB1; K12.1; DRK1  
 A/Genes-references: GDB:128081; OMIM:600397  
 A/Map position: 20q13.2-20q13.2  
 C/Superfamily: potassium channel 1 protein drkl

Query Match 22.6%; Score 750; DB 2; Length 858;  
 Best Local Similarity 29.2%; Pred. No. 1.7e-43;  
 Matches 189; Conservative 114; Mismatches 220; Indels 124; Gaps 18;

27 MPLPAD--KMKODELIVNVSGRRFQT-WRTLEVPDTLG-----STEKEFF----- 74  
 16 LPPEMEIVSKACSRVRLNVGLAHVLMR-TLDELPTRLCKLDCVTHSLLEVCD 74  
 75 -FNEDEYFPPDRDEVEFVCLNPFRTGKLHYPREICISAYDELAAYGILPEIIGDCY 133  
 75 DYSGLDDEYFPPDRPGAFSTILNPFYRGLHMEEMCALFSQGLDWGIDEIYESCCQ 134  
 134 EYKDKRENAERLMDNDSENNQ-----SMPSLSRQTMWRAFEHPHSTALVYVV 188  
 135 ARYHOKQNEBELKRAETLREBEGEPNTCCAEKRKLDLLEKPNSSVAAKILAIT 194  
 189 TGEFIAVSITNVETVPCGTGVSKEPLCGERYSA-----FECCLTACMIITVEYL 243  
 195 SIMFIVSTALSLNTLP-----BLQSLDEEGOSTNDPOLAHVAVCIAMTWEYL 246  
 244 RLFAAPSRYPFRISVMSIIDVVAIMPYIGLVMTNN-----EDVSGAVTLRVFVR 236  
 247 RLFSPPKMKFPGKPLNAIDLALIPYVTIFLTESNKSVLQFQNVARVVQIFRIMILR 306  
 297 IFFRSRISQGRITGLKSCASGLFLSLTMAIIFPATWVYAKKSASASTIPA 356  
 307 ILKLARSTGLQSGFLTRSYNELGLILFLAMGIMIFSLVFAEKDDDTFKSIPA 366  
 357 SFWYITVMTGLGDMVPKTIAGKIFGSIKSGVLVIALPVVIVNSFRIYHONORA 416  
 367 SFWMATITMTVVGDIYPTKILGKIYGVLCIAGVIALPIPIVNNSEPFKEQKQ 426  
 417 DKRAOKKARLARIIVAKTSSNAYLHSGKNGLL-----NEALELGTPEEH 464  
 427 EKAIKREA-LER-----AKRNGSIVNMKDAFARSIEEMDIVVEKNGEN 471  
 465 MGRITSLIESQHHLHLEKTTNHEFIDEQFQNCMESSMOWPSTRBPSLSHGGLT 524  
 472 MGRKDKV--QDNLSNPKWMTYRTL--SETSSKSPETEQSPK----- 514  
 525 TTCSSRSKKTTHLPNGLPATRLRSMOELSTIHIQSEOPSLTSSSLNKADGLRP 584  
 515 -----ARSSSSPQL-----NVQLEDMYNNKAKQSQPIANTKSSAASQKKEHL-- 560  
 585 NCKTSQITTAIISIPPLALPEGESRPPSPAGPNTNIPSITSNV 631  
 561 -----EMESIPSPVAF-----LPTRTGVI 580

RESULT 7  
 S00480  
 potassium channel protein A (clone Sh-beta) - fruit fly (Drosophila melanogaster)  
 C/Species: Drosophila melanogaster  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 17-Nov-2000  
 C/Accession: S00480; S01111  
 R/Pongs, O.; Kecskemethy, N.; Mueller, R.; Krah-Jentgens, I.; Baumann, A.; Kiltz, H.H.;  
 EMBO J. 7, 1087-1096, 1988

A/Title: Shaker encodes a family of putative potassium channel proteins in the nervous sy  
 A/Reference number: S00479; WUID:88296413; PMID:2456921  
 A/Accession: S00480  
 A/Molecule type: DNA  
 A/Residues: 1-643 <RON>  
 A/Cross-references: EMBL:X07132; NID:98602; PIDN:CAA30144.1; PID:98603  
 A/Note: the clone is designated as Sh-beta  
 R/Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.  
 Nature 331, 137-142, 1988  
 A/Title: Multiple potassium-channel components are produced by alternative splicing at th  
 A/Reference number: S00508; WUID:88122563; PMID:2448635  
 A/Accession: S01111  
 A/Molecule type: mRNA  
 A/Residues: 1-643 <SCH>  
 A/Note: the clone is designated as ShD1  
 R/Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.  
 Nature 332, 740, 1988  
 A/Reference number: S01113  
 A/Contents: annotation; erratum  
 C/Genetic:  
 A/Gene: Shaker  
 A/Genes-references: FlyBase:FBgn003380  
 C/Superfamily: potassium channel protein drkl  
 C/Keywords: alternative splicing; transmembrane protein

Query Match 22.2%; Score 736.5; DB 2; Length 643;  
 Best Local Similarity 31.7%; Pred. No. 1.3e-48;  
 Matches 181; Conservative 106; Mismatches 171; Indels 113; Gaps 14;

40 ELIVLVSGRRFQMTTLEHYPTDLGSTEKEF-FNEDEYFPPDRDEVEFVCLNPF 98  
 85 ERVIVNVSGRLRFETQRTLNQFPTDLGDPARLRFDPRLREYFPPDRSPSDALYY 144  
 99 RT-GKLHYPREICISAYDELAAYGILPEIIGCCYKDKRENAERLMDNDSENNQ 157  
 145 QSGGRLRRPNNVLDVSEIRKYE-----LGOAINKRE-----DEGFIKEE 189  
 158 ESMPSLSRQTMWRAFEHPHSTALVYVYVTFGLFVAVITNVETP----- 206  
 190 RPLPDNEKQKRWLLFEYPESSQARVVAIISVILLISIVIFCLETLPEFKAYVENTT 249  
 207 -CGTVGSKELPCGERYSVAFFCLDTACVMIFFVEYLRLFAAPSRYPFRSVMISIDV 265  
 250 TNGTKLEBDEVP--DITDPFFLEITLCIMFFELTVRFELCPNKLNFCRDVWNYIDII 306  
 266 AIMPYIGLV-----MTNEDVGAFF-TLVFVPRIFPKSRH 303  
 307 AIIPIYITLATTVAEEDTLNLPKAVSPQDKSSNQAMSLAIIKVLRLVRFRIFKLSRH 366  
 304 SOGRLITGLTKSCASGLFLSLTMAIIFPATWVYAKKSASASTIPAFWYITV 363  
 367 SKGLQILGRILKASMEGLILFLFIVLFSAYVPAEAGSENFPSISIPAFWVAVY 426  
 364 TMTTLGDMVPKTIAGKIFGSIKSGVLVIALPVVIVNSFRIYHONQDKRAQK 423  
 427 TMTTVYGDMTPVGVKQIVGSLCAIAGVLTIALPVVIVNSFRIYHRTDDEEQSON 486  
 424 KARLARIIVAKTSSNAUL-----HSKNGL-----LNEALELGTPEEHGKT 468  
 487 FNVH-----TSCPYLPGLTGQMKKSSLSSESSDMMDLDGVESITGLTETPGNS 537  
 469 -----TSLIESQHHLHLEKTTNHEFIDEQ-----FEQNCM 502  
 538 AVAPFLGAQOQOQOQPVASSLSMSIDQQLHPLOQLTOTQLVQOQOQOQOQOQOQOQ 597  
 503 ESSMQ-----NYPSTRSPSLSHPGIT 524  
 598 OTQOQOQOQOQSHNTINASAAATGSGSSGSLT 628

RESULT 8  
 CHRTD1  
 potassium channel protein drkl - rat









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Db      541 SGPILNTKEMAPQSQ--POEELEMGSPMPVAPLPRTEGVIDKMSMSIDSFISCADPF 598
      512 -----TRSP--SLSHPGILTTT-----CCSRREKKTTHLPNSN-----LQAT 546
Qy      599 PEATPSPHPLASLSKSGSTAPVEYMGALGASGGRMETNPPIEYRSRSGFPVESPSS 658
      547 RLRS-----MOELSTHIOGSEQPSLTTSRSSIMLKADD-GRPNCKTSQITTAISIP 600
      659 SKMTHNPMKRLKLVKVFLEGGDPTPL-----PALGLHDLRLRRGGARAVALEGASILD 714
Qy      601 PPALTPP-----GESRPPSPASPGPNTNI 623
      715 KPVLSPESSSIYTTASARTPPRSPKHTAI 743

RESULT 13
66669
potassium channel (Kv1.5) - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66669
R/Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A/Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rabbit heart and facilit
A/Reference number: S66669; MUID:96032538; PMID:7556635
A/Accession: S66669
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-598 <SAS>
A/Cross-references: UNIPROT:P50638; EMBL:D45025; NID:G1060972; PIDN:BA08082.1; PID:di00
C/Superfamily: potassium channel protein drkl

Query Match      21.7%; Score 719; DB 2; Length 598;
Best Local Similarity 35.0%; Pred. No. 2.6e-47;
Matches 166; Conservative 85; Mismatches 141; Indels 82; Gaps 9;

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```

Qy      42 IVLVNSGRFPQRTTLERYPDTLIGSTKEF--FNNEDTKYFFDRDPFVCVNFYRT 100
      106 VLINISGLREFQTGLTAQPNNTLGDPAKRLRFPPLNENYFEDNRSPFGILYYYS 165
Db      101 -GKLHYPRYECISAYDELAIFYGILPEIIGDCYEEYKORKRENAERLMDNDSENNQES 159
      166 GGRLLRPVNSLDVFADEIRFYQ-----LGDAMERFRE-----DEGFIDKEKP 210
Qy      160 MPSTSPQRTMRAFFENPHTLTALVFFYTGFIASVTNVEYTP----- 206
      211 LPRNEFQRYWLIFFYESSGSARAIAIVSVILISITFCLETLPEFRDERELLRHP 270
Qy      207 -----CGTV---PGSKELPCGER--YGAFFCLDTACMIFFVEYLLRLPA 247
      271 VPIQPPAPALGANGSAVAPASGSTYVAPLPRTLADPFIVYTTVCVIMTFELLVRFPA 330
Db      248 APSRPRFIRSVMSIIDVVAIMPYYIGLVMTNNEVSGA-----FVTLRVF 292
      331 CPKSAEFSRNIMNIDIVAFIPYFITLGTLEAQCGGGGQNGOQAMSLAIRVIRLV 390
Qy      293 RVPRIRFPRSHSGRLTIGTLKSCASEIGFLPSLTMAIIFATYMAFEKSSASKPT 352
      391 RVPRIRFPLSHSGRLTIGTLKSCASEIGFLPSLTMAIIFATYMAFEKSSASKPT 450
Db      353 SIPASFVYITVTTTGLGYDMVPKTIAGKIFGSLGSLGVLTALPVPVIVNSFRIRYQ 412
      451 SIDAFAFMVAVYTTTGYDMRPITVGGKIVGSLCAAGLTALVVPVIVNSFRIRYR 510
Qy      413 NQPADKRA-----QKKARLARIRVAKTSSNAYLSKENG 448
      511 ETDHEQALKEBGSRGSTSDAGGQRKASWSKSLCKAGGSLTADSVRRG 564

```

RESULT 14  
A49507  
potassium channel Kv1.5 - mouse

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C/Species: Mus musculus (house mouse)
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: A49507; B49507
R/Altali, B.; Lénage, F.; Zillan, P.; Guillemaire, E.; Honore, E.; Waldmann, R.; Hugnot,
J. Biol. Chem. 268, 24283-24289, 1993
A/Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+) c
A/Reference number: A49507; MUID:94043264; PMID:8226976
A/Accession: A49507
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-602 <ATT>
A/Cross-references: UNIPROT:Q61762; GB:I22218; NID:G435603; PIDN:AAA33365.1; PID:G435604
A/Accession: B49507
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 201-602 <AT2>
A/Cross-references: GB:I22218
C/Superfamily: potassium channel protein drkl
C/Keywords: alternative splicing

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Query Match      21.7%; Score 719; DB 2; Length 602;
Best Local Similarity 34.3%; Pred. No. 2.6e-47;
Matches 176; Conservative 93; Mismatches 168; Indels 76; Gaps 12;

Qy      30 APADKNRQDELIVLVNSGRFPQRTTLERYPDTLIGSTKEF--FNNEDTKYFFDRDP 88
      101 APQSGSLHQRVILINISGLREFQTGLTAQPNNTLGDPAKRLRFPPLNENYFEDNRN 160
Qy      89 EVPRCVLNFYRT-GKLHYPRYECISAYDELAIFYGILPEIIGDCYEEYKORKRENAERL 147
      161 PSFGILYYQSGGRLLRPVNSLDVFADEIRFYQ-----LGDAMERFRE----- 206
Qy      148 MDDNDSENNQESMPSTSPQRTMRAFFENPHTLTALVFFYTGFIASVTNVEYTP-- 206
      207 -DEGFIDKEKPRLPRNEFQRYWLIFFYESSGSARAIAIVSVILISITFCLETLPE 265
Db      207 -----CGT--VPKSKELPCGERSYVA-----FFCLDTACV 234
Qy      266 FRVRELLRHPVPQPPAPAPAGTNAGSGVLSST--TVAPLPRTLADPFIVERTCV 323
      235 MIFVEYLLRLFAAPSRKPRFSVMSIIDVVAIMPYYIGLVMTNNEVSGA----- 285
Db      324 IMFFELLVRFPAKSAEFSRNIMNIDIVAFIPYFITLGTLEAQCGGGGQNGOQAM 383
Qy      286 -----FVTLRVPRVIRKPRFSSHSGRLTIGTLKSCASEIGFLPSLTMAIIFATYMFY 341
      384 SLAIRVIRLVKRVIRKLSRHSKGLTIGTLKASMRKGLIIFLFIQVILFSSAYRF 443
Qy      342 AEKGSASKPTSIAPASFVYITVTTTGLGYDMVPKTIAGKIFGSLGSLGVLTALPVPV 401
      444 AEADNQSGLSSIDDAFMVAVYTTTGYDMRPITVGGKIVGSLCAAGLTALPVPV 503
Qy      402 IVNSFRIRYHONQADKRAKRLARIRVA-----KTSSNAYLSKENG--N 451
      504 IVNSFRIRYHNETHEQALKEEGIQREESGLDTGQKRVKSCSKSFH-KTGGPLEST 562
Db      452 EALELTGPEEENMGKTTSLIESQHHILHLCLE 484
      563 DSIRSGCEPLEKCHLKAKSNVDLRSLYALCLD 595

```

RESULT 15  
A43531  
potassium channel Kv1.3 - rat  
N/Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel RGK5  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1992 #sequence\_revision 28-Oct-1992 #text\_change 09-Jul-2004  
C/Accession: A43531; JH0168; S06708  
R/Douglas, J.; Osborne, P.B.; Cai, Y.C.; Walkinson, M.; Christie, M.J.; Adelman, J.P.  
J. Immunol. 144, 4841-4850, 1990  
A/Title: Characterization and functional expression of a rat genomic DNA clone encoding  
A/Reference number: A43531; MUID:90278098; PMID:2351830  
A/Accession: A43531

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-525 <DOU>  
A:Cross-references: UNIPROT:P15384; GB:M30312  
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Polander, K.; Lunt  
Neuron 4, 929-939, 1990  
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectif  
A:Reference number: JH0166; MUID:90297965; PMID:2361015  
A:Accession: JH0168  
A:Molecule type: DNA  
A:Residues: 1-180, 'G', 182-525 <SMA>  
A:Cross-references: GB:M31744; NID:9205104; PIDN:AAA41500.1; PID:9205105  
A:Experimental source: brain  
A:Note: only a list of differences from sequence S06708 is given  
R:Stuehmer, W.; Ruppertsberg, J.P.; Schroeder, K.H.; Sakmann, B.; Stocker, M.; Giese, K.F  
EMBO J. 8, 3235-3244, 1989  
A:Title: Molecular basis of functional diversity of voltage-gated potassium channels in  
A:Reference number: S06708; MUID:90059914; PMID:2555158  
A:Accession: S06708  
A:Molecule type: mRNA  
A:Residues: 1-105, 'L', 107-180, 'G', 182-525 <STU>  
A:Cross-references: EMBL:X16001; NID:957034; PIDN:CAA34132.1; PID:957035  
C:Superfamily: potassium channel protein drkl  
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane pro  
F:185-203/Domain: transmembrane #status predicted <TM1>  
F:245-266/Domain: transmembrane #status predicted <TM2>  
F:278-298/Domain: transmembrane #status predicted <TM3>  
F:313-331/Domain: transmembrane #status predicted <TM4>  
F:348-367/Domain: transmembrane #status predicted <TM5>  
F:383-392/Domain: transmembrane beta strand #status predicted <TM61>  
F:393-401/Domain: transmembrane beta strand #status predicted <TM62>  
F:409-431/Domain: transmembrane #status predicted <TM6>  
F:470/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic

Query Match 21.6%; Score 718.5; DB 2; Length 525;  
Best Local Similarity 31.0%; Pred. No. 2.4e-47;  
Matches 178; Conservative 104; Mismatches 179; Indels 113; Gaps 16;

QY 10 PPAAPAAIGMMPVANC-----PMP--LAPADKNKRODELIVLVNNGRRPOTWRTT 57  
DB 12 PEAAGGGGGDEPPGGCGVGGCGDREYPLPALPAGEDCCGERVIVINISGLRFETQTKT 71  
QY 58 LERYPDTLLGSTEKEF--FENEDTKEYFPDRODEVRCLNPFYRT--GKXLYPRYECISAYD 115  
DB 72 LCQPPETLLGDPKRMRFYDPLRNEYFPDRKNSPFDALYYQSGRIKRPVNPVDIDIFS 131  
QY 116 DELAFYGLIPRIIGDCYEEYKRENAERLMDNDSENNQESMPSLSFQTMWRAPEN 175  
DB 132 EIRIFYQ-----LGEAMEKFR-----DEGFLAREERPLPRRDFQKQVLLFEY 176  
QY 176 PHTSTLAIYFYVTGFTIYAVSVITNVETVPGTIVGSKELPC----- 218  
DB 177 PESSRPAGIAIVSLVILISIVIFCLETLR--EPRDEKDYAPSPQDVEAANNSTSGA 234  
QY 219 ---GERVVAFCUDTACVMIPTVEXYLRLFAAPSRVRFISVMSIIDVNAIMPYIGLV 275  
DB 235 SSGASSFSDPFFVETLCIIMFSEFLLVRFACPSKATFSRINMNLIDIVALIPYFITLG 294  
QY 276 M-----TNMEDVSGAFV--TLRVPRVRFIFKFSRHSQGLRIIGYTLKSCASELGLIFS 327  
DB 295 TELAEKQNGQAMSLALIRYIRLVVRIRIFKLSRHSKGLQILGQTLKASMEELGLIFP 354  
QY 328 LTMALIFATWFAEKSSASKFTSIPASFYTTIVMTTLGYGDMVPKTIAGKIFGSI 387  
DB 355 LFIGVILFSSAVYFAEADDPSSGFNSIPDAFWAVVMTVGYGDMHPVTIGKIVGSLC 414  
QY 388 SLSGVLVIALVPVIVSNFRIYHONQKADKRAQKARLARIRVAKTGSSNAYLHSKRN 447  
DB 415 AIAAGVLTIALVPVIVSNFNYFHRETEGE--QAQ-----YMH----- 451  
QY 448 GLNLAEALITGTPEEHMGKTTSLIESQHHLLHCLKTYNHEFIDEQMFEQNCMESSMQ 507  
DB 452 --VGSCHLSSSAEELRKARANSSTLSKSEYVIE--EGGMNHSARFPQTIPK----- 498

QY 508 NYPSTRSPSLSHPLGTLTTCCSRRSKKTTHLPNS 541  
DB 499 -----TGNSTATCT-----TNNPNNS 514

Search completed: April 6, 2005, 07:17:45  
Job time : 116.785 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 04:33:59 ; Search time 595.111 Seconds  
(without alignments)  
547.263 Million cell updates/sec

Title: US-10-062-879-4  
Perfect score: 3320  
Sequence: 1 MAAVAAVMPFARAATGWM.....PGPNTIPSITSNVKVSVL 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3295.5	99.3	655	1 KCD3_HUMAN	Q9UK17 homo sapien
2	3288.5	99.1	655	1 KCD3_RAT	Q62897 rattus norv
3	3278.5	98.8	655	1 KCD3_MOUSE	Q920V1 mus musculi
4	3269.5	98.5	655	1 KCD3_RABIT	Q92CIS oryctolagus
5	3266.5	98.4	655	2 Q8WNC2	Q8WNC2 mustela put
6	3126	94.2	658	2 Q9PTD3	Q9PTD3 gallus gall
7	2843.5	85.6	659	2 Q57662	Q57662 xenopus lae
8	2590	78.0	638	2 Q72W36	Q72W36 brachydanto
9	2530	76.2	630	2 Q8HYZ1	Q8HYZ1 mustela put
10	2524	76.0	630	1 KCD2_RABIT	P59995 oryctolagus
11	2523	76.0	630	1 KCD2_MOUSE	Q920V2 mus musculi
12	2519	75.9	630	1 KCD2_RAT	Q62881 rattus norv
13	2517	75.8	630	1 KCD2_HUMAN	Q92AV8 homo sapien
14	2517	75.8	632	2 Q8WNC3	Q8WNC3 gallus gall
15	2141.5	64.5	651	1 KCD1_MOUSE	Q03719 mus musculi
16	2132.5	64.2	647	1 KCD1_HUMAN	Q9NA22 homo sapien
17	2032.5	61.2	660	2 Q95PC8	Q95PC8 panulirus i
18	2026.5	61.0	660	2 Q95PC7	Q95PC7 panulirus i
19	2023.5	60.9	680	2 Q95PC6	Q95PC6 panulirus i
20	1986.5	59.8	579	2 Q95PC5	Q95PC5 panulirus i
21	1984.5	59.8	585	2 Q95PC4	Q95PC4 panulirus i
22	1981	59.7	546	2 Q26040	Q26040 panulirus i
23	1981	59.7	551	2 Q95PC0	Q95PC0 panulirus i
24	1966	59.2	561	2 Q95PC9	Q95PC9 panulirus i
25	1954.5	58.9	608	2 Q95PC3	Q95PC3 panulirus i
26	1915.5	57.7	490	1 CTRK_DROME	P17971 drosophila
27	1908.5	57.5	490	1 Q7Q1S7	Q7Q1S7 anopheles g
28	1905	57.4	800	2 Q6R4N6	Q6R4N6 ciona intes
29	1859.5	56.0	633	2 Q8RAD3	Q8RAD3 halocynthia
30	1786	53.8	471	2 Q8RAD2	Q8RAD2 halocynthia
31	1770	53.3	609	2 Q95XD1	Q95XD1 caenorhabdi

32	1654.5	49.8	372	2 Q75LS7	Q75LS7 homo sapien
33	1328.5	40.0	478	2 P91784	P91784 polychaeta
34	1303	33.2	236	2 Q619B6	Q619B6 rattus norv
35	837	25.2	409	2 P91783	P91783 polychaeta
36	770	23.2	907	1 KCB2_RAT	Q63099 rattus norv
37	768	23.1	911	2 Q727D0	Q727D0 homo sapien
38	767.5	23.1	908	2 Q18476	Q18476 loligo peal
39	766	23.1	898	2 Q91592	Q91592 xenopus lae
40	766	23.1	911	1 KCB2_HUMAN	Q92853 homo sapien
41	758	22.8	985	1 CTRK_DROME	P17970 drosophila
42	756	22.8	911	1 KCB2_RABIT	Q95111 oryctolagus
43	754.5	22.7	816	2 Q98SV4	Q98SV4 ictalurus p
44	750.5	22.6	876	2 Q91593	Q91593 xenopus lae
45	750	22.6	858	1 KCB1_HUMAN	Q14721 homo sapien

## ALIGNMENTS

RESULT 1  
KCD3\_HUMAN STANDARD; PRT; 655 AA.  
ID Q9UK17; O60576; O60577; Q9UH85; Q9UH86; Q9UK16;  
AC 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated  
DB potassium channel subunit Kv4.3).  
GN Name=KCND3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND  
RP FUNCTION.  
RC TISSUE=Heart;  
RX MEDLINE=99061682; PubMed=9843794;  
RA Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomasek G.F.;  
RT "Isolation and characterization of the human gene encoding Ito:  
RT further diversity by alternative mRNA splicing.";  
RL Am. J. Physiol. 275:H1963-H1970(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain, and Heart;  
RX MEDLINE=99218223; PubMed=10200233;  
RA Dilks D., Ling H.-P., Cockett M., Sokol P., Nunn R.;  
RT "Cloning and expression of the human Kv4.3 potassium channel.";  
RL J. Neurophysiol. 81:1974-1977(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX Calmele T.P.G., Faivre J.-F., Javre J.-L., Cheval B., Rouanet S.,  
RA Bril A.;  
RT "Long and short human isoforms of the Kv4.3 channel: cloning,  
RT expression, electrophysiology, pharmacology and phosphorylation by  
RT protein kinase C.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
RC TISSUE=Brain cortex;  
RX MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;  
RA Isbrandt D., Leichter T., Waldechuetz R., Zhu X.-R., Luhmann U.,  
RA Michel U., Sauter K., Pongs O.;  
RT "Gene structures and expression profiles of three human KCND (Kv4)  
RT potassium channels mediating A-type currents (ITO) and I(SA).";  
RL Genomics 64:144-154(2000).  
RN [5]  
RP INTERACTION WITH KCNIP2, KCNE1, KCNE2, SCN1B AND KCNA1.  
RX MEDLINE=22233757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9;  
RA Deschenes I., Tomasek G.F.;  
RT "Modulation of Kv4.3 current by accessory subunits.";

RL FEBS Lett. 528:183-188(2002).

CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.

CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4 (By similarity). Interacts with KCNE1, KCNE2, SCN1B and KCNA1.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Name=1; Synonyms=KCNDB3L, Long;

CC IsoId=09UK17-1; Sequence=Displayed;

CC Name=2; Synonyms=KCNDB3S, Short;

CC IsoId=09UK17-2; Sequence=VSP\_008826;

CC TISSUE SPECIFICITY: Highly expressed in heart and brain, in particular in cortex, cerebellum, amygdala and caudate nucleus. Detected at lower levels in liver, skeletal muscle, kidney and pancreas. Isoform 1 predominates in most tissues. Isoform 1 and isoform 2 are detected at similar levels in brain, skeletal muscle and pancreas.

CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.

CC -----

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CC -----

DR EMBL; AF048712; AAC05121.1; -

DR EMBL; AF048713; AAC05122.1; -

DR EMBL; AF187963; AAF01044.1; -

DR EMBL; AF187964; AAF01045.1; -

DR EMBL; AF205856; AAF20924.1; -

DR EMBL; AF205857; AAF20925.1; -

DR EMBL; AF120491; AAD38898.1; -

DR EMBL; AF166011; AAF68177.1; -

DR EMBL; AF166009; AAF68177.1; JOINED.

DR EMBL; AF166010; AAF68177.1; JOINED.

DR EMBL; AF166011; AAF68178.1; -

DR EMBL; AF166009; AAF68178.1; JOINED.

DR HSSP; Q16968; 1A68.

DR GeneW; HGNC:6239; KCND3.

DR MIT; 605411; -

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR001622; K+channel\_pore.

DR InterPro; IPR003091; K\_channel.

DR InterPro; IPR003131; K\_tetra.

DR InterPro; IPR004056; KV4channel.

DR InterPro; IPR003968; KV\_channel.

DR InterPro; IPR005820; M+channel\_nlg.

DR InterPro; IPR003975; Shal\_channel.

DR Pfam; PF00520; Ion\_trans\_1.

DR Pfam; PF02214; K\_tetra\_1.

DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PR01518; KV4CHANNEL.

DR PRINTS; PR01491; KVCHANNEL.

DR PRINTS; PR01497; SHALCHANNEL.

KM Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane; Transport; Voltage-gated channel.

KW DOMAIN 1 181 Cytoplasmic (Potential).

FT TRANSMEM 182 202 Segment S1 (Potential).

FT TRANSMEM 222 242 Segment S2 (Potential).

FT	DOMAIN	243	256	Cytoplasmic (Potential).
FT	TRANSMEM	257	277	Segment S3 (Potential).
FT	TRANSMEM	287	307	Segment S4 (Potential).
FT	DOMAIN	308	320	Cytoplasmic (Potential).
FT	TRANSMEM	321	341	Segment S5 (Potential).
FT	TRANSMEM	360	380	Segment H5 (pore-forming) (Potential).
FT	TRANSMEM	382	402	Segment S6 (Potential).
FT	DOMAIN	403	655	Cytoplasmic (Potential).
FT	SITE	372	372	Selectivity filter (By similarity).
FT	VARSPLIC	468	506	Missing (in isoform 2).
FT	CONFLICT	239	239	/Prid=VSP_008826.
FT	CONFLICT	375	375	V -> G (in Ref. 1).
FT	CONFLICT	408	408	P -> L (in Ref. 1).
FT	CONFLICT	452	452	R -> G (in Ref. 2).
FT	CONFLICT	531	531	T -> Q (in Ref. 2).
FT	CONFLICT	564	564	A -> D (in Ref. 2).
FT	CONFLICT	646	646	A -> T (in Ref. 1).
FT	CONFLICT	654	654	V -> A (in Ref. 3 and 4).
SO	SEQUENCE	655 AA;	73479 MW;	ADCB502A97204764 CRC64;

  

Query Match	99.3%	Score 3295.5;	DB 1;	Length 655;
Best Local Similarity	96.9%	Pred. No. 7.7e-198;		
Matches 635;	Conservative 0;	Mismatches 1;	Indels 19;	Gaps 1;

  

QY	1	MAAGVAAWLPFAFAAAIGWMPVANCMPPLAPADKNKRODELIVLVNSGRRFQWRRTLLER	60
DB	1	MAAGVAAWLPFAFAAAIGWMPVANCMPPLAPADKNKRODELIVLVNSGRRFQWRRTLLER	60
QY	61	YPTTLGSTEKEPEFEDTKEVFRDDEYFRVCLNFTRTGKHAYREICISAYDEELAF	120
DB	61	YPTTLGSTEKEPEFEDTKEVFRDDEYFRVCLNFTRTGKHAYREICISAYDEELAF	120
QY	121	YGLPELIGCCCEYKDRRENAERLMDNDSENNQESNPSSFPQTMRAENPHTST	180
DB	121	YGLPELIGCCCEYKDRRENAERLMDNDSENNQESNPSSFPQTMRAENPHTST	180
QY	181	LALVYYVTGFFIYAVSVITNVVETVPCGTVPVSGKELPCGGRYSVAFCLDTACMIFTV	240
DB	181	LALVYYVTGFFIYAVSVITNVVETVPCGTVPVSGKELPCGGRYSVAFCLDTACMIFTV	240
QY	241	YLRLFAAPSRYPFRISVMSIDVVAIMPYIGLVMTNEDVSGAFYTLRVFVFRIEKF	300
DB	241	YLRLFAAPSRYPFRISVMSIDVVAIMPYIGLVMTNEDVSGAFYTLRVFVFRIEKF	300
QY	301	SRHSQGRILGYTLKSCASELGLFLSLTMAIIFPAVMPYAKGSASAKFTSIPASFMY	360
DB	301	SRHSQGRILGYTLKSCASELGLFLSLTMAIIFPAVMPYAKGSASAKFTSIPASFMY	360
QY	361	TIYMTTLGYGDMVPKTIAGKIFGSIISGLVIVLPPVIVSNFSRIYHQNQRADKRR	420
DB	361	TIYMTTLGYGDMVPKTIAGKIFGSIISGLVIVLPPVIVSNFSRIYHQNQRADKRR	420
QY	421	AQKARLARIYVAKTGSNNAYLHSGKNGLNELBELTGPBEHMGKTSILISQHHLL	480
DB	421	AQKARLARIYVAKTGSNNAYLHSGKNGLNELBELTGPBEHMGKTSILISQHHLL	480
QY	481	HCEKTT-----NHERIDQMEONQESSMONTYPTSPSSHP	521
DB	481	HCEKTT-----NHERIDQMEONQESSMONTYPTSPSSHP	521
QY	522	GLTTCCSRSSKKTTHLNSNLPRTLRSQMOELSTHIQSEOPSLTSSSINLKADG	581
DB	522	GLTTCCSRSSKKTTHLNSNLPRTLRSQMOELSTHIQSEOPSLTSSSINLKADG	581
QY	541	GLTTCCSRSSKKTTHLNSNLPRTLRSQMOELSTHIQSEOPSLTSSSINLKADG	600
DB	541	GLTTCCSRSSKKTTHLNSNLPRTLRSQMOELSTHIQSEOPSLTSSSINLKADG	600
QY	582	LRPNCSTQITTAIISIPPPALTPGESSRPPASPCPNTNIDSTSNVVKSVL	636
DB	582	LRPNCSTQITTAIISIPPPALTPGESSRPPASPCPNTNIDSTSNVVKSVL	636
QY	601	LRENCKTSQITTAIISIPPPALTPGESSRPPASPCPNTNIDSTSNVVKSVL	655
DB	601	LRENCKTSQITTAIISIPPPALTPGESSRPPASPCPNTNIDSTSNVVKSVL	655

  

RESULT 2	KCD3 RAT	STANDARD;	PRT;	655 AA.
ID	KCD3_RAT	STANDARD;	PRT;	655 AA.

AC Q62897; 008723; P70622; Q63286; Q99P42;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated  
DE potassium channel subunit Kv4.3).  
GN Name=Kcnd3;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
RX MEDLINE=96428386; PubMed=8831489;  
RA Dixon J.E., Shi W., Wang H.-S., McDonald C., Yu H., Wymore R.S.,  
RA Cohen I.S., McKinnon D.;  
RT "Role of the Kv4.3 K+ channel in ventricular muscle. A molecular  
RT correlate for the transient outward current.";  
RL Circ. Res. 79:659-668(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=96317227; PubMed=8734615;  
RA Sexodio P., Vega-Saenz de Miera E., Rudy B.;  
RT "Cloning of a novel component of A-type K+ channels operating at  
RT subthreshold potentials with unique expression in heart and brain.";  
RL J. Neurophysiol. 75:2174-2179(1996).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 3), FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Hippocampus;  
RX MEDLINE=97154683; PubMed=9001401; DOI=10.1016/S0014-5793(96)01388-9;  
RA Tsaur M.-L., Chou C.-C., Shih Y.-H., Wang H.-L.;  
RT "Cloning, expression and CNS distribution of Kv4.3, an A-type K+  
RT channel alpha subunit.";  
RL FEBS Lett. 400:215-220(1997).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Smooth muscle, and Vas deferens;  
RX MEDLINE=98111009; PubMed=9450548; DOI=10.1016/S0014-5793(97)01483-X;  
RA Ohya S., Tanaka M., Oku T., Asai Y., Watanabe M., Giles W.R.,  
RA Imaizunari Y.;  
RT "Molecular cloning and tissue distribution of an alternatively spliced  
RT variant of an A-type K+ channel alpha-subunit, Kv4.3 in the rat.";  
RL FEBS Lett. 420:47-53(1997).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;  
RX MEDLINE=21402960; PubMed=11427525; DOI=10.1074/jbc.M101058200;  
RA Song M., Helguera G., Eghbali M., Zhu N., Zarei M.M., Olcese R.,  
RA Toro L., Stelani B.;  
RT "Remodeling of Kv4.3 potassium channel gene expression under the  
RT control of sex hormones.";  
RL J. Biol. Chem. 276:31883-31890(2001).  
RN [6]  
RP SEQUENCE OF 455-606 FROM N.A. (ISOFORM 1).  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=97460452; PubMed=9314834;  
RA Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Levitan E.S.;  
RT "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel subunit  
RT mRNAs in ventricles of renovascular hypertensive rats.";  
RL Circ. Res. 81:533-539(1997).  
RN [7]  
RP INTERACTION WITH KCNIP1, KCNIP2 AND KCNIP3.  
RX MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;  
RA An W.F., Bowby M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,  
RA Hinson J.W., Matteson K.I., Strassler B.W., Trimmer J.S., Rhodes K.J.;  
RT "Modulation of A-type potassium channels by a family of calcium  
RT sensors";  
RL Nature 403:553-556(2000).  
RN [8]  
RP SUBCELLULAR LOCATION.  
RX MEDLINE=22128857; PubMed=12006572; DOI=10.1074/jbc.M203651200;  
RA Takimoto K., Yang E.-K., Conforti L.;

RT "Palmitoylation of KChIP splicing variants is required for efficient  
RT cell surface expression of Kv4.3 channels.";  
RL J. Biol. Chem. 277:26904-26911(2002).  
RN [9]  
RP INTERACTION WITH KCNIP4.  
RX MEDLINE=21664433; PubMed=11805342; DOI=10.1073/pnas.022509299;  
RA Holmgvist M.H., Cao J., Hernandez-Pineda R., Jacobson M.D.,  
RA Carroll K.I., Sung M.A., Betty M., Ge P., Glibrid K.J., Brown M.E.,  
RA Jurnan M.E., Lawson D., Slios-Santiago I., Xie Y., Covarrubias M.,  
RA Rhodes K.J., Stefano P.S., An W.F.;  
RT "Elimination of fast inactivation in Kv4 A-type potassium channels by  
RT an auxiliary subunit domain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:1035-1040(2002).  
RN [10]  
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
RP inactivating A-type potassium channels. May contribute to I(TO)  
RP current in heart and I(Sa) current in neurons. Channel properties  
RP are modulated by interactions with other alpha subunits and with  
RP regulatory subunits.  
RN [11]  
RP SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.  
RN Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
RN KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNA1 (by  
RN similarity).  
RN [12]  
RP SUBCELLULAR LOCATION: Integral membrane protein. Interaction with  
RN palmitoylated KCNIP2 and KCNIP3 enhances cell surface expression.  
RN [13]  
RP ALTERNATIVE PRODUCTS:  
RN Event=Alternative splicing; Named isoforms=3;  
RN Name=1; Synonyms=Kv4.3 long form;  
RN IsoId=Q62897-1; Sequence=Displayed;  
RN Name=2;  
RN IsoId=Q62897-2; Sequence=VSP\_008831;  
RN Name=3;  
RN IsoId=Q62897-3; Sequence=VSP\_008831, VSP\_008832;  
RN [14]  
RP TISSUE SPECIFICITY: Highly expressed in brain, in particular in  
RN the retrosplenial cortex, medial habenula, anterior thalamus,  
RN hippocampus, cerebellum and lateral geniculate and superior  
RN colliculus. Highly expressed in heart atrium and throughout the  
RN ventricle wall, in lung and vas deferens.  
RN [15]  
RP DOMAIN: The segment S4 is probably the voltage-sensor and is  
RN characterized by a series of positively charged amino acids at  
RN every third position.  
RN [16]  
RP SIMILARITY: Belongs to the potassium channel family. D (Shal)  
RN subfamily.  
RN [17]  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U42975; AAC52695.1; -;  
CC EMBL: U75448; AAB18337.1; -;  
CC EMBL: L48619; AAB80459.1; -;  
CC EMBL: AF334791; AAK07651.1; -;  
CC EMBL: AB003587; BAA24525.1; -;  
CC EMBL: U92897; AAB53321.1; -;  
CC HSSP: Q16968; 1A68.  
CC InterPro: IPR005821; Ion trans.  
CC InterPro: IPR001622; K+channel\_pore.  
CC InterPro: IPR003091; K\_channel.  
CC InterPro: IPR003131; K\_tetra.  
CC InterPro: IPR004056; KV43channel.  
CC InterPro: IPR003968; Kv channel.  
CC InterPro: IPR005820; M-channel\_nlg.  
CC InterPro: IPR003975; Shal channel.  
CC Pfam: PF00520; Ion trans\_1.  
CC Pfam: PF02214; K\_tetra\_1.  
CC PRINTS: PR00169; KCHANNEL.  
CC PRINTS: PR01518; KV43CHANNEL.  
CC PRINTS: PR01491; KV3CHANNEL.  
CC PRINTS: PR01497; SHALCHANNEL.  
CC Alternative splicing; Ion transport; Ionic channel; Multigene family;

KM Potassium; Potassium channel; Potassium transport; Transmembrane;  
 KM Transport; Voltage-gated channel.  
 FT DOMAIN 1 181 Cytoplasmic (Potential).  
 FT TRANSMEM 182 202 Segment S1 (Potential).  
 FT TRANSMEM 222 242 Segment S2 (Potential).  
 FT TRANSMEM 243 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 277 Segment S3 (Potential).  
 FT TRANSMEM 287 307 Segment S4 (Potential).  
 FT TRANSMEM 308 320 Cytoplasmic (Potential).  
 FT TRANSMEM 321 341 Segment S5 (Potential).  
 FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).  
 FT TRANSMEM 382 402 Segment S6 (Potential).  
 FT DOMAIN 403 655 Cytoplasmic (Potential).  
 FT SITE 367 372 Selectivity filter (By similarity).  
 FT VARSPIC 488 506 Missing (in isoform 2 and isoform 3).  
 FT VARSPIC 608 655 /Ftrid=VSP\_008831.  
 FT VARSPIC 608 655 VAVSVL -> QDOEPGRVVTCKDEITLCT (in isoform 3).  
 FT CONFLICT 124 124 /Ftrid=VSP\_008832.  
 FT CONFLICT 404 404 L -> H (in Ref. 3).  
 FT CONFLICT 569 569 S -> T (in Ref. 2 and 5).  
 FT CONFLICT 631 631 S -> T (in Ref. 3).  
 FT CONFLICT 654 654 P -> A (in Ref. 2).  
 FT CONFLICT 654 654 V -> A (in Ref. 1 and 4).  
 SQ SEQUENCE 655 AA; 73513 MW; 26BC512BD069C09 CRC64;  
 Query Match 99.1%; Score 3288.5; DB 1; Length 655;  
 Best Local Similarity 96.8%; Pred. No. 2.1e-197;  
 Matches 634; Conservative 1; Mismatches 1; Indels 19; Gaps 1;  
 QY 1 MAAGVAAAMLPFAAAGMPPVANCMPPLAPADKNKRDGLVLANSGRRFQWRTTLER 60  
 DB 1 MAAGVAAAMLPFAAAGMPPVANCMPPLAPADKNKRDGLVLANSGRRFQWRTTLER 60  
 QY 61 YPDTLLGSTEKEPEFNEDETEKEFPDRDPVEFRVCLNFTYRTGKLHYPRYECISAYDELA 120  
 DB 61 YPDTLLGSTEKEPEFNEDETEKEFPDRDPVEFRVCLNFTYRTGKLHYPRYECISAYDELA 120  
 QY 121 YGILPEITIGCCYEEYDRKRENAERLMDNDSNNQNSPSSISFRQTMRAENPTST 180  
 DB 121 YGILPEITIGCCYEEYDRKRENAERLMDNDSNNQNSPSSISFRQTMRAENPTST 180  
 QY 181 LAIVFYVYTGFFLAIVSVITNVETPCGTGPGSKELCGGRYSVAFCLDTACVMIPTVE 240  
 DB 181 LAIVFYVYTGFFLAIVSVITNVETPCGTGPGSKELCGGRYSVAFCLDTACVMIPTVE 240  
 QY 241 YLLRLFAAPSRYPFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRFRVRIEKF 300  
 DB 241 YLLRLFAAPSRYPFRIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRFRVRIEKF 300  
 QY 301 SRHSQGRIRIGYTLKSCASGLGLFSLTMAIIIFAVMYAEKGSASAKFTSIPAFWY 360  
 DB 301 SRHSQGRIRIGYTLKSCASGLGLFSLTMAIIIFAVMYAEKGSASAKFTSIPAFWY 360  
 QY 361 TIYMTLTGSDMWPKTIAGKIFGSCISGLVIALPVPIVSNFRIYHONORADKRR 420  
 DB 361 TIYMTLTGSDMWPKTIAGKIFGSCISGLVIALPVPIVSNFRIYHONORADKRR 420  
 QY 421 AOKKARLARIRVAKTSSNAYLHRSKNGLLNEALELTGPEEBHMGKTTSLIESQHHL 480  
 DB 421 AOKKARLARIRVAKTSSNAYLHRSKNGLLNEALELTGPEEBHMGKTTSLIESQHHL 480  
 QY 481 HCLEKTT-----NHFIDEMFQONCMESMOMYESTRSPSLSSHP 521  
 DB 481 HCLEKTT-----NHFIDEMFQONCMESMOMYESTRSPSLSSHP 521  
 QY 522 GLTTTCCSRSSKKTTHLPSNLPATRLRSQMOELSTHIQSGEOPSLTSSSSNLKADG 581  
 DB 522 GLTTTCCSRSSKKTTHLPSNLPATRLRSQMOELSTHIQSGEOPSLTSSSSNLKADG 581  
 QY 582 LRPNCKTSQITTAISIPTPALTPBESRPPSPAPNTNIPSTSNVAVSVL 636  
 DB 582 LRPNCKTSQITTAISIPTPALTPBESRPPSPAPNTNIPSTSNVAVSVL 636

DB 601 LRPNCKTSQITTAISIPTPALTPBESRPPSPAPNTNIPSTSNVAVSVL 655  
 RESULT 3  
 ID KC03\_MOUSE STANDARD; PRT; 655 AA.  
 AC Q9Z0V1; Q8CC44; Q9Z0V0;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated potassium channel subunit Kv4.3).  
 GN Name=Kcnd3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN (1)  
 RC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;  
 RA Tanaka H., Janzen K., Minkfein R.J., Fiset C., Clark R.B., Giles W.R.;  
 RT "Cloning and functional characterization of mouse heart K+ channel alpha subunits, Kv1.5, Kv4.2 and Kv4.3";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RC SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki I., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S., Nikaado I., Osato Y., Saito R., Suzuki H., Yamana I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schirral L.M., Kanpin A., Matsuda H., Batelov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chotia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough U., Grimmer S., Gustlincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L., Konekaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikti H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arahawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN (3)  
 RC INTERACTION WITH KCNIP3.  
 RX MEDLINE=21481767; PubMed=11598014; DOI=10.1093/emboj/20.20.5715;  
 RA Liles B., Franz O., Sewing S., Bruns R., Neuhoff H., Roeper J.;  
 RT "Tuning pacemaker frequency of individual dopaminergic neurons by Kv4.3 and KChip3.1 transcription";  
 RL EMBO J. 20:5715-5724 (2001).  
 RN (4)  
 RC INTERACTION WITH KCND2 AND KCNIP2.  
 RX MEDLINE=21906624; PubMed=11909823;  
 RX DOI=10.1161/01.RES.0000012664.05949.B0;  
 RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S., Nerbonne J.M.;  
 RT "Role of heteromultimers in the generation of myocardial transient outward K+ currents";  
 RL Circ. Res. 90:586-593 (2002).



CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
 CC inactivating A-type potassium channels. May contribute to I(TO)  
 CC current in heart and I(Sa) current in neurons. Channel properties  
 CC are modulated by interactions with other alpha subunits and with  
 CC regulatory subunits.  
 CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2.  
 CC Associates with the regulatory subunits KCNP1, KCNP2, KCNP3 and  
 CC KCNP4. Interacts with KCNE1, KCNE2, SCN1B and KCNA1 (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=Kv4.3L;  
 CC IsoId=Q9Z0V1-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Kv4.3M;  
 CC IsoId=Q9Z0V1-2; Sequence=VSP\_008827;  
 CC Name=3;  
 CC IsoId=Q9Z0V1-3; Sequence=VSP\_008828, VSP\_008829;  
 CC Note=May be due to intron retention. No experimental  
 CC confirmation available;  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shall)  
 CC subfamily.  
 CC -----  
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 CC -----  
 CC EMBL; AF107781; AAD16973.1; -  
 CC EMBL; AF107782; AAD16974.1; -  
 CC EMBL; AK033962; BAC28529.1; -  
 CC HSSP; Q16968; 1A68  
 CC MGD; MGI:1928743; Kcnd3.  
 CC InterPro; IPR005821; Ion\_trans.  
 CC InterPro; IPR001622; K+channel\_pore.  
 CC InterPro; IPR003091; K\_channel.  
 CC InterPro; IPR003131; K\_tetra.  
 CC InterPro; IPR004056; Kv43\_channel.  
 CC InterPro; IPR003968; Kv\_channel.  
 CC InterPro; IPR005820; M+channel\_nlg.  
 CC InterPro; IPR003975; Shal\_channel.  
 CC Pfam; PF00220; Ion\_trans; 1.  
 CC Pfam; PF02214; K\_tetra; 1.  
 CC PRINTS; PR00169; KCHANNEL.  
 CC PRINTS; PR01518; KV43CHANNEL.  
 CC PRINTS; PR01491; KVCHANNEL.  
 CC PRINTS; PR01497; SHALCHANNEL.  
 CC Alternative splicing; Ion transport; Ionic channel; Multigene family;  
 CC Potassium; Potassium channel; Potassium transport; Transmembrane;  
 CC Transposum; Voltage-gated channel.  
 CC DOMAIN 1 181  
 CC TRANSMEM 182 202 Cytoplasmic (Potential).  
 CC TRANSMEM 222 242 Segment S1 (Potential).  
 CC DOMAIN 243 256 Segment S2 (Potential).  
 CC TRANSMEM 257 277 Cytoplasmic (Potential).  
 CC TRANSMEM 287 307 Segment S3 (Potential).  
 CC DOMAIN 308 320 Segment S4 (Potential).  
 CC TRANSMEM 321 341 Cytoplasmic (Potential).  
 CC TRANSMEM 360 380 Segment S5 (Potential).  
 CC TRANSMEM 382 402 Segment H5 (pore-forming) (Potential).  
 CC DOMAIN 403 655 Segment S6 (pore-forming) (Potential).  
 CC SITE 367 372 Selectivity filter (By similarity).  
 CC VASPLIC 488 531 GHSYVDPLSLVSTSTKNEHFDIQMFQNCHESSMONT  
 CC PST -> VSSSLPPASLTSQSGCTHVIIPRESSVFPQ  
 CC SKTVSLPLG (in isoform 3).  
 CC /FTId=VSP\_008828.  
 CC Missing (in isoform 2).  
 CC VASPLIC 488 506

FT /FTId=VSP\_008827.  
 FT VASPLIC 532 655 Missing (in isoform 3).  
 FT /FTId=VSP\_008829.  
 SQ SEQUENCE 655 AA; 73462 MW; 17FC5EAEC868B33 CRC64;  
 Query Match 98.8%; Score 3278.5; DB 1; Length 655;  
 Best Local Similarity 96.5%; Pred. No. 8.9e-197;  
 Matches 632; Conservative 1; Mismatches 3; Indels 19; Gaps 1;  
 QY 1 MAAGVAAALPFAARAALGMPVANCMPPLAPADKKKKODELIVLVNNGRRFQTWRTTLER 60  
 DB 1 MAAGVAAALPFAARAALGMPVANCMPPLAPADKKKKODELIVLVNNGRRFQTWRTTLER 60  
 QY YPDTLLSGTEKEFFNEPTKEKFFPPRDEVRVCVNFPRGTGLHPRYECISAYDELA 120  
 DB 61 YPDTLLSGTEKEFFNEPTKEKFFPPRDEVRVCVNFPRGTGLHPRYECISAYDELA 120  
 QY YGILPEIIGDCCYBEYKORKTENMERLMDNDSENNQSMPSLSFQTMWRAFENPHST 180  
 DB 121 YGILPEIIGDCCYBEYKORKTENMERLMDNDSENNQSMPSLSFQTMWRAFENPHST 180  
 QY LALVEYVYTGFFIAVSITNVEVTPCGTVPSKELPCGERYSVAFPCLDIACVMI 240  
 DB 181 LALVEYVYTGFFIAVSITNVEVTPCGTVPSKELPCGERYSVAFPCLDIACVMI 240  
 QY LALVEYVYTGFFIAVSITNVEVTPCGTVPSKELPCGERYSVAFPCLDIACVMI 240  
 DB 181 LALVEYVYTGFFIAVSITNVEVTPCGTVPSKELPCGERYSVAFPCLDIACVMI 240  
 QY YLLRLFAAPSRKRFIRSVMSIIDVVALMPYITGLVMTNNEVSGAFVTLRFRVRIRKF 300  
 DB 241 YLLRLFAAPSRKRFIRSVMSIIDVVALMPYITGLVMTNNEVSGAFVTLRFRVRIRKF 300  
 QY SRHSGGLILGVTLLKSCASEGFLFSLTMMIIFPATMFAEKSSASKFTSPASFMY 360  
 DB 301 SRHSGGLILGVTLLKSCASEGFLFSLTMMIIFPATMFAEKSSASKFTSPASFMY 360  
 QY SRHSGGLILGVTLLKSCASEGFLFSLTMMIIFPATMFAEKSSASKFTSPASFMY 360  
 DB 301 SRHSGGLILGVTLLKSCASEGFLFSLTMMIIFPATMFAEKSSASKFTSPASFMY 360  
 QY TIVTWTLLGYDMPVKTIAGKIFGSLGSLVIALPVPYIVSNFSRIYHONRADKRR 420  
 DB 361 TIVTWTLLGYDMPVKTIAGKIFGSLGSLVIALPVPYIVSNFSRIYHONRADKRR 420  
 QY AOKKARLARIRVAKTGGSSNATLHSGRNLINBALELTGTPEBEHMKTTSLIESGHHLL 480  
 DB 421 AOKKARLARIRVAKTGGSSNATLHSGRNLINBALELTGTPEBEHMKTTSLIESGHHLL 480  
 QY HCLEKTT-----NHEFIDEQMFQNCHESSMONTPTSPSLSSHP 521  
 DB 481 HCLEKTT-----NHEFIDEQMFQNCHESSMONTPTSPSLSSHP 521  
 QY HCLEKTTGLSLVDDPLLSVSTSTIKNHEFIDEQMFQNCHESSMONTPTSPSLSSHS 540  
 DB 481 HCLEKTTGLSLVDDPLLSVSTSTIKNHEFIDEQMFQNCHESSMONTPTSPSLSSHS 540  
 QY GLTTCCSRSKKKTTHLPNSNLPATRLRSWQELSTLHIQSEOPSLTTSRSLSLNKADG 581  
 DB 541 GLTTCCSRSKKKTTHLPNSNLPATRLRSWQELSTLHIQSEOPSLTTSRSLSLNKADG 581  
 QY LRPNCKTSQITTAIISTPTPALTPEGSRPPSPGPNNTIPISTTSNVVYKVSU 636  
 DB 601 LRPNCKTSQITTAIISTPTPALTPEGSRPPSPGPNNTIPISTTSNVVYKVSU 636  
 Db 601 LRPNCKTSQITTAIISTPTPALTPEGSRPPSPGPNNTIPISTTSNVVYKVSU 655  
 RESULT 4  
 KCD3\_RABIT  
 ID KCD3\_RABIT STANDARD; PRT; 655 AA.  
 AC O9TIT5;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 3 (Voltage-gated  
 DE potassium channel subunit Kv4.3).  
 GN Name=KCND3;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_Taxid=9986;  
 OX [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=New Zealand white; TISSUE=Corneal endothelium;  
 RP Rae J.L.;  
 RA "Ion channels in cornea endothelium.";  
 RT

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE OF 73-645 FROM N.A. (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=22117972; PubMed=12122138;  
 RA Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G., Obeso A., Gantofina M.D., Gonzalez C.;  
 RT "Molecular identification of Kv alpha subunits that contribute to the oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit carotid body."  
 RT J. Physiol. (Lond.) 542:369-382(2002).  
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(to) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.  
 CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCMB1 (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Name=1; Synonyms=long;  
 CC IsoId=Q9YTT5-1; Sequence=displayed;  
 CC Name=2; Synonyms=short;  
 CC IsoId=Q9YTT5-2; Sequence=VSP\_008830;  
 CC TISSUE SPECIFICITY: Detected in carotid body chemoreceptor cells and in frontal cortex.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal) subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; AF198445; AAF06021.1; -;  
 CC EMBL; AF493549; AAM46843.1; -;  
 CC HSSP; Q16968; 1A68.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K-channel\_pore.  
 DR InterPro; IPR003091; K\_channel.  
 DR InterPro; IPR003131; K\_tetra.  
 DR InterPro; IPR004056; KV43channel.  
 DR InterPro; IPR003968; Kv channel.  
 DR InterPro; IPR005820; M-channel\_nlg.  
 DR InterPro; IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PRO0169; KCHANNEL.  
 DR PRINTS; PRO1518; KV43CHANNEL.  
 DR PRINTS; PRO1491; KVCHANNEL.  
 DR PRINTS; PRO1497; SHALCHANNEL.  
 KW Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane; Transmembrane; Voltage-gated channel.  
 FT DOMAIN 1 181 Cytoplasmic (Potential).  
 FT TRANSMEM 182 202 Segment S1 (Potential).  
 FT TRANSMEM 222 242 Segment S2 (Potential).  
 FT DOMAIN 243 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 277 Segment S3 (Potential).  
 FT TRANSMEM 287 307 Segment S4 (Potential).  
 FT DOMAIN 308 320 Cytoplasmic (Potential).  
 FT TRANSMEM 321 341 Segment S5 (Potential).  
 FT TRANSMEM 360 380 Segment H5 (pore-forming) (Potential).  
 FT TRANSMEM 382 402 Segment S6 (Potential).

FT DOMAIN 403 655 Cytoplasmic (Potential).  
 FT SITE 367 372 Selectivity filter (By similarity).  
 FT VARSPLIC 488 506 Missing (in isoform 2).  
 FT FTID=VSP\_008830.  
 SQ SEQUENCE 655 AA; 73380 MW; C6AE9E895415FAF9 CRG64;  
 Query Match 98.5%; Score 3269.5; DB 1; Length 655;  
 Best Local Similarity 96.2%; Pred. No. 3.2e-196;  
 Matches 630; Conservative 2; Mismatches 4; Indels 19; Gaps 1;  
 QY 1 MAAGVAAVLPEFAAAALIGMPVANCMPPLADKNGKROBELLYLVNSGRRFQWRITLLER 60  
 DB 1 MAAGVAAVLPEFAAAALIGMPVANCMPPLADKNGKROBELLYLVNSGRRFQWRITLLER 60  
 QY 61 YPDTLLGSTEKEKEFFNEPTKEVEFDPRPEVFCVLFNYFTGKLHYRYECISAYDDELAF 120  
 DB 61 YPDTLLGSTEKEKEFFNEPTKEVEFDPRPEVFCVLFNYFTGKLHYRYECISAYDDELAF 120  
 QY 121 YGILPEIIGDCYEEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNHTST 180  
 DB 121 YGILPEIIGDCYEEYKDKRENAERLMDNDSENNOESMPSLSFRQTMRAEPNHTST 180  
 QY 181 LALVEFYVGFPLAVSVITNVVETVPCGTPGSKELPCGERYSVAFFCLDTACVMLFTYE 240  
 DB 181 LALVEFYVGFPLAVSVITNVVETVPCGTPGSKELPCGERYSVAFFCLDTACVMLFTYE 240  
 QY 241 YLRLFAASRYRFFIRSVNSIIDVVAIMPYIGLVVNTNEDVSGAEVTLRVFRFRIKPE 300  
 DB 241 YLRLFAASRYRFFIRSVNSIIDVVAIMPYIGLVVNTNEDVSGAEVTLRVFRFRIKPE 300  
 QY 301 SRHSQGLRLIGYTLKSCASLEGFLSLTMAIITFTWTFYAEKGSASAKFTSIIPASFWY 360  
 DB 301 SRHSQGLRLIGYTLKSCASLEGFLSLTMAIITFTWTFYAEKGSASAKFTSIIPASFWY 360  
 QY 361 TIVYMTTIGVDMVPTIAGIKRIGSICSLGVIVLAPVIVSNSRITVHQQRDKRR 420  
 DB 361 TIVYMTTIGVDMVPTIAGIKRIGSICSLGVIVLAPVIVSNSRITVHQQRDKRR 420  
 QY 421 AQKKARLARIYAKTSSNAYLHSSKNGGLNEALLETGPDEEHMKTTSLIRSOHHLL 480  
 DB 421 AQKKARLARIYAKTSSNAYLHSSKNGGLNEALLETGPDEEHMKTTSLIRSOHHLL 480  
 QY 481 HCLEKTT-----NHEFIDQMFQNCMESSMONTYSTRSPSSSHP 521  
 DB 481 HCLEKTTGSLVDDBLLSVRTSTINKHEFIDQMFQNCMESSMONTYSTRSPSSSHP 521  
 QY 522 GLTTCCSRRSKKTTLPLNSNLPATRLRSMOELSTHIGSBOPSLTTSSSINLKADG 581  
 DB 522 GLTTCCSRRSKKTTLPLNSNLPATRLRSMOELSTHIGSBOPSLTTSSSINLKADG 581  
 QY 582 LRPNCKTSQITTAIISIPPPALTPGESRPPASGPMNTIPSITSNVKVSVL 636  
 DB 601 LRPNCKTSQITTAIISIPPPALTPGESRPPASGPMNTIPSITSNVKVSVL 655  
 RESULT 5  
 Q8WNO2 PRELIMINARY; PRT; 655 AA.  
 ID Q8WNO2  
 AC Q8WNO2;  
 DT 01-MAR-2002 (Trembl) 20, Created)  
 DT 01-MAR-2002 (Trembl) 20, Last sequence update)  
 DT 01-OCT-2003 (Trembl) 25, Last annotation update)  
 DE Voltage-gated potassium channel Kv4.3 long form.  
 OS Muscula putorius furo (Fetret).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Muscula.  
 OC NCBI\_TaxID=9669;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=21896086; PubMed=11897837;  
 RA Patel S.P., Campbell D.L., Morales M.J., Strauss H.C.;

RT "Heterogeneous expression of KChIP2 isoforms in the ferret heart."  
 RL J. Physiol. 539:649-656(2002).  
 DR EMBL; AF454388; AAL51038.1; -.  
 DR HSSP; Q63881; 1S6C.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PR01518; KV43CHANNEL.  
 DR PRINTS; PR01491; KVCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 DR Ion transport; Ionic channel; Transmembrane; Transport.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 655 AA; 73375 MW; 3DD3E94819FEF6C1 CRC64;

Query Match 98.4%; Score 3266.5; DB 2; Length 655;  
 Best Local Similarity 95.9%; Pred. No. 5e-196;  
 Matches 628; Conservative 4; Mismatches 4; Indels 19; Gaps 1;

OY 1 MAAGVAAALPPARAAAIAGMPVANCMPMLAPADKXKRODELIVLVSGRRFQMTTLIER 60  
 DB 1 MAAGVAAALPPARAAAIAGMPVANCMPMLAPADKXKRODELIVLVSGRRFQMTTLIER 60  
 OY 61 YPDLLGSTEKEFFENEDTKEYFPDRDEVEFRVCVLFYRTGKLHYPRYECISAYDELAIF 120  
 DB 61 YPDLLGSTEKEFFENEDTKEYFPDRDEVEFRVCVLFYRTGKLHYPRYECISAYDELAIF 120  
 OY 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAFENPHST 180  
 DB 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAFENPHST 180  
 OY 181 LALVFYVYTGFFIAVSITNVETVPCGTVGSKELPCGERSVAFPCLDIACWIFVE 240  
 DB 181 LALVFYVYTGFFIAVSITNVETVPCGTVGSKELPCGERSVAFPCLDIACWIFVE 240  
 OY 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLVFRVRIKPF 300  
 DB 241 YLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLVFRVRIKPF 300  
 OY 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVVFYAEKSSASKFTSIPASFW 360  
 DB 301 SRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVVFYAEKSSASKFTSIPASFW 360  
 OY 361 TIVMTTLGVDMPVKTAKIGFISGSLGVLVIALVPIVSNFSRIYHONQADRR 420  
 DB 361 TIVMTTLGVDMPVKTAKIGFISGSLGVLVIALVPIVSNFSRIYHONQADRR 420  
 OY 421 AOKKARLARIRVATKSSNAIYHSGKGLTEALEHMTPEBEHVGKSTLSIESHHLL 480  
 DB 421 AOKKARLARIRVATKSSNAIYHSGKGLTEALEHMTPEBEHVGKSTLSIESHHLL 480  
 OY 481 HCLEKTT-----NHEFTDEQMEONCMSSMONTPTSRPSLSHP 521  
 DB 481 HCLEKTT-----NHEFTDEQMEONCMSSMONTPTSRPSLSHP 521  
 OY 522 GLTTTCSSRSRKTTHLPNSNLPATRLASMOELSTIHQSEOBPLTTSRSLSNKADG 581  
 DB 522 GLTTTCSSRSRKTTHLPNSNLPATRLASMOELSTIHQSEOBPLTTSRSLSNKADG 581  
 OY 582 LRPNCKTSQITTAIISITPPALTPEGSRPPSPGPNNTNIPSTSNVAVSVL 636  
 DB 582 LRPNCKTSQITTAIISITPPALTPEGSRPPSPGPNNTNIPSTSNVAVSVL 636  
 OY 601 LRPNCKTSQITTAIISITPPALTPEGSRPPSPGPNNTNIPSTSNVAVSVL 655  
 DB 601 LRPNCKTSQITTAIISITPPALTPEGSRPPSPGPNNTNIPSTSNVAVSVL 655

RESULT 6  
 Q9PTD3 PRELIMINARY; PRT; 658 AA.  
 AC Q9PTD3;

DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Potassium channel Kv4.3.  
 GN Name=KCND3;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OK NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-bred White Leghorn; TISSUE=Lens epithelium;  
 RA Rae J.L.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF209722; AAF22832.1; -.  
 DR HSSP; Q63881; 1S6C.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR001622; K\_channel\_pore.  
 DR InterPro; IPR004056; KV43channel.  
 DR InterPro; IPR003968; Kv\_channel.  
 DR InterPro; IPR003091; K\_channel.  
 DR InterPro; IPR003131; K\_tetra.  
 DR InterPro; IPR005820; M-channel\_nlg.  
 DR InterPro; IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PR00169; KVCHANNEL.  
 DR PRINTS; PR01491; KVCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 DR Ion transport; Ionic channel; Transmembrane; Transport.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 658 AA; 73896 MW; 0F8743DAF8B12A8 CRC64;

Query Match 94.2%; Score 3126; DB 2; Length 658;  
 Best Local Similarity 91.9%; Pred. No. 3.1e-187;  
 Matches 605; Conservative 19; Mismatches 12; Indels 22; Gaps 4;

OY 1 MAAGVAAALPPARAAAIAGMPVANCMPMLAPADKXKRODELIVLVSGRRFQMTTLIER 60  
 DB 1 MAAGVAAALPPARAAAIAGMPVANCMPMLAPADKXKRODELIVLVSGRRFQMTTLIER 60  
 OY 61 YPDLLGSTEKEFFENEDTKEYFPDRDEVEFRVCVLFYRTGKLHYPRYECISAYDELAIF 120  
 DB 61 YPDLLGSTEKEFFENEDTKEYFPDRDEVEFRVCVLFYRTGKLHYPRYECISAYDELAIF 120  
 OY 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAFENPHST 179  
 DB 121 YGILPEIIGDCCYEEYKDRKRENAERLMDNDSENNOGSMPSLSFRQTMRAFENPHST 180  
 OY 180 TLALVFYVYTGFFIAVSITNVETVPCGTVGSKELPCGERSVAFPCLDIACWIFV 239  
 DB 180 TLALVFYVYTGFFIAVSITNVETVPCGTVGSKELPCGERSVAFPCLDIACWIFV 240  
 OY 240 EYLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLVFRVRIK 299  
 DB 240 EYLLRLFAAPSRVRFIRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLVFRVRIK 300  
 OY 300 FSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVVFYAEKSSASKFTSIPASFW 359  
 DB 300 FSRHSQGLRIIGYTLKSCASELGFLLFSLTMAIIIFATVVFYAEKSSASKFTSIPASFW 360  
 OY 360 YTIIVMTTLGVDMPVKTAKIGFISGSLGVLVIALVPIVSNFSRIYHONQADRR 419  
 DB 360 YTIIVMTTLGVDMPVKTAKIGFISGSLGVLVIALVPIVSNFSRIYHONQADRR 420

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QY 420 RAQKARLARIRVAKTGSSNAVLHKKRGNLNEALELTG-TPEEHMGKTTSLIESQH 478
DB 421 RAQKARLARIRVAKTGSSNAVLHKKRGNLNEALELTGTEDEQHTKTSILIESQH 480
QY 479 LHCLKERTT-----NHEPIDEQMFQONCMESSMONTPESTRSGLS 519
DB 481 LHCLKERTTGLSLVDDPLLSVTRSTIKNEHFIDEQLFEQNCMESSMONTPESTRSGLS 540
QY 520 HPELTTCCSRRSKTTTHLPSNLPATRLRSMOELSTHIQSEOPSLTTRSSSLNKD 579
DB 541 HHELTSSCCSRKTKTHLPNSVVPATRLRSWOELSTHIQSEOPSLTTRSSSLNKD 600
QY 580 DGLRPNCKTSQITTAIISIPTPALTPEGSRPPSPGPTNI-PSITSNVKAVSL 636
DB 601 DGLRPNCKAQTITTAIISIPTPALTPEGSRPPSPGPTNIISITTSNVKAVSL 658

RESULT 7
057662 ID 057662 PRELIMINARY; PRT; 659 AA.
AC 057662;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Potassium channel xkv4.3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; U89265; AAB94379.1; -.
DR HSSP; Q63881; 156C.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0008076; C:Voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:Protein binding; IEA.
DR GO; GO:0005249; F:Voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPRO00210; BTB POZ.
DR InterPro; IPRO05821; Ion trans.
DR InterPro; IPRO01622; K+channel pore.
DR InterPro; IPRO04056; KV43channel.
DR InterPro; IPRO03968; KV_channel.
DR InterPro; IPRO03091; K_channel.
DR InterPro; IPRO03131; K_tetra.
DR InterPro; IPRO05820; M+channel nlg.
DR InterPro; IPRO03975; Shal_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1518; KV43CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
DR PRINTS; PRO1497; SHALCHANNEL.
DR SMART; SM00225; BTB_1.
DR PROSITE; PS50097; BTB_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 659 AA; 74515 MW; 73F5CF339C6A0F47 CRC64;

Query Match 85.6%; Score 2843.5; DB 2; Length 659;
Best Local Similarity 84.1%; Pred. No. 1.4e-169;
Matches 556; Conservative 39; Mismatches 39; Indels 27; Gaps 7;
QY 1 MAAGVAAAMLPFAAAGMPPVANCMPMLPADGNKKODELIVLVNAGRRFQRTTLER 60
DB 1 MAGGVAAAMLPFAAAGMPPVANCMPMLPADGNKKODELIVLVNAGRRFQRTTLER 60
QY YPDTLGSTEKEPFNFEDTKEYPFDNDPEVFRCLVNFRTGKLHYPRYECSIAVDLAP 120
DB YPDTLGSTEKEPFNFEDTKEYPFDNDPEVFRCLVNFRTGKLHYPRYECSIAVDLAP 120

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DB 61 YPDNLGPEKEPFNEETKEYFPDRDPEVFRSLNFPRTGLHPRYVISAAYDELS 120
QY 121 YGILPEIIDDCCYEYKDKRRENAERLMDNDSENNOESMPSLSFQTMRAFENHTST 180
DB 121 YGILPEIIDDCCYEYKDKRRENAERLMDNDSENNOESMPSLSFQTMRAFENHTST 180
QY 181 LALVFPYVTGFFLAVSVITNVVEVTPDGVTPGSKELPCGERYSVAEFCIDTACWIFVE 240
DB 181 LALVFPYVTGFFLAVSVITNVVEVTPDGVTPGSKELPCGERYSVAEFCIDTACWIFVE 240
QY 241 YLLRLFAAPSRFRFSRVN---SIIDVVAIMPYIYGLVNTN-NEVSGAFVTLRVVR 296
DB 241 YLLRLFAAPSRFRFSRVN---SIIDVVAIMPYIYGLVNTNNEVSGAFVTLRVVR 300
QY 297 IFKFSHSGGLRIIGYLLKSCASELGLFLPSLTMAIIFATVWFYAEKSSASKFTSIDA 356
DB 301 IFKFSHSGGLRIIGYLLKSCASELGLFLPSLTMAIIFATVWFYAEKSSASKFTSIDA 360
QY 357 SFWYTIIVMTTIGYGMVPEKTIAGKIEG-SICSLGVLVIALPVVIVSNFSRIYQNR 415
DB 361 SFWYTIIVMTTIGYGMVPEKTIAGKIEFPHLNSLGLVIALPDPVAVNFSRIYQNR 420
QY 416 ADKRAQKARLARIRVAKTGSSNAVLHKKRGNLNEALELTCTPEEHMGKTTSLIESQ 475
DB 421 ADKRAQKARLARIRVAKTGSSNAVLHKKRGNLNEALELTCTPEEHMGKTTSLIESQ 480
QY 476 HHHLLHCLKERTTTHHEF-IDE-----QMEQNCMESSMONTPESTRSP 515
DB 481 HHHLLHCLKERTTGLSLVDDPLLSVTRSTIDHEPBCSLMOMFQONREMSCKNVPSTATA 540
QY 516 SLSSHGGLTTSCSRRSKTKTHLPNSNLPATRLRSWOELSTHIQSEOPSLTTRSSSLN 575
DB 541 SLSSHGGLTTSCSRRSKTKTHLPNSNVPATRLRSWOELSTHIQSEOPSLTTRSSSLN 600
QY 576 LKADDLARNCKTSQITTAIISIPTPALTPEGSRPPSPGPTNIISITTSNVKAVS 635
DB 601 LKSEDEMRNCKASQITTAIISIPTPALTPEGSRPPSPGPTNIISITTSNVKAVS 658
QY 636 L 636
DB 659 L 659

RESULT 8
072W36 ID 072W36 PRELIMINARY; PRT; 638 AA.
AC 072W36;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Potassium voltage-gated channel, Shal-related family, member 3.
GN OBFNames-zgc:55306.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lotteliello N.A., Peters G.J., Abramson R.D., Muljani S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC045304; AAH45304.1; -.  
 DR HSSP; O63981; 1S6C.  
 DR ZFIN; ZDB-GENE-030131-5626; zgc:55306.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR001622; K+channel.pore.  
 DR InterPro; IPR003968; Kv\_channel.  
 DR InterPro; IPR003091; K\_channel.  
 DR InterPro; IPR003131; K\_tetra.  
 DR InterPro; IPR005820; M-channel.nlg.  
 DR InterPro; IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans\_1.  
 DR Pfam; PF02214; K\_tetra\_1.  
 DR PRINTS; PR0169; KCHANNEL.  
 DR PRINTS; PR01518; KV4CHANNEL.  
 DR PRINTS; PR01491; KVCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 KW Ion transport; ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 638 AA; 72053 MW; 038645FB28947F47 CRC64;

Query Match 78.0%; Score 2590; DB 2; Length 638;  
 Best Local Similarity 77.8%; Pred. No. 9,7e-154;  
 Matches 501; Conservative 71; Mismatches 58; Indels 14; Gaps 10;

QY 1 MAAGVAAALPPARAAALIGMPVANCMPPLAPADKKRQDELIVLVNSGRFPQWRTTLE 60  
 DB 1 MAAGVAAALPPARAAALIGMPVANCMPVAPPSNKKRQDELIVLVNSGRFPQWRTTLD 60  
 QY 61 YPDTLLGSTEKEFFFNEDTKKEFFPRDPEVFCVLFNRTGKLHYPRYECISAYDELA 120  
 DB 61 YPDTLLGSSSEKKEFFNEETREYFFPRDPPVFSIINFRTGLHYPRYECISAYDELA 120  
 QY 121 YGILPEIIGDCCYEYKDKRKRENAERLMDNDSENNOESPISFQRTWRAFPENPHST 180  
 DB 121 FGIIEPIISDCYEYKDKRKRENTERLMDNLE-DNKDSKLEPMRTRETMWRFAFENPHST 179  
 QY 181 LALVEYVYTGFEIIVSVITNVEVPCGTPGSKELPCGERYSVAFFCLDTACWIFTE 240  
 DB 180 MALVYVYVYTGFEIIVSVITNVEVPCGMPQGRDUPGCEGRTAEAFPCMDTACWIFTE 239  
 QY 241 YLLRLFAAPSRIRFRSWSIIVDAVIMPYIIGLVNTNEDVSGAFVTLRVVRIRIPE 300  
 DB 240 YLMRLFAAPSRIRFRSWSIIVDAVILPYIIGLVNTNEDVSGAFVTLRVVRIRIPE 299  
 QY 301 SRHSGGLIILGYTLKSCASELGLFLFSILMAIIFATWFAVEKSSSSAKFTSPASFPY 360  
 DB 300 SRHSGGLIILGYTLKSCASELGLFLFSILMAIIFATWFAVEKSSSSAKFTSPASFPY 359  
 QY 361 TIVMTTLIGYDMVEXTKIAGKIFGSIISGLVIALPVVIVSNFSRIYHONQADKKR 420  
 DB 360 TIVMTTLIGYDMVEXTKIAGKIFGSIISGLVIALPVVIVSNFSRIYHONQADKKR 419

QY 421 AOK-KARLARIIVAKTSSNAYLHSGKGLINLEALTELGTPEE-EHMGKTTLSIESOH 477  
 DB 420 AOKVQKARLARIKRIKSSGSTAFILSKRG-LNOSTELTGSLEEDQOLKKTSLIESQH 478  
 QY 478 HLHLCLEKTNHEFIDQWFEQNCMESSMONYSTRSPSLSHPGITTTCSRRSKTTH 537  
 DB 479 HLHLCLEKTNHEFIDQWFEQNLQYQVLTALQNPFS-QSPFLSSEBEGITGCCRRPKNIQ 537  
 QY 538 LPSNLPRATRLSMOELSTIHIQSEKQPSLTSSSLINKADGLRPNKTS-QITTAII 596  
 DB 538 PLNATHTSHHTNIQELSLHIQCEQOPLNTRSSLLMDSGLNCKSSGLVTTAII 597  
 QY 597 SIPTPPA-----LTPGESRPPSPGPMPTNIRISINNVKSVL 636  
 DB 598 SIPTPPSNNSRASPDPAPPNPDEAP-PLIN-PSST-DVVKISAL 638

RESULT 9  
 ID 08HYZ1 PRELIMINARY; PRT; 630 AA.  
 AC 08HYZ1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Voltage-gated potassium channel Kv4.2.  
 OS Musceta putorius furo (Ferret).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Mustela.  
 OX NCBI\_TaxID=9669;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Patel S.P., Strauss H.C.;  
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY147192; AAN39878.1; -.  
 DR HSSP; O63981; 1S6C.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR001622; K+channel.pore.  
 DR InterPro; IPR004055; Kv42channel.  
 DR InterPro; IPR003968; Kv\_channel.  
 DR InterPro; IPR003091; K\_channel.  
 DR InterPro; IPR003131; K\_tetra.  
 DR InterPro; IPR005820; M-channel.nlg.  
 DR InterPro; IPR003975; Shal\_channel.  
 DR Pfam; PF00520; Ion\_trans\_1.  
 DR Pfam; PF02214; K\_tetra\_1.  
 DR PRINTS; PR00169; KCHANNEL.  
 DR PRINTS; PR01517; KV42CHANNEL.  
 DR PRINTS; PR01491; KVCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 DR SMART; SM00225; BTB; 1.  
 KW Ion transport; ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 630 AA; 70565 MW; DA4CFD16598A9842 CRC64;

Query Match 76.2%; Score 2530; DB 2; Length 630;  
 Best Local Similarity 76.1%; Pred. No. 5.4e-150;  
 Matches 488; Conservative 68; Mismatches 69; Indels 16; Gaps 6;

QY 1 MAAGVAAALPPARAAALIGMPVANCMPPLAPADKKR-QDELIVLVNSGRFPQWRTTLE 59  
 DB 1 MAAGVAAALPPARAAALIGMPVAPSPROEKRTQDMLIVLVNSGRFPQWRTTLE 60  
 QY 60 RYPTLLGSTEKEFFFNEDTKKEFFPRDPEVFCVLFNRTGKLHYPRYECISAYDELA 119  
 DB 61 RYPTLLGSSSRDFFYHETQYFFPRDPPDFRHLNFRYRQKLYPRHCEISAYDELA 120

Qy	120	FYGLIPEIIGDCCYEYKORKEKMERLMDNDSENNQGS -MSELSFRQMTMAFENPHT 178
Db	121	FFGLIPEIIGDCCYEYKORREKMERLDDADDTDTGTSALPTMTARQWRMAFENPHT 180
Qy	179	STLALVFFVYTGFFLAVSVYTNVVEVTPCGTVPGS -KELPCGERYSVAFCLDTACWMTF 237
Db	181	STMALVFFVYTGFFLAVSVYTNVVEVTPCGSSFGHIKELPCGERVYVAFCLDTACWMTF 240
Qy	238	TVEYLRLTFAASRYRFRFSVWSIIDVVAIMPYIGLWMTNNEVSGAFPTLTVFVFR 297
Db	241	TVEYLRLTFAASRYRFRFSVWSIIDVVAILEPYIGLWMTNNEVSGAFPTLTVFVFR 300
Qy	298	FKFSNHSOGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMEYAKSGSSAKFTSIPAS 357
Db	301	FKFSNHSOGLRIIGYTLKSCASELGLFLSLTMAIIIFATVMEYAKSGSSAKFTSIPAS 360
Qy	358	FWYTLVTMTTLLGDMVWPKTIAGKIFGSIICSLSGVLVIALPVVYIVSNFRITYHONRAD 417
Db	361	FWYTLVTMTTLLGDMVWPKTIAGKIFGSIICSLSGVLVIALPVVIVSNFRITYHONRAD 420
Qy	418	KRRACKKRLARIRVAKTGSSNAVYLSKRNGLINEMALTELGTPEEHMGKTSLSIOH 477
Db	421	KRRACKKRLARIRVAKTGSSNAVYLSKRNGLINEMALTELGTPEEHMGKTSLSIOH 479
Qy	478	HLHLCKLEKTNHEFIDQMFQONCMSSMQONYPESTRSPSLSSHPGLLTTTCCSRRSKKTTH 537
Db	480	HLHLCKLEKTNHEFIDQMFQONCMSSMQONYPESTRSPSLSSHPGLLTTTCCSRRSKKTFR 539
Qy	538	LPNSULPATRLRSMQGLSTIITHIQGSQPSLTSRRSLNKLADGLAPNCKTSQITTAIIS 557
Db	540	IPNAVVSQSHRSVOELSTIQICRVERTPLNSRSSLSLNKMECVCVLCNCEQPVYTAIIS 559
Qy	598	IPTPALTPREGSRP--PPASQGPNTNIPSTSNVVKVSVL 636
Db	600	IPTPEVTPTEGGDRPESPEYSGS-----NIYRVSL 630
RESULT 10		
KCD2_RABIT		
ID	KCD2_RABIT	STANDARD; PRT; 630 AA.
AC	P59955;	
DT	29-MAR-2004 (Rel. 43, Created)	
DT	29-MAR-2004 (Rel. 43, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Potassium voltage-gated channel subfamily D member 2 (Voltage-gated potassium channel subunit Kv4.2).	
GN	Name=KCND2;	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
OX	NCBI_TaxID=9986;	
RY	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=New Zealand white; TISSUE=Cornea;	
RA	Rae J.L.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE OF 15-614 FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.	
EX	MEDLINE=22117972; PubMed=12122138;	
RA	Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T., Sanz-Alfayate G.,	
RA	Obeso A., Gantofrino M.D., Gonzalez C.;	
RT	"Molecular identification of Kv alpha subunits that contribute to the	
RT	oxygen-sensitive K(+) current of chemoreceptor cells of the rabbit	
RT	carotid body";	
RL	J. Physiol. (Lond.) 542:369-382(2002).	
CC	-1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly	
CC	inactivating A-type potassium channels. May contribute to I(To)	
CC	current in heart and I(Sa) current in neurons. Channel properties	
CC	are modulated by interactions with other alpha subunits and with	
CC	regulatory subunits.	
CC	-1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.	
CC	Associates with the regulatory subunits KCNP1, KCNP2, KCNP3 and	

Query	Match	Best Local Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Score	DB 10	Score	DB 11	Score	DB 12	Score	DB 13	Score	DB 14	Score	DB 15	Score	DB 16	Score	DB 17	Score	DB 18	Score	DB 19	Score	DB 20	Score	DB 21	Score	DB 22	Score	DB 23	Score	DB 24	Score	DB 25	Score	DB 26	Score	DB 27	Score	DB 28	Score	DB 29	Score	DB 30	Score	DB 31	Score	DB 32	Score	DB 33	Score	DB 34	Score	DB 35	Score	DB 36	Score	DB 37	Score	DB 38	Score	DB 39	Score	DB 40	Score	DB 41	Score	DB 42	Score	DB 43	Score	DB 44	Score	DB 45	Score	DB 46	Score	DB 47	Score	DB 48	Score	DB 49	Score	DB 50	Score	DB 51	Score	DB 52	Score	DB 53	Score	DB 54	Score	DB 55	Score	DB 56	Score	DB 57	Score	DB 58	Score	DB 59	Score	DB 60	Score	DB 61	Score	DB 62	Score	DB 63	Score	DB 64	Score	DB 65	Score	DB 66	Score	DB 67	Score	DB 68	Score	DB 69	Score	DB 70	Score	DB 71	Score	DB 72	Score	DB 73	Score	DB 74	Score	DB 75	Score	DB 76	Score	DB 77	Score	DB 78	Score	DB 79	Score	DB 80	Score	DB 81	Score	DB 82	Score	DB 83	Score	DB 84	Score	DB 85	Score	DB 86	Score	DB 87	Score	DB 88	Score	DB 89	Score	DB 90	Score	DB 91	Score	DB 92	Score	DB 93	Score	DB 94	Score	DB 95	Score	DB 96	Score	DB 97	Score	DB 98	Score	DB 99	Score	DB 100	Score	DB 101	Score	DB 102	Score	DB 103	Score	DB 104	Score	DB 105	Score	DB 106	Score	DB 107	Score	DB 108	Score	DB 109	Score	DB 110	Score	DB 111	Score	DB 112	Score	DB 113	Score	DB 114	Score	DB 115	Score	DB 116	Score	DB 117	Score	DB 118	Score	DB 119	Score	DB 120	Score	DB 121	Score	DB 122	Score	DB 123	Score	DB 124	Score	DB 125	Score	DB 126	Score	DB 127	Score	DB 128	Score	DB 129	Score	DB 130	Score	DB 131	Score	DB 132	Score	DB 133	Score	DB 134	Score	DB 135	Score	DB 136	Score	DB 137	Score	DB 138	Score	DB 139	Score	DB 140	Score	DB 141	Score	DB 142	Score	DB 143	Score	DB 144	Score	DB 145	Score	DB 146	Score	DB 147	Score	DB 148	Score	DB 149	Score	DB 150	Score	DB 151	Score	DB 152	Score	DB 153	Score	DB 154	Score	DB 155	Score	DB 156	Score	DB 157	Score	DB 158	Score	DB 159	Score	DB 160	Score	DB 161	Score	DB 162	Score	DB 163	Score	DB 164	Score	DB 165	Score	DB 166	Score	DB 167	Score	DB 168	Score	DB 169	Score	DB 170	Score	DB 171	Score	DB 172	Score	DB 173	Score	DB 174	Score	DB 175	Score	DB 176	Score	DB 177	Score	DB 178	Score	DB 179	Score	DB 180	Score	DB 181	Score	DB 182	Score	DB 183	Score	DB 184	Score	DB 185	Score	DB 186	Score	DB 187	Score	DB 188	Score	DB 189	Score	DB 190	Score	DB 191	Score	DB 192	Score	DB 193	Score	DB 194	Score	DB 195	Score	DB 196	Score	DB 197	Score	DB 198	Score	DB 199	Score	DB 200	Score	DB 201	Score	DB 202	Score	DB 203	Score	DB 204	Score	DB 205	Score	DB 206	Score	DB 207	Score	DB 208	Score	DB 209	Score	DB 210	Score	DB 211	Score	DB 212	Score	DB 213	Score	DB 214	Score	DB 215	Score	DB 216	Score	DB 217	Score	DB 218	Score	DB 219	Score	DB 220	Score	DB 221	Score	DB 222	Score	DB 223	Score	DB 224	Score	DB 225	Score	DB 226	Score	DB 227	Score	DB 228	Score	DB 229	Score	DB 230	Score	DB 231	Score	DB 232	Score	DB 233	Score	DB 234	Score	DB 235	Score	DB 236	Score	DB 237	Score	DB 238	Score	DB 239	Score	DB 240	Score	DB 241	Score	DB 242	Score	DB 243	Score	DB 244	Score	DB 245	Score	DB 246	Score	DB 247	Score	DB 248	Score	DB 249	Score	DB 250	Score	DB 251	Score	DB 252	Score	DB 253	Score	DB 254	Score	DB 255	Score	DB 256	Score	DB 257	Score	DB 258	Score	DB 259	Score	DB 260	Score	DB 2
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Db 241 TTEYLRLAARSRFRPFRSVMSIIDVAILPYIIGLWNTDNEVSGARVTIARFRVRI 300
Qy 298 FRFSHSGCLRLITGLTKSCASGLGFLPGLTMAIIIFATVFWYAEKSSASKFTSIPAS 357
Db 301 FRFSHSGCLRLITGLTKSCASGLGFLPGLTMAIIIFATVFWYAEKSSASKFTSIPAS 360
Qy 368 FWYTVVMTTGLGGMVPRKTAGKIFGSLCSLGLVIALPVPVIVSNRSRIYHONORD 417
Db 361 FWYTVVMTTGLGGMVPRKTAGKIFGSLCSLGLVIALPVPVIVSNRSRIYHONORD 420
Qy 418 KRAQKARLARIRVAKTGSSNAVLHKKRGLNLELTGTPEER--HMGKTSILIEIS 475
Db 421 KRAQKARLARIRVAKTGSSNAVLHKKRGLNLELTGTPEER--HMGKTSILIEIS 477
Qy 476 HHHLLHCEKTNHFEIDQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQ 535
Db 478 HHHLLHCEKTNHFEIDQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQF 537
Qy 536 THLPNSNLPATRLRSMOELSTHIGSGPSLITRSSNLTKADGLRNCCTQTITAI 595
Db 538 FRIPANVSGSGRGVQELSTIQRICVERTPLSNRSSSLNAAWECVKNLNCQPYVTAI 597
Qy 596 ISIPPPALTEGESRP--PPASPPNTIPISTSNVAVSVL 636
Db 598 ISIPPPALTEGESRP--PPASPPNTIPISTSNVAVSVL 630

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RESULT 11
KCD2_MOUSE STANDARD: PRT: 630 AA.
ID_KCD2_MOUSE Q8CHB7; Q9JJD0;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated
DE potassium channel subunit Kv4.2).
GN Name=Kv4.2; Synonyms=Kiaa1044;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Heart ventricle;
RA Tanaka H., Janzen K., Winkler R.J., Fiset C., Clark R.B., Giles W.R.;
RT "Cloning and functional characterization of mouse heart K+ channel
RT alpha subunits, Kv1.5, Kv4.2 and Kv4.3."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library."
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22353125; PubMed=12465718;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT 1. The complete nucleotide sequences of 100 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 9:179-188(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros, and Olfactory bulb;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,

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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balcarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbett L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner U., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Borls A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [5]
RP PHOSPHORYLATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20497051; PubMed=11040264;
RA Varga A.W., Anderson A.E., Adams J.P., Vogel H., Sweatt J.D.;
RT "Input-specific immunolocalization of differentially phosphorylated
RT Kv4.2 in the mouse brain."
RL Learn. Memory 7:321-332(2000).
RN [6]
RP INTERACTION WITH KCNIP3, NOTAGENESIS OF SER-552, AND PHOSPHORYLATION.
RX MEDLINE=22338839; PubMed=12451113;
RA Schrader L.A., Anderson A.E., Mayne A., Pfaffinger P.J., Sweatt J.D.;
RT "PKA modulation of Kv4.2-encoded A-type potassium channels requires
RT formation of a supramolecular complex."
RL J. Neurosci. 22:10123-10133(2002).
RN [7]
RP INTERACTION WITH KCND3 AND KCNIP2.
RX MEDLINE=21906624; PubMed=11909823;
RX DOI=10.1161/01.RBS.0000012664.05949.E0;
RA Guo W., Li H., Almond F., Johns D.C., Rhodes K.J., Trimmer J.S.,
RA Nerbonne J.M.;
RT "Role of heteromultimers in the generation of myocardial transient
RT outward K+ currents."
RL Circ. Res. 90:586-593(2002).
RN [8]
RP FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly
RP inactivating A-type potassium channels. May contribute to I(TO)
RP current in heart and I(Sa) current in neurons. Channel properties
RP are modulated by interactions with other alpha subunits and with
RP regulatory subunits.
RN [9]
RP SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.
RP Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and
RP and FLNC (by similarity).
RN [10]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RP TISSUE SPECIFICITY: Detected in brain, especially in hippocampus,
RP medial habenular nucleus, striatum, amygdala, cortex and
RP cerebellum.
RN [11]
RP DOMAIN: The segment S4 is probably the voltage-sensor and is
RP characterized by a series of positively charged amino acids at
RP every third position.
RN [12]
RP SIMILARITY: Belongs to the potassium channel family. D (Shal)
RP subfamily.
RN [13]
RP CAUTION: Ref.2 sequence differs from that shown due to a
RP frameshift in position 520.
RN [14]
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RT "A role for frequenin, a Ca<sup>2+</sup>-binding protein, as a regulator of Kv4  
 RT K<sup>+</sup>-currents.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12808-12813(2001).  
 RN [5]  
 RP INTERACTION WITH KCNIP4.  
 RX MEDLINE=21964093; PubMed=11847232; DOI=10.1074/jbc.M200897200;  
 RA Morohashi Y., Hatanaka N., Ohya S., Takikawa R., Matubiki T.,  
 RA Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.;  
 RT "Molecular cloning and characterization of CALP/KCIP4, a novel EF-  
 RT hand protein interacting with presenilin 2 and voltage-gated potassium  
 RT channel subunit Kv4.";  
 RL J. Biol. Chem. 277:14965-14975(2002).  
 RN [6]  
 RP MUTAGENESIS OF 627-VAL--LEU-630, AND INTERACTION WITH DLG4.  
 RX MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;  
 RA Wong W., Newell B.W., Junglof D.G.W., Jones O.T., Schlichter L.C.;  
 RT "Cell surface targeting and clustering interactions between  
 RT heterologously expressed PSD-95 and the Shal voltage-gated potassium  
 RT channel, Kv4.2.";  
 RL J. Biol. Chem. 277:20423-20430(2002).  
 RN [7]  
 RP INTERACTION WITH DPP6.  
 RX MEDLINE=22464931; PubMed=12575952; DOI=10.1016/S0896-6273(02)01185-6;  
 RA Nadal M.S., Ozaita A., Amarillo Y., Vega-Saenz de Miera E., Ma Y.,  
 RA Mo W., Goldberg E.M., Mismari Y., Ikebara Y., Neubert T.A., Rudy B.;  
 RT "The CD6-related dipeptidyl aminopeptidase-like protein DPP6 is a  
 RT critical component of neuronal A-type K<sup>+</sup> channels.";  
 RL Neuron 37:449-461(2003).  
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
 CC inactivating A-type potassium channels. May contribute to I(TO)  
 CC current in heart and I(Sa) current in neurons. Channel properties  
 CC are modulated by interactions with other alpha subunits and with  
 CC regulatory subunits.  
 CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.  
 CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
 CC KCNIP4. Interacts with FLNA and FLNC (By similarity). Interacts  
 CC with DPP6, DLG4 and FRET.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Interaction with  
 CC DPP6, DLG4 or FRET may increase cell surface expression.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart and throughout the  
 CC brain, with similar levels in cortex and hypothalamus, and much  
 CC higher levels in hippocampus, dentate gyrus and the habenular  
 CC nucleus of the thalamus. Detected at similar levels in heart  
 CC atrium and ventricle. Detected in aorta, cardiac and smooth  
 CC muscle.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- PTM: Phosphorylated on serine and threonine residues (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)  
 CC subfamily.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a  
 CC frameshift in position 477.  
 CC  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC  
 CC EMBL, S64320; AAB19939.1; -  
 CC EMBL, M59980; AAA40929.1; ALT\_FRAME.  
 CC PIR, J00271; J00271.  
 CC PDB, 186C; X-ray; B=1-30.  
 CC InterPro: IPR005621; Ion trans.  
 CC InterPro: IPR001622; K+channel pore.  
 CC InterPro: IPR003091; K\_channel.  
 CC InterPro: IPR003131; K\_tetra.  
 CC InterPro: IPR004055; KV42channel.  
 CC InterPro: IPR003968; Kv\_channel.

DR InterPro: IPR005620; M-channel nlg.  
 DR InterPro: IPR003975; Shal\_channel.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR Pfam: PF02214; K\_tetra; 1.  
 DR PRINTS: PR00169; KCHANNEL.  
 DR PRINTS: PR01517; KV42CHANNEL.  
 DR PRINTS: PR01491; KVCHANNEL.  
 DR PRINTS: PR01497; SHALCHANNEL.  
 KM 3D-structure; Ion transport; Ionic channel, Multigene family;  
 KW Phosphorylation; Potassium; Potassium channel; Potassium transport;  
 KW Transmembrane; Transport; Voltage-gated channel;  
 FT DOMAIN 1 183  
 FT TRANSMEM 184 204 Segment S1 (potential).  
 FT TRANSMEM 225 245 Segment S2 (potential).  
 FT DOMAIN 246 259 Cytoplasmic (potential).  
 FT TRANSMEM 260 280 Segment S3 (potential).  
 FT TRANSMEM 290 310 Segment S4 (potential).  
 FT DOMAIN 311 323 Cytoplasmic (potential).  
 FT TRANSMEM 324 344 Segment S5 (potential).  
 FT TRANSMEM 363 383 Segment S6 (potential).  
 FT TRANSMEM 385 405 Segment S6 (potential).  
 FT DOMAIN 406 630 Cytoplasmic (potential).  
 FT SITE 370 375 Selectivity filter (By similarity).  
 FT MOD\_RES 38 38 Phosphoserine (By similarity).  
 FT MOD\_RES 552 552 Phosphothreonine (By similarity).  
 FT MOD\_RES 602 602 Phosphoserine (By similarity).  
 FT MOD\_RES 607 607 Phosphothreonine (By similarity).  
 FT MOD\_RES 616 616 Phosphoserine (By similarity).  
 FT MUTAGEN 627 630 Missing: Abolishes interaction with DLG4.  
 SQ SEQUENCE 630 AA; 70548 MW; PDE578A5113BABF CnG64;

Query Match 75.9%; Score 2519; DB 1; Length 630;  
 Best Local Similarity 75.8%; Pred. No. 2.6e-149;  
 Matches 486; Conservative 69; Mismatches 70; Indels 16; Gaps 6;  
 QY 1 MAAGVAAALPPARAALIGMVAACMPPLADADKKR-ODELIVLVNSGRBPPQRTTLE 59  
 DB 1 MAAGVAAALPPARAALIGMVAACMPPLADADKKR-ODELIVLVNSGRBPPQRTTLE 60  
 QY RYPDTLLGSTEKEFFNEEDTKEFFEDRDEVRFCVNFRTGKLYPRYECISAYDELA 119  
 DB RYPDTLLGSSRRDPFYPHETQYFFDRDPDIFRHILNFRYRGKLYPHRECISAYDELA 120  
 QY 120 FYGLIPETIGCCYBEYKDRRENAERLMDNDSENNQES-MPSISFQOTMMRAEENHT 178  
 DB 120 FYGLIPETIGCCYBEYKDRRENAERLMDNDSENNQES-MPSISFQOTMMRAEENHT 178  
 QY 121 FFGIIPETIGCCYBEYKDRRENAERLMDNDSENNQES-MPSISFQOTMMRAEENHT 180  
 DB 121 FFGIIPETIGCCYBEYKDRRENAERLMDNDSENNQES-MPSISFQOTMMRAEENHT 180  
 QY 179 STIALVFYVTGFFIAVSVINVTVEVPCGVPPS-KEIPGGRYSVAFFCLDTACWIF 237  
 DB 179 STIALVFYVTGFFIAVSVINVTVEVPCGVPPS-KEIPGGRYSVAFFCLDTACWIF 237  
 QY 181 STIALVFYVTGFFIAVSVINVTVEVPCGVPPS-KEIPGGRYSVAFFCLDTACWIF 240  
 DB 181 STIALVFYVTGFFIAVSVINVTVEVPCGVPPS-KEIPGGRYSVAFFCLDTACWIF 240  
 QY 238 TVEYLRLFAAPSRFRFRSVMISIIDVAIMPYIIGLVMTNNEVSGAFTLVRAVFRVRI 297  
 DB 238 TVEYLRLFAAPSRFRFRSVMISIIDVAIMPYIIGLVMTNNEVSGAFTLVRAVFRVRI 297  
 QY 241 TVEYLRLFAAPSRFRFRSVMISIIDVAIMPYIIGLVMTNNEVSGAFTLVRAVFRVRI 300  
 DB 241 TVEYLRLFAAPSRFRFRSVMISIIDVAIMPYIIGLVMTNNEVSGAFTLVRAVFRVRI 300  
 QY 298 FKFSRHSQGLRIIGYTKSCASELGFILFSLTMAIIFPATYFAEKSSASKFTSIDPAS 357  
 DB 298 FKFSRHSQGLRIIGYTKSCASELGFILFSLTMAIIFPATYFAEKSSASKFTSIDPAS 357  
 QY 301 FKFSRHSQGLRIIGYTKSCASELGFILFSLTMAIIFPATYFAEKSSASKFTSIDPAS 360  
 DB 301 FKFSRHSQGLRIIGYTKSCASELGFILFSLTMAIIFPATYFAEKSSASKFTSIDPAS 360  
 QY 358 FMYITVMTTIGYDMPVKTAGKIFGSGISGLGVYALVPVYVSFSAIHYONORAD 417  
 DB 358 FMYITVMTTIGYDMPVKTAGKIFGSGISGLGVYALVPVYVSFSAIHYONORAD 417  
 QY 361 FMYITVMTTIGYDMPVKTAGKIFGSGISGLGVYALVPVYVSFSAIHYONORAD 420  
 DB 361 FMYITVMTTIGYDMPVKTAGKIFGSGISGLGVYALVPVYVSFSAIHYONORAD 420  
 QY 418 KRAQKARLARIRVAKTGSNAAYLHSGKNGLNEALELGTPEBEHNGKTSLSLESGH 477  
 DB 418 KRAQKARLARIRVAKTGSNAAYLHSGKNGLNEALELGTPEBEHNGKTSLSLESGH 477  
 QY 421 KRAQKARLARIRVAKTGSNAAYLHSGKNGLNEALELGTPEBEHNGKTSLSLESGH 479  
 DB 421 KRAQKARLARIRVAKTGSNAAYLHSGKNGLNEALELGTPEBEHNGKTSLSLESGH 479  
 QY 478 HLHCLKETTTHERTIDEQMFQONCESSMOMVYBSTRPSLSHSGLTTCSSRSKTKTH 537  
 DB 478 HLHCLKETTTHERTIDEQMFQONCESSMOMVYBSTRPSLSHSGLTTCSSRSKTKTH 537  
 QY 480 HLHCLKETTTHERTIDEQMFQONCESSMOMVYBSTRPSLSHSGLTTCSSRSKTKTH 539  
 DB 480 HLHCLKETTTHERTIDEQMFQONCESSMOMVYBSTRPSLSHSGLTTCSSRSKTKTH 539  
 QY 538 LNSNLPATRLRSQMOELSTHIGQSEOPSLTSSSLNLEKDDGAPRPKCTSOITTAIS 597  
 DB 538 LNSNLPATRLRSQMOELSTHIGQSEOPSLTSSSLNLEKDDGAPRPKCTSOITTAIS 597

Db 540 IPNANVSGSHRGVQELSTIQIRCVERTPLSRSSLNKMECVKLNCEOPYTTAITS 599  
 QY 598 ITPPALTEGESRP--PPASPGPNTNIPSTSNVVKAVL 636  
 Db 600 ITPPVTTPGDDRPESPEYSGS-----NIVRVNAL 630  
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 ID\_KCND2\_HUMAN STANDARD; PRT; 630 AA.  
 AC O9N2V8; O95012; O95021; Q9UBV7; Q9UN98; Q9UN99;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 2 (Voltage-gated  
 DE potassium channel subunit Kv4.2).  
 GN Name=KCND2; Synonyms=K11A1044;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99061682; Pubmed=9843794;  
 RA Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.;  
 RT "Isolation and characterization of the human gene encoding Ito:  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:197-205(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=9937452; Pubmed=10470851;  
 RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XIV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:197-205(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. TISSUE SPECIFICITY, AND FUNCTION.  
 RX MEDLINE=20017432; Pubmed=10551270;  
 RA Zhu X.-R., Wolf A., Schwarz M., Isbrandt D., Pongs O.;  
 RT "Characterization of human Kv4.2 mediating a rapidly-inactivating  
 RT transient voltage-sensitive K<sup>+</sup> current.";  
 RL Recept. Channels 6:387-400(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=20195625; Pubmed=10729221; DOI=10.1006/geno.2000.6117;  
 RA Isbrandt D., Leichter T., Waldehuetz R., Zhu X.-R., Luhmann U.,  
 RA Michel U., Sauter K., Pongs O.;  
 RT "Gene structures and expression profiles of three human KCND (Kv4)  
 RT potassium channels mediating A-type currents I(TO) and I(SA).";  
 RL Genomics 64:144-154(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2616434; Pubmed=12690205; DOI=10.1126/science.1083423;  
 RA Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayashi K.,  
 RA Herbrick J.-A., Carson A.R., Parker-Katiraei L., Skeag J., Klatza R.,  
 RA Zhang J., Hudek A.K., Li M., Haddad M., Duggan G.B., Fernandez B.A.,  
 RA Kanematsu D., Gentile S., Christopoulos C.C., Choufani S.,  
 RA Kanematsu D., Zheng X.H., Lai Z., Nusser D., Zhang Q., Gu Z., Lu F.,  
 RA Zeesman S., Nowacznyk M.J., Teshima I., Chitayat D., Shuman C.,  
 RA Weisberg R., Zackai E.H., Grebe T.A., Cox S.R., Kitzpatrick S.J.,  
 RA Rahman N., Friedman J.M., Heng H.H.O., Pellicci P.G., De-Coco F.,  
 RA Belloni E., Shaffer L.G., Pober B., Morton C.C., Ferguson H.,  
 RA Bruns G.A.P., Korf B.R., Quade B.J., Lyon A.H., Ferguson H.,  
 RA Higgins A.W., Leach N.T., Herrick S.R., Lemay E., Parra C.G.,  
 RA Kim H.-G., Summers A.W., Gripp K.W., Roberts W., Szatmari P.,  
 RA Winsor E.J.T., Grzeschik K.-H., Teedi A., Minassian B.A., Kere J.,  
 RA Aramengo L., Putana M.A., Estivill X., Wilson M.D., Koop B.F.,  
 RA Tosi S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B.,

RA Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner H.,  
 RA Doehner K., Rommens J.M., Vincent J.B., Venter J.C., Li P.W.,  
 RA Mural R.J., Adams M.D., Teui L.-C.;  
 RT "Human chromosome 7: DNA sequence and biology.";  
 RL Science 300:767-772(2003).  
 RN [6]  
 RP MUTAGENESIS OF 601-PRO-604, SUBCELLULAR LOCATION, AND INTERACTION  
 RP WITH FLNA AND FLNC.  
 RX MEDLINE=20556633; Pubmed=11102480;  
 RA Petrecca K., Miller D.M., Shrier A.;  
 RT "Localization and enhanced current density of the Kv4.2 potassium  
 RT channel by interaction with the actin-binding protein filamin.";  
 RL J. Neurosci. 20:8736-8744(2000).  
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
 CC inactivating A-type potassium channels. May contribute to I(TO)  
 CC current in heart and I(Sa) current in neurons. Channel properties  
 CC are modulated by interactions with other alpha subunits and with  
 CC regulatory subunits.  
 CC -1- SUBUNIT: Homotrimer or heterotrimer with KCND1 and/or KCND3.  
 CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
 CC KCNIP4. Interacts with DPP6, DLG4 and FREQ (by similarity).  
 CC Interacts with FLNA and FLNC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Detected in  
 CC dendrites in cultured hippocampal neurons.  
 CC -1- TISSUE SPECIFICITY: Highly expressed throughout the brain.  
 CC Expression is very low or absent in other tissues.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- PTM: Phosphorylated on serine and threonine residues (by  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)  
 CC subfamily.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; AF121104; AAD22053.1; -;  
 CC EMBL; AB028967; BAAB2996.2; AL1\_INIT.  
 CC EMBL; AJ010969; CAB56841.1; -;  
 CC EMBL; AF166008; AAF65618.1; -;  
 CC EMBL; AF166007; AAF65618.1; JOINED.  
 CC EMBL; AC004888; AAC83405.1; -;  
 CC EMBL; AC004946; -; NOT ANNOTATED CDS.  
 CC EMBL; AF142568; AAD52159.1; -;  
 CC HSSP; Q16968; 1A68.  
 CC GeneW; HGNC:6238; KCND2.  
 CC H-InvDB; HIX007027; -;  
 CC MIM; 605410; -;  
 CC InterPro; IPR005821; Ion trans.  
 CC InterPro; IPR001622; K+channel\_pore.  
 CC InterPro; IPR003091; K channel.  
 CC InterPro; IPR003131; K tetra.  
 CC InterPro; IPR004055; KV42channel.  
 CC InterPro; IPR003868; KV\_channel.  
 CC InterPro; IPR005820; M+channel\_nlg.  
 CC InterPro; IPR003975; Shal channel.  
 CC Pfam; PF00520; Ion trans; 1.  
 CC Pfam; PF02214; K tetra; 1.  
 CC PRINTS; PR00169; KCHANNEL.  
 CC PRINTS; PR01517; KV42CHANNEL.  
 CC PRINTS; PR01491; KVCHANNEL.  
 CC PRINTS; PR01497; SHALCHANNEL.  
 CC Ion transport; Ionic channel; Multigene family; Phosphorylation;  
 CC Potassium; Potassium channel; Potassium transport; Transmembrane;  
 CC Transport; Voltage-gated channel.  
 CC DOMAIN 1 183 Cytoplasmic (potential).  
 CC TRANSMEM 184 204 Segment S1 (potential).

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FT TRANSMEM 225 245 Segment S2 (Potential).
FT DOMAIN 246 259 Cytoplasmic (Potential).
FT TRANSMEM 260 280 Segment S3 (Potential).
FT TRANSMEM 290 310 Segment S4 (Potential).
FT DOMAIN 311 323 Cytoplasmic (Potential).
FT TRANSMEM 324 344 Segment S5 (Potential).
FT TRANSMEM 363 383 Segment H5 (pore-forming) (Potential).
FT TRANSMEM 385 405 Segment S6 (Potential).
FT DOMAIN 406 630 Cytoplasmic (Potential).
FT SITE 370 375 Selectivity filter (By similarity).
FT MOD_RES 38 38 Phosphochreonine (By similarity).
FT MOD_RES 552 552 Phosphoserine (By similarity).
FT MOD_RES 602 602 Phosphochreonine (By similarity).
FT MOD_RES 607 607 Phosphochreonine (By similarity).
FT MOD_RES 616 616 Phosphoserine (By similarity).
FT MUTAGEN 601 604 PTP->ATPA: Abolishes interaction with PLNC.
FT CONFLICT 450 450 N->S (in Ref. 1).
FT CONFLICT 464 464 Q->P (in Ref. 1).
FT CONFLICT 550 550 Q->R (in Ref. 1).
FT CONFLICT 553 553 I->V (in Ref. 1).
SQ SEQUENCE 630 AA; 70536 MW; 0C11B62FFA220421 CRC64;

Query Match 75.8%; Score 2518; DB 1; Length 630;
Best Local Similarity 75.8%; Pred. No. 3e-149; Indels 16; Gaps 6;
Matches 486; Conservative 69; Mismatches 70;

QY 1 MAAGVAAALPPARAALIGMPVANCMPPLADPKNR-ODELIVANSGRRFQWRTTLE 59
DB 1 MAAGVAAALPPARAALIGMPVANCMPPLADPKNR-ODELIVANSGRRFQWRTTLE 60
QY 60 RYPTLLGSTEKEFFENEDTKEYFPDRDPEVRCVLANFYRTGKLYHPYECISAYDELA 119
DB 61 RYPTLLGSSERBDFEYHETQYFEDRDPDIFRHILNFYRTGKLYHPYECISAYDELA 120
QY 120 FYGILPEIIGCCYEEYDRKRENAERLMDNDSENNQES-MPSLSPFQTMWRAPENPT 178
DB 121 FFGILPEIIGCCYEEYDRKRENAERLMDNDSENNQES-MPSLSPFQTMWRAPENPT 180
QY 179 STLAIVFYVYVGFPIAVSVITNVVETVPCGVPGS-KELPCGERSVAFPCLDTCAMIF 237
DB 181 STLAIVFYVYVGFPIAVSVITNVVETVPCGVPGS-KELPCGERSVAFPCLDTCAMIF 240
QY 238 TVEYLLRLFAAPBSRYRFRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 297
DB 241 TVEYLLRLFAAPBSRYRFRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLILIGYTLKSCASELGFLLPSLTMAIIFATWYFAEKSSASKFTSIPAS 357
DB 301 FKFSRHSQGLILIGYTLKSCASELGFLLPSLTMAIIFATWYFAEKSSASKFTSIPAS 360
QY 358 FWYITVMTTIGYGMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIHYONQAD 417
DB 361 FWYITVMTTIGYGMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIHYONQAD 420
QY 418 KRRQKARLARIRVAKTGSSNAYLHAKRNGLLNEALELTGTPEEHNGKTTSLIESQH 477
DB 421 KRRQKARLARIRVAKTGSSNAYLHAKRNGLLNEALELTGTPEEHNGKTTSLIESQH 479
QY 478 HLLHCEKTTNHEFDQMFQONCMESMOMYPSRSPSLSSHPLTTTCCSRKKTTH 537
DB 480 HLLHCEKTTNHEFDQMFQONCMESMOMYPSRSPSLSSHPLTTTCCSRKKTTH 539
QY 538 LPNSNLPATRLRSMOELSTIHIOGSEQPSLTTSSRLSLKADDDGAPNCKTSQITTAIS 597
DB 540 LPNSNLPATRLRSMOELSTIHIOGSEQPSLTTSSRLSLKADDDGAPNCKTSQITTAIS 599
QY 598 IPTPALTPGEGSRP--PPASPGPNTNIPSTISNVYKSVL 636
DB 600 IPTPALTPGEGSRP--PPASPGPNTNIPSTISNVYKSVL 630

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O8UW33
ID O8UW33 PRELIMINARY; PRT; 632 AA.
AC O8UW33;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Shal-like voltage-gated potassium channel.
GN Name=kv4.2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakai Y., Sokolowski B.H.A.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF075160; AAL56633.1; -.
DR HSSP; O63881; 1S6C.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0008076; C:Voltage-gated potassium channel complex; IEA.
DR GO; GO:0005515; F:Protein binding; IEA.
DR GO; GO:0005249; F:Voltage-gated potassium channel activity; IEA.
DR GO; GO:0006813; P:Potassium ion transport; IEA.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01517; KV4CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 632 AA; 70982 MW; 147C92979F2297D9 CRC64;

Query Match 75.8%; Score 2517; DB 2; Length 632;
Best Local Similarity 76.2%; Pred. No. 3.5e-145; Indels 16; Gaps 6;
Matches 489; Conservative 62; Mismatches 75;

QY 1 MAAGVAAALPPARAALIGMPVANCMPPLADPKNR-ODELIVANSGRRFQWRTTLE 59
DB 1 MAAGVAAALPPARAALIGMPVANCMPPLADPKNR-ODELIVANSGRRFQWRTTLE 60
QY 60 RYPTLLGSTEKEFFENEDTKEYFPDRDPEVRCVLANFYRTGKLYHPYECISAYDELA 119
DB 61 RYPTLLGSSERBDFEYHETQYFEDRDPDIFRHILNFYRTGKLYHPYECISAYDELA 120
QY 120 FYGILPEIIGCCYEEYDRKRENAERLMDNDSENNQES-MPSLSPFQTMWRAPENPT 178
DB 121 FFGILPEIIGCCYEEYDRKRENAERLMDNDSENNQES-MPSLSPFQTMWRAPENPT 180
QY 179 STLAIVFYVYVGFPIAVSVITNVVETVPCGVPGS-KELPCGERSVAFPCLDTCAMIF 237
DB 181 STLAIVFYVYVGFPIAVSVITNVVETVPCGVPGS-KELPCGERSVAFPCLDTCAMIF 240
QY 238 TVEYLLRLFAAPBSRYRFRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 297
DB 241 TVEYLLRLFAAPBSRYRFRSVMSIIDVVAIMPYYIGLVMTNEDVSGAFVTLRVFRVRI 300
QY 298 FKFSRHSQGLILIGYTLKSCASELGFLLPSLTMAIIFATWYFAEKSSASKFTSIPAS 357
DB 301 FKFSRHSQGLILIGYTLKSCASELGFLLPSLTMAIIFATWYFAEKSSASKFTSIPAS 360
QY 358 FWYITVMTTIGYGMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIHYONQAD 417
DB 361 FWYITVMTTIGYGMVPKTIAGKIFGSIICSLGVLVIALPVPVIVSNFSRIHYONQAD 420
QY 418 KRRQKARLARIRVAKTGSSNAYLHAKRNGLLNEALELTGTPEEHNGKTTSLIESQH 476
DB 421 KRRQKARLARIRVAKTGSSNAYLHAKRNGLLNEALELTGTPEEHNGKTTSLIESQH 480
QY 477 HLLHCEKTTNHEFDQMFQONCMESMOMYPSRSPSLSSHPLTTTCCSRKKTTH 536

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Db 481 HLLHCLIEKTTNHEFVDEQIYESCNEVSTVNRPPSHSPSLSSQOGVTGTCSSRRHKTY 540  
 Qy 537 HLPNSNLPATRLSRMDELSTHIOGSEOPSLTSSSLNKADGLPNCSTQITTAII 596  
 Db 541 RINTNLTGSRHSVGLSTIQRVCERTPLSNRSRLNKVECVLNEQPIVTTAII 600  
 Qy 597 SIPTPALTPGESSRP--PASPQEPNTNIPSTISNVKVSYL 636  
 Db 601 SIPTPVTPTEGDDRPESPESYSGG-----NIVRSAL 632  
 RESULT 15  
 KCD1\_MOUSE STANDARD; PRT; 651 AA.  
 ID KCD1\_MOUSE  
 AC 003719; 08CC68;  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium voltage-gated channel subfamily D member 1 (Voltage-gated  
 potassium channel subunit Kv4.1) (msh1).  
 GN Name=Kcnd1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=91239573; PubMed=2034678;  
 RA Pak M.D., Baker K., Covarrubias M., Butler A., Ratcliffe A.,  
 RA Salikoff L.,  
 RT "msh1, a subfamily of A-type K<sup>+</sup> channel cloned from mammalian  
 brain".  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4386-4390(1991).  
 RN [2]  
 RP SEQUENCE OF 145-647 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Epithelium;  
 RX MEDLINE=22354683; PubMed=1246885; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltac K., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sendelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,  
 RA Sultana R., Takemata Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Zimin P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs".  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP INTERACTION WITH KCNIP1.  
 RX MEDLINE=21316019; PubMed=11423117; DOI=10.1016/S0014-5793(01)02560-1;  
 RA Nakamura T.Y., Nandi S., Pountney D.J., Artman M., Rudy B.,  
 RA Coetzee W.A.,  
 RT "Different effects of the Ca(2+)-binding protein, KChIP1, on two Kv4

RT subfamily members, Kv4.1 and Kv4.2.";  
 RL FBS Lett. 499:205-209(2001).  
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly  
 CC inactivating A-type potassium channels. May contribute to I<sub>to</sub>  
 CC current in the heart and I(Sa) current in neurons. Channel  
 CC properties are modulated by subunit assembly.  
 CC -1- SUBUNIT: Homodimer or heterodimer with KCND2 and/or KCND3.  
 CC Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and  
 CC KCNIP4 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- SIMILARITY: Belongs to the potassium channel family. D (Shal)  
 CC subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; M64226; AAA39745.1; -;  
 DR EMBL; AK033805; BAC28480.1; -;  
 DR PIR; A39372; A39372.  
 DR HSSP; O16968; 1A68.  
 DR MGD; MGI:96671; Kcnd1.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003091; K channel.  
 DR InterPro; IPR003131; K tetra.  
 DR InterPro; IPR004054; Kv4channel.  
 DR InterPro; IPR003968; Kv channel.  
 DR InterPro; IPR005820; M+channel\_nlg.  
 DR InterPro; IPR003975; Shal channel.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR Pfam; PF02214; K\_tetra; 1.  
 DR PRINTS; PR00169; KCHANNEL.  
 DR PRINTS; PR01516; KV4CHANNEL.  
 DR PRINTS; PR01491; KYCHANNEL.  
 DR PRINTS; PR01497; SHALCHANNEL.  
 KW Ion transport; Ionic channel; Multigene family; Potassium;  
 KW Potassium channel; Potassium transport; Transmembrane; Transport;  
 KW Voltage-gated channel.  
 FT DOMAIN 1 184 Cytoplasmic (Potential).  
 FT TRANSMEM 185 205 Segment S1 (Potential).  
 FT TRANSMEM 227 247 Segment S2 (Potential).  
 FT DOMAIN 248 261 Cytoplasmic (Potential).  
 FT TRANSMEM 262 282 Segment S3 (Potential).  
 FT TRANSMEM 292 312 Segment S4 (Potential).  
 FT DOMAIN 313 325 Cytoplasmic (Potential).  
 FT TRANSMEM 326 346 Segment S5 (Potential).  
 FT TRANSMEM 365 385 Segment H5 (pore-forming) (Potential).  
 FT TRANSMEM 387 407 Segment S6 (Potential).  
 FT DOMAIN 408 651 Cytoplasmic (Potential).  
 FT SITE 372 377 Selectivity filter (By similarity).  
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 651 AA; 71697 MW; 801DEC3C56C721F CRC64;  
 Query Match 64.5%; Score 2141.5; DB 1; Length 651;  
 Best local Similarity 65.7%; Pred. No. 1,1e-125;  
 Matches 434; Conservative 76; Mismatches 116; Indels 35; Gaps 13;  
 Qy 1 MAAGVAAWLPFPADAAIGMVPVANCMPAPADAKRQDELIVLVNSGRRFQWRTTLER 60  
 Db 1 MAAGVATWLPFPAAAVGWLPLAQOPLPAPAEVKASRGDEVLVVNSGRFETWKTLLDR 60  
 Qy YPTTLGSTEKEFEFEDTEVEFDDDPVFRVLPFRGKLAHYRGCISAYDEELAF 120  
 Db YPTTLGSSSEKEFFAYAESEGFDPDRPDVFRVLPFRGKLAHYRGCISAYDEELAF 120



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